

|    |            |             |            |            |            |      |
|----|------------|-------------|------------|------------|------------|------|
|    | TTGGGCAAGG | AATTTTCAGTG | ACACAAACAC | AAATGCTTCG | TGCCTTTACA | 900  |
|    | GCTATTGCTA | ATGATGGAGT  | TATGCTGGAG | CCAAAATTTA | TAAGTGCTAT | 950  |
|    | TTATGATACT | AACAATCAGT  | CTGTACGTAA | GTCACAAAAA | GAAATAGTAG | 1000 |
|    | GAAATCCTGT | TTCCAAAGAG  | GCAGCAAGCA | CAACTCGAAA | TCACATGATC | 1050 |
| 5  | TTAGTTGGGA | CGGACCCTCT  | ATATGGAAC  | ATGTATAATC | ACTACACAGG | 1100 |
|    | AAAGCCAATT | ATAACAGTTC  | CTGGACAAAA | TGTAGCAGTT | AAATCCGGTA | 1150 |
|    | CGGCTCAAAT | CGCTGATGAG  | AAAAATGGAG | GATACTTGGT | TGGTTCTACC | 1200 |
|    | AATTATATTT | TCTCAGTTGT  | GACTATGAAT | CCTGCTGAAA | ATCCTGATTT | 1250 |
|    | TATCTTGAT  | GTAACGGTTC  | AACAGCCTGA | GCATTATTCA | GGTATCCAGT | 1300 |
| 10 | TGGGAGAATT | TGCCACCCCA  | ATCTTGGAGC | GGGCTTCAGC | TATGAAAGAA | 1350 |
|    | TCTCTCAATC | TTCAATCTCC  | AGCCAAAAAT | TTAGATAAAG | TTACGACAGA | 1400 |
|    | ATCTTCTTAT | GCAATGCCTA  | GCATCAAGGA | TATTTACCT  | GGTGAGTTGG | 1450 |
|    | CGGAAGCCTT | ACGCCGAAAT  | ATTGTGCAAC | CAATCGTTGT | AGGTACTGGA | 1500 |
|    | ACAAAGATTA | AAGAGACTTC  | TGTAGAAGAA | GGGACCAATC | TTGCACCAAA | 1550 |
| 15 | CCAACAAGTT | CTCCTTTTAT  | CGGATAAGGT | AGAAGAAATT | CCAGACATGT | 1600 |
|    | ATGGCTGGAA | AAAAGAGACT  | GCCGAGACCT | TTGCTAAATG | GTTGGATATT | 1650 |
|    | GAAGTGAAT  | TTGAAGGTTT  | AGGTTCCGTT | GTTTCAAG   |            | 1689 |

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## 2) INFORMATION FOR SEQ ID NO: 1047

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1690 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | CAAAAAAGAA | TTGGAAGCTG | CAGAGGTCAA | GGGGATTGAT | TTTACAACCA | 50   |
|    | GTCCCAACCG | TAGTTACCCA | AACGGACAAT | TTGCTTCTAG | TTTTATCGGA | 100  |
|    | CTAGCTCAGC | TCCATGAAAA | TGAAGATGGC | AGCAAGAGCT | TGCTGGGAAC | 150  |
| 40 | TTCTGGAATG | GAGAGTTCCT | TGAACAGTAT | TCTTGCAGGG | ACAGACGGCA | 200  |
|    | TTATTACCTA | TGAAAAGGAT | CGTCTGGGTA | ATATTGTACC | CGGAACAGAA | 250  |
|    | CAAGTTTCCC | AACAAACGGT | AGATGGCAAG | GATGTTTACA | CAACCATTTT | 300  |
|    | CAGCCCCCTC | CAGTCCTTTA | TGGAAACCCA | GATGGATGCT | TTTCAAGAGA | 350  |
|    | AGGTAAAGG  | AAAGTACACG | ACAGCGACTT | TGGTCAGTGC | TAAAACAGGG | 400  |
| 45 | GAAATTCTGG | CAACAACGCA | ACGACCGACC | TTTGATGCAG | ATACAAAAGA | 450  |
|    | AGGCATTACA | GAGGACTTTG | TTTGGCGTGA | TATCCTTTAC | CAAAGTAACT | 500  |
|    | ATGAGCCAGG | TTCCCCTATG | AAAGTGATGA | TGTTGGCTGC | TGCTATTGAT | 550  |
|    | AATAATACCT | TTCCAGGGGG | AGAAGTCTTC | AATAGTAGTG | AGTTAAAAAT | 600  |
|    | TGCAGATGTC | ACGATTCGAG | ATTGGGACGT | CAATGAAGGA | TTGACTGGTG | 650  |
| 50 | GCAGAATGAT | GACCTTTTCT | CAAGGGTTCG | CTCACTCAAG | TAACGTGGGG | 700  |
|    | ATGACGCTTC | TTGAGCAAAA | GATGGGAGAT | GCTACATGGC | TTGATTATCT | 750  |
|    | AAATCGCTTT | AAATTTGGTG | TTCCGACTCG | TTTTGGCTTG | ACGGATGAAT | 800  |
|    | ATGCAGGCCA | ACTTCCAGCT | GACAATATCG | TAAATATTGC | TCAGAGTTCA | 850  |
| 55 | TTTGGACAAG | GGATTTCAGC | GACCCAGACG | CAAATGATTC | GTGCCTTCAC | 900  |
|    | GGCTATTGCC | AACGATGGAG | TCATGTTAGA | ACCTAAATTT | ATCAGTGCCA | 950  |
|    | TTTATGATCC | AAATGATCAA | ACTGCTCGGA | AATCACAAAA | AGAAGTTGTG | 1000 |
|    | GGAAATCCTG | TGTCTAAAGA | TGCAGCGAGC | TTGACGCGAA | CGCATATGGT | 1050 |
|    | TTTAGTCGGT | ACCGATCCAG | TATATGGAAC | TATGTATAAT | CATAAGACAG | 1100 |
|    | GGAAACCAAC | TGTAAGTGT  | CCTGGGCAAA | ATGTAGCCCT | CAAGTCTGGT | 1150 |
| 60 | ACGGCTCAGA | TTGCCGATGA | GAAAAATGGA | GGTTACTTAG | TTGGTACGAC | 1200 |

|    |            |            |            |             |             |      |
|----|------------|------------|------------|-------------|-------------|------|
|    | CAATTACATT | TTTTCGGCTG | TATCGATGAA | CCCTGCTGAA  | AATCCTGATT  | 1250 |
|    | TTATTCTCTA | TGTGACGGTT | CAACAGCCTG | AGCATTATTC  | AGGTATTTCAG | 1300 |
|    | TTGGGGGAAT | TTGCCAATCC | TATCTTGGA  | AGGGCAGTGG  | CTATGAAAGA  | 1350 |
|    | TTCCCTTAAC | CTCCAATCTA | CCGCTAAAAC | GTTAAATCAG  | GTAACCAATC  | 1400 |
| 5  | AAAGCGCTTA | TGCCATGCCT | AGCATCAAGG | ACATTTCCACC | TGGCGATTG   | 1450 |
|    | GCGGAAGCCT | TACGTGCGCA | TATTGTGCAA | CCAATCGTTG  | TAGGAACAGG  | 1500 |
|    | AACAAAAATT | AAAGAATCAT | CTGTAGAAGA | AGGGACGGAT  | CTTGACACTA  | 1550 |
|    | ACCAGCAAGT | TCTTCTCTTA | TCTGATAAAG | CAGAGGAAGT  | TCCAGATATG  | 1600 |
|    | TATGGTTGGA | CAAAAGAGAC | TGCTGAGACC | TTTGCTAAGT  | GGCTCAATAT  | 1650 |
| 10 | AGAACTTGAA | TTTGAAGGTT | CGGGCTCTAC | TGTGCAGAAG  |             | 1690 |

## 2) INFORMATION FOR SEQ ID NO: 1048

15

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1682 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
| 30 | AAAAGAGTTG | GAAACTGCAG | AGGTCAAGGG | GATTGATTTT | ACAACCAGTC | 50   |
|    | CCAATCGTAG | TTACCCAAAC | GGACAATTTG | CTTCTAGCTT | TATTGGCTTA | 100  |
|    | GCCCAACTTC | ATGAAAATGA | GGATGGTAGT | AAGAGTTTGT | TAGGGACTTC | 150  |
|    | TGGTTTGGAG | AGTTCTTTAA | ATACCATTCT | TGCTGGGACA | GACGGTATTA | 200  |
|    | TTACCTATGA | AAAAGACCGT | GTAGGAAATA | TCGTACCAGG | TACAGAACTG | 250  |
| 35 | GTATCGCAAC | AAACTGTGGA | TGGCAAGGAT | GTTTATACAA | CATTGTCTAG | 300  |
|    | TCCGCTACAA | TCTTTCATGG | AAACTCAGAT | GGATGCCTTT | CTAGAAAAAG | 350  |
|    | TAAAAGGTAA | GTATATGACC | GCGACCTTGG | TCAGTGCAAA | GACCGGTGAA | 400  |
|    | ATCCTCGCTA | CCACCCAACG | ACCTACCTTT | AATGCAGATA | CTAAAGAAGG | 450  |
|    | AATCACTGAG | GACTTTGTTT | GGCGTGATAT | TCTTTATCAA | AGTAACTATG | 500  |
| 40 | AACCAGGATC | AGCCATGAAG | GTTATGACGT | TAGCTTCTTC | TATTGATAAT | 550  |
|    | AATACCTTCC | CAAGTGGAGA | ATACTTCAAT | AGCAGTGAAT | TCAAAATAGC | 600  |
|    | GGATGCGACG | ACTCGAGATT | GGGATGTTAA | TGAAGGTTTG | ACTACTGGTG | 650  |
|    | GGATGATGAC | TTTCTTACAA | GGTTTCGCTC | ACTCCAGTAA | TGTTGGAATG | 700  |
|    | AGTCTACTTG | AACAAAAAAT | GGGAGATGCT | ACTTGGTTGG | ATTATCTAAA | 750  |
| 45 | ACGCTTTAAA | TTTGGGGTTC | CAACTCGCTT | TGGCTTGACA | GATGAATACG | 800  |
|    | CTGGTCAACT | TCCAGCTGAT | AATATTGTTA | GTATTGCTCA | AAGCTCATTT | 850  |
|    | GGGCAAGGAA | TTTCAGTGAC | ACAAACACAA | ATGCTTCGTG | CCTTTACAGC | 900  |
|    | TATTGCTAAT | GATGGAGTTA | TGCTGGAGCC | AAAATTTATA | AGTGCTATTT | 950  |
|    | ATGATACTAA | CAATCAGTCT | GTACGTAAGT | CACAAAAAGA | AATAGTAGGA | 1000 |
| 50 | AATCCTGTTT | CCAAAGAGGC | AGCAAGCACA | ACTCGAAATC | ACATGATCTT | 1050 |
|    | AGTTGGGACG | GACCCTCTAT | ATGGAACTAT | GTATAATCAC | TACACAGGAA | 1100 |
|    | AGCCAATTAT | AACAGTTCCT | GGACAAAATG | TAGCAGTTAA | ATCCGGTACG | 1150 |
|    | GCTCAAATCG | CTGATGAGAA | AAATGGAGGA | TACTTGGTTG | GTTCTACCAA | 1200 |
|    | TTATATTTTC | TCAGTTGTGA | CTATGAATCC | TGCTGAAAAT | CCTGATTTTA | 1250 |
| 55 | TCTTGTATGT | AACGGTTCAA | CAGCCTGAGC | ATTATTCAGG | TATCCAGTTG | 1300 |
|    | GGAGAATTTG | CCACCCCAAT | CTTGGAGCGG | GCTTCAGCTA | TGAAAGAATC | 1350 |
|    | TCTCAATCTT | CAATCTCCAG | CCAAAAATTT | AGATAAAGTT | ACGACAGAAT | 1400 |
|    | CTTCTTATGC | AATGCCTAGC | ATCAAGGATA | TTTCACCTGG | TGAGTTGGCG | 1450 |
|    | GAAGCCTTAC | GCCGAAATAT | TGTGCAACCA | ATCGTTGTAG | GTAAGTGAAC | 1500 |
| 60 | AAAGATTAAA | GAGACTTCTG | TAGAAGAAGG | GACCAATCTT | GCACCAAACC | 1550 |

|            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------|
| AACAAGTTCT | CCTTTTATCG | GATAAGGTAG | AAGAAATTCC | AGACATGTAT | 1600 |
| GGCTGGAAAA | AAGAGACTGC | TGAAACCTTT | GCTAAATGGT | TGGATATTGA | 1650 |
| GTTGGAATTT | GAAGGTTTCA | GTTCCGTCGT | TC         |            | 1682 |

5

## 2) INFORMATION FOR SEQ ID NO: 1049

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1241 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## 15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
(B) STRAIN: R690

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049

|                |            |             |            |            |      |
|----------------|------------|-------------|------------|------------|------|
| GCAGCGTTGC     | GTGATACCGT | TGAAAAAACC  | ATTAAAAACT | GTTTGGATTT | 50   |
| TGAAAGGAGA     | CAGGAGCATG | AATAGAATAA  | AAGTTGCAAT | ACTGTTTGGG | 100  |
| 25 GGTGCTCAG   | AGGAGCATGA | CGTATCGGTA  | AAATCTGCAA | TAGAGATAGC | 150  |
| CGCTAACATT     | AATAAAGAAA | AATACGAGCC  | GTTATACATT | GGAATTACGA | 200  |
| AATCTGGTGT     | ATGGAAAATG | TGCGAAAAAC  | CTTGCGCGGA | ATGGGAAAAC | 250  |
| GACAATTGCT     | ATTCAGCTGT | ACTCTCGCCG  | GATAAAAAAA | TGCACGGATT | 300  |
| ACTTGTTAAA     | AAGAACCATG | AATATGAAAT  | CAACCATGTT | GATGTAGCAT | 350  |
| 30 TTTTCAGCTTT | GCATGGCAAG | TCAGGTGAAG  | ATGGATCCAT | ACAAGGTCTG | 400  |
| TTTGAATTGT     | CCGGTATCCC | TTTTGTAGGC  | TGCGATATTC | AAAGCTCAGC | 450  |
| AATTTGTATG     | GACAAATCGT | TGACATACAT  | CGTTGCGAAA | AATGCTGGGA | 500  |
| TAGCTACTCC     | CGCCTTTTGG | GTTATTAATA  | AAGATGATAG | GCCGGTGGCA | 550  |
| GCTACGTTTA     | CCTATCCTGT | TTTTGTAAAG  | CCGGCGCGTT | CAGGCTCATC | 600  |
| 35 CTTCGGTGTG  | AAAAAAGTCA | ATAGCGCGGA  | CGAATTGGAC | TACGCAATTG | 650  |
| AATCGGCAAG     | ACAATATGAC | AGCAAAATCT  | TAATTGAGCA | GGCTGTTTCG | 700  |
| GGCTGTGAGG     | TCGGTTGTGC | GGTATTGGGA  | AACAGTGCCG | CGTTAGCTGT | 750  |
| TGGCGAGGTG     | GACCAAATCA | GGCTGCAGTA  | CGGAATCTTT | CGTATTCATC | 800  |
| AGGAAGTCGA     | GCCGGAAAAA | GGCTCTGAAA  | ACGCAGTTAT | AACCGTTCCC | 850  |
| 40 GCAGACCTTT  | CAGCAGAGGA | GCGAGGACGG  | ATACAGGAAA | CGGCAAAAAA | 900  |
| AATATATAAA     | GCGCTCGGCT | GTAGAGGTCT  | AGCCCGTGTG | GATATGTTTT | 950  |
| TACAAGATAA     | CGGCCGCATT | GTAAGTGAACG | AAGTCAATAC | TCTGCCCGGT | 1000 |
| TTCACGTCAT     | ACAGTCGTTA | TCCCCGTATG  | ATGGCCGCTG | CAGGTATTGC | 1050 |
| ACTTCCCGAA     | CTGATTGACC | GCTTGATCGT  | ATTAGCGTTA | AAGGGGTGAT | 1100 |
| 45 AAGCATGGAA  | ATAGGATTTA | CTTTTTTAGA  | TGAAATAGTA | CACGGTGTTT | 1150 |
| GTTGGGACGC     | TAAATATGCC | ACTTGGGATA  | ATTCACCGG  | AAAACCGGTT | 1200 |
| GACGGTTATG     | AAGTAAATCG | CATTGTAGGG  | ACATACGAAT | T          | 1241 |

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## 2) INFORMATION FOR SEQ ID NO: 1050

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1249 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

60

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R691

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050

|    |             |             |             |            |            |      |
|----|-------------|-------------|-------------|------------|------------|------|
|    | TCACACCGCA  | TACGGCCTAT  | TATACCGAGC  | AAGCGTTGCG | TGATACCGTT | 50   |
|    | GAAAAAACCA  | TTAAAAACTG  | TTTGGATTTT  | GAAAGGAGAC | AGGAGCATGA | 100  |
|    | ATAGAATAAA  | AGTTGCAATA  | CTGTTTGGGG  | GTTGCTCAGA | GGAGCATGAC | 150  |
| 10 | GTATCGGTAA  | AATCTGCAAT  | AGAGATAGCC  | GCTAACATTA | ATAAAGAAAA | 200  |
|    | ATACGAGCCG  | TTATACATTG  | GAATTACGAA  | ATCTGGTGTA | TGGAAAATGT | 250  |
|    | GCGAAAAACC  | TTGCGCGGAA  | TGGGAAAACG  | ACAATTGCTA | TTCAGCTGTA | 300  |
|    | CTCTCGCCGG  | ATAAAAAAAT  | GCACGGATTA  | CTTGTTAAAA | AGAACCATGA | 350  |
|    | ATATGAAATC  | AACCATGTTG  | ATGTAGCATT  | TTCAGCTTTG | CATGGCAAGT | 400  |
| 15 | CAGGTGAAGA  | TGGATCCATA  | CAAGGTCTGT  | TTGAATTGTC | CGGTATCCCT | 450  |
|    | TTTGTAGGCT  | GCGATATTCA  | AAGCTCAGCA  | ATTTGTATGG | ACAAATCGTT | 500  |
|    | GACATACATC  | GTTGCGAAAA  | ATGCTGGGAT  | AGCTACTCCC | GCCTTTTGGG | 550  |
|    | TTATTAATAA  | AGATGATAGG  | CCGGTGGCAG  | CTACGTTTAC | CTATCCTGTT | 600  |
|    | TTTGTTAAGC  | CGGCGCGTTC  | AGGCTCATCC  | TTCGGTGTGA | AAAAAGTCAA | 650  |
| 20 | TAGCGCGGAC  | GAATTGGACT  | ACGCAATTGA  | ATCGGCAAGA | CAATATGACA | 700  |
|    | GCAAAATCTT  | AATTGAGCAG  | GCTGTTTCGG  | GCTGTGAGGT | CGGTTGTGCG | 750  |
|    | GTATTGGGAA  | ACAGTGCCGC  | GTTAGCTGTT  | GGCGAGGTGG | ACCAAATCAG | 800  |
|    | GCTGCAGTAC  | GGAATCTTTC  | GTATTCATCA  | GGAAGTCGAG | CCGGAAAAAG | 850  |
|    | GCTCTGAAAA  | CGCAGTTATA  | ACCGTTCCCC  | CAGACCTTTC | AGCAGAGGAG | 900  |
| 25 | CGAGGACGGA  | TACAGGAAAC  | GGCAAAAAAA  | ATATATAAAG | CGCTCGGCTG | 950  |
|    | TAGAGGTCTA  | GCCCGTGTGG  | ATATGTTTTT  | ACAAGATAAC | GGCCGCATTG | 1000 |
|    | TACTGAACGA  | AGTCAATACT  | CTGCCCGGTT  | TCACGTCATA | CAGTCGTTAT | 1050 |
|    | CCCCGTATGA  | TGGCCGCTGC  | AGGTATTGCA  | CTTCCCGAAC | TGATTGACCG | 1100 |
|    | CTTGATCGTA  | TTAGCGTTAA  | AGGGGTGATA  | AGCATGGAAA | TAGGATTTAC | 1150 |
| 30 | TTTTTTTAGAT | GAAATAGTAC  | ACGGTGTTTCG | TTGGGACGCT | AAATATGCCA | 1200 |
|    | CTTGGGATAA  | TTTCAACCGGA | AAACCGGTTG  | ACGGTTATGA | AGTAAATCG  | 1249 |

## 35 2) INFORMATION FOR SEQ ID NO: 1051

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1272 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R481

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 50 | TATACCGAGC | AAGCGTTGCG | TGATACCGTT | GAAAAAACCA | TTAAAAACTG | 50  |
|    | TTTGGATTTT | GAAAGGAGAC | AGGAGCATGA | ATAGAATAAA | AGTTGCAATA | 100 |
|    | CTGTTTGGGG | GTTGCTCAGA | GGAGCATGAC | GTATCGGTAA | AATCTGCAAT | 150 |
|    | AGAGATAGCC | GCTAACATTA | ATAAAGAAAA | ATACGAGCCG | TTATACATTG | 200 |
| 55 | GAATTACGAA | ATCTGGTGTA | TGGAAAATGT | GCGAAAAACC | TTGCGCGGAA | 250 |
|    | TGGGAAAACG | ACAATTGCTA | TTCAGCTGTA | CTCTCGCCGG | ATAAAAAAAT | 300 |
|    | GCACGGATTA | CTTGTTAAAA | AGAACCATGA | ATATGAAATC | AACCATGTTG | 350 |
|    | ATGTAGCATT | TTCAGCTTTG | CATGGCAAGT | CAGGTGAAGA | TGGATCCATA | 400 |
|    | CAAGGTCTGT | TTGAATTGTC | CGGTATCCCT | TTTGTAGGCT | GCGATATTCA | 450 |
| 60 | AAGCTCAGCA | ATTTGTATGG | ACAAATCGTT | GACATACATC | GTTGCGAAAA | 500 |



|    |             |            |            |            |            |      |
|----|-------------|------------|------------|------------|------------|------|
|    | ATGCTGGGAT  | AGCTACTCCC | GCCTTTTGGG | TTATTAATAA | AGATGATAGG | 550  |
|    | CCGGTGGCAG  | CTACGTTTAC | CTATCCTGTT | TTTGTTAAGC | CGGCGCGTTC | 600  |
|    | AGGCTCATCC  | TTCGGTGTGA | AAAAAGTCAA | TAGCGCGGAC | GAATTGGACT | 650  |
|    | ACGCAATTGA  | ATCGGCAAGA | CAATATGACA | GCAAAATCTT | AATTGAGCAG | 700  |
| 5  | GCTGTTTCGG  | GCTGTGAGGT | CGGTTGTGCG | GTATTGGGAA | ACAGTGCCGC | 750  |
|    | GTTAGTTGTT  | GGCGAGGTGG | ACCAAATCAG | GCTGCAGTAC | GGAATCTTTC | 800  |
|    | GTATTCATCA  | GGAAGTCGAG | CCGGAAAAAG | GCTCTGAAAA | CGCAGTTATA | 850  |
|    | ACCGTTCCCG  | CAGACCTTTC | AGCAGAGGAG | CGAGGACGGA | TACAGGAAAC | 900  |
|    | GGCAAAAAAA  | ATATATAAAG | CGCTCGGCTG | TAGAGGTCTA | GCCCGTGTGG | 950  |
| 10 | ATATGTTTTT  | ACAAGATAAC | GGCCGCATTG | TACTGAACGA | AGTCAATACT | 1000 |
|    | CTGCCCCGTT  | TCACGTCATA | CAGTCGTTAT | CCCCGTATGA | TGGCCGCTGC | 1050 |
|    | AGGTATTGCA  | CTTCCCGAAC | TGATTGACCG | CTTGATCGTA | TTAGCGTTAA | 1100 |
|    | AGGGGTGATA  | AGCATGGAAA | TAGGATTTAC | TTTTTTAGAT | GAAATAGTAC | 1150 |
|    | ACGGTGTTTCG | TTGGGACGCT | AAATATGCCA | CTTGGGATAA | TTTCACCGGA | 1200 |
| 15 | AAACCGGTTG  | ACGGTTATGA | AGTAAATCGC | ATTGTAGGGA | CATACGAATT | 1250 |
|    | GGCTTGAATC  | GCTTTTTTGA | GG         |            |            | 1272 |

## 20 2) INFORMATION FOR SEQ ID NO: 1052

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: R492

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052

|    |             |            |            |            |            |      |
|----|-------------|------------|------------|------------|------------|------|
| 35 | TCCCCCGGCA  | TACGGCCTAT | TATACCGAGC | AAGCGTTGCG | TGATACCGTT | 50   |
|    | GAAAAAACCA  | TTAAAAACTG | TTTGGATTTT | GAAAGGAGAC | AGGAGCATGA | 100  |
|    | ATAGAATAAA  | AGTTGCAATA | CTGTTTGGGG | GTTGCTCAGA | GGAGCATGAC | 150  |
|    | GTATCGGTAA  | AATCTGCAAT | AGAGATAGCC | GCTAACATTA | ATAAAGAAAA | 200  |
| 40 | ATACGAGCCG  | TTATACATTG | GAATTACGAA | ATCTGGTGTA | TGGAAAATGT | 250  |
|    | GCGAAAAACC  | TTGCGCGGAA | TGGGAAAACG | ACAATTGCTA | TTCAGCTGTA | 300  |
|    | CTCTCGCCGG  | ATAAAAAAAT | GCACGGATTA | CTTGTTAAAA | AGAACCATGA | 350  |
|    | ATATGAAATC  | AACCATGTTG | ATGTAGCATT | TTCAGCTTTG | CATGGCAAGT | 400  |
|    | CAGGTGAAGA  | TGGATCCATA | CAAGGTCTGT | TTGAATTGTC | CGGTATCCCT | 450  |
| 45 | TTTGTAGGCT  | GCGATATTCA | AAGCTCAGCA | ATTTGTATGG | ACAAATCGTT | 500  |
|    | GACATACATC  | GTTGCGAAAA | ATGCTGGGAT | AGCTACTCCC | GCCTTTTGGG | 550  |
|    | TTATTAATAA  | AGATGATAGG | CCGGTGGCAG | CTACGTTTAC | CTATCCTGTT | 600  |
|    | TTTGTTAAGC  | CGGCGCGTTC | AGGCTCATCC | TTCGGTGTGA | AAAAAGTCAA | 650  |
|    | TAGCGCGGAC  | GAATTGGACT | ACGCAATTGA | ATCGGCAAGA | CAATATGACA | 700  |
| 50 | GCAAAATCTT  | AATTGAGCAG | GCTGTTTCGG | GCTGTGAGGT | CGGTTGTGCG | 750  |
|    | GTATTGGGAA  | ACAGTGCCGC | GTTAGCTGTT | GGCGAGGTGG | ACCAAATCAG | 800  |
|    | GCTGCAGTAC  | GGAATCTTTC | GTATTCATCA | GGAAGTCGAG | CCGGAAAAAG | 850  |
|    | GCTCTGAAAA  | CGCAGTTATA | ACCGTTCCCG | CAGACCTTTC | AGCAGAGGAG | 900  |
|    | CGAGGACGGA  | TACAGGAAAC | GGCAAAAAAA | ATATATAAAG | CGCTCGGCTG | 950  |
| 55 | TAGAGGTCTA  | GCCCGTGTGG | ATATGTTTTT | ACAAGATAAC | GGCCGCATTG | 1000 |
|    | TACTGAACGA  | AGTCAATACT | CTGCCCCGTT | TCACGTCATA | CAGTCGTTAT | 1050 |
|    | CCCCGTATGA  | TGGCCGCTGC | AGGTATTGCA | CTTCCCGAAC | TGATTGACCG | 1100 |
|    | CTTGATCGTA  | TTAGCGTTAA | AGGGGTGATA | AGCATGGAAA | TAGGATTTAC | 1150 |
|    | TTTTTTTAGAT | GAAATAGTAC | ACGGTGTTTC | TTGGGACGCT | AAATATGCCA | 1200 |
| 60 | CTTGGGATAA  | TTTCACCGGA | AAACCGGTTG | ACGGTTA    |            | 1237 |

## 2) INFORMATION FOR SEQ ID NO: 1053

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: R581

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053

|    |            |            |             |            |            |      |
|----|------------|------------|-------------|------------|------------|------|
| 20 | CATACGGCCT | ATTATACCGA | GCAAGCGTTG  | CGTGATACCG | TTGAAAAAAC | 50   |
|    | CATTAAAAAC | TGTTTGGATT | TTGAAAGGAG  | ACAGGAGCAT | GAATAGAATA | 100  |
|    | AAAGTTGCAA | TACTGTTTGG | GGGTTGCTCA  | GAGGAGCATG | ACGTATCGGT | 150  |
|    | AAAATCTGCA | ATAGAGATAG | CCGCTAACAT  | TAATAAAGAA | AAATACGAGC | 200  |
|    | CGTTATACAT | TGGAATTACG | AAATCTGGTG  | TATGGAAAAT | GTGCGAAAAA | 250  |
| 25 | CCTTGCGCGG | AATGGGAAAA | CGACAATTGC  | TATTCAGCTG | TACTCTCGCC | 300  |
|    | GGATAAAAAA | ATGCACGGAT | TACTTGTTAA  | AAAGAACCAT | GAATATGAAA | 350  |
|    | TCAACCATGT | TGATGTAGCA | TTTTTCAGCTT | TGCATGGCAA | GTCAGGTGAA | 400  |
|    | GATGGATCCA | TACAAGGTCT | GTTTGAATTG  | TCCGGTATCC | CTTTTGTAGG | 450  |
|    | CTGCGATATT | CAAAGCTCAG | CAATTTGTAT  | GGACAAATCG | TTGACATACA | 500  |
| 30 | TCGTTGCGAA | AAATGCTGGG | ATAGCTACTC  | CCGCCTTTTG | GGTTATTAAT | 550  |
|    | AAAGATGATA | GGCCGGTGGC | AGCTACGTTT  | ACCTATCCTG | TTTTTGTTAA | 600  |
|    | GCCGGCGCGT | TCAGGCTCAT | CCTTCGGTGT  | GAAAAAAGTC | AATAGCGCGG | 650  |
|    | ACGAATTGGA | CTACGCAATT | GAATCGGCAA  | GACAATATGA | CAGCAAAATC | 700  |
|    | TTAATTGAGC | AGGCTGTTTC | GGGCTGTGAG  | GTCGGTTGTG | CGGTATTGGG | 750  |
| 35 | AAACAGTGCC | GCGTTAGCTG | TTGGCGAGGT  | GGACCAAATC | AGGCTGCAGT | 800  |
|    | ACGGAATCTT | TCGTATTCAT | CAGGAAGTCG  | AGCCGGAAAA | AGGCTCTGAA | 850  |
|    | AACGCAGTTA | TAACCGTTCC | CGCAGACCTT  | TCAGCAGAGG | AGCGAGGACG | 900  |
|    | GATACAGGAA | ACGGCAAAAA | AAATATATAA  | AGCGCTCGGC | TGTAGAGGTC | 950  |
|    | TAGCCCGTGT | GGATATGTTT | TTACAAGATA  | ACGGCCGCAT | TGTACTGAAC | 1000 |
| 40 | GAAGTCAATA | CTCTGCCCGG | TTTCACGTCA  | TACAGTCGTT | ATCCCCGTAT | 1050 |
|    | GATGGCCGCT | GCAGGTATTG | CACTTCCCGA  | ACTGATTGAC | CGCTTGATCG | 1100 |
|    | TATTAGCGTT | AAAGGGGTGA | TAAGCATGGA  | AATAGGATTT | ACTTTTTTAG | 1150 |
|    | ATGAAATAGT | ACACGGTGTT | CGTTGGGACG  | CTAAATATGC | CACTTGGGAT | 1200 |
|    | AATTTACCGG | GAAAACCGGT | TGACGGGTAT  | GAAAGTAAAT | CGCATTGTAG | 1250 |
| 45 | GGACATTCGA | ATT        |             |            |            | 1263 |

## 2) INFORMATION FOR SEQ ID NO: 1054

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1054

|    |             |            |            |            |            |      |
|----|-------------|------------|------------|------------|------------|------|
| 5  | CGGCCTATTA  | TNCCGAGCAA | GCGTTGCGTG | ATACCGTTGA | AAAAACCATT | 50   |
|    | AAAAACTGTT  | TGGATTTTGA | AAGGAGACAG | GAGCATGAAT | AGAATAAAAG | 100  |
|    | TTGCAATACT  | GTTTGGGGGT | TGCTCAGAGG | AGCATGACGT | ATCGGTAAAA | 150  |
|    | TCTGCAATAG  | AGATAGCCGC | TAACATTAAT | AAAGAAAAAT | ACGAGCCGTT | 200  |
|    | ATACATTGGA  | ATTACGAAAT | CTGGTGTATG | GAAAATGTGC | GAAAAACCTT | 250  |
| 10 | GCGCGGAATG  | GGAAAACGAC | AATTGCTATT | CAGCTGTACT | CTCGCCGGAT | 300  |
|    | AAAAAAATGC  | ACGGATTACT | TGTTAAAAAG | AACCATGAAT | ATGAAATCAA | 350  |
|    | CCATGTTGAT  | GTAGCATTTT | CAGCTTTGCA | TGGCAAGTCA | GGTGAAGATG | 400  |
|    | GATCCATACA  | AGGTCTGTTT | GAATTGTCCG | GTATCCCTTT | TGTAGGCTGC | 450  |
|    | GATATTCAAA  | GCTCAGCAAT | TTGTATGGAC | AAATCGTTGA | CATACATCGT | 500  |
| 15 | TGCGAAAAAT  | GCTGGGATAG | CTACTCCCGC | CTTTTGGGTT | ATTAATAAAG | 550  |
|    | ATGATAGGCC  | GGTGGCAGCT | ACGTTTACCT | ATCCTGTTTT | TGTTAAGCCG | 600  |
|    | GCGCGTTCAG  | GCTCATCCTT | CGGTGTGAAA | AAAGTCAATA | GCGCGGACGA | 650  |
|    | ATTGGACTAC  | GCAATTGAAT | CGGCAAGACA | ATATGACAGC | AAAATCTTAA | 700  |
|    | TTGAGCAGGC  | TGTTTCGGGC | TGTGAGGTCG | GTTGTGCGGT | ATTGGGAAAC | 750  |
| 20 | AGTGCCGCGT  | TAGTTGTTGG | CGAGGTGGAC | CAAATCAGGC | TGCAGTACGG | 800  |
|    | AATCTTTTCGT | ATTCATCAGG | AAGTCGAGCC | GGAAAAAGGC | TCTGAAAACG | 850  |
|    | CAGTTATAAC  | CGTTCCCGCA | GACCTTTCAG | CAGAGGAGCG | AGGACGGATA | 900  |
|    | CAGGAAACGG  | CAAAAAAAT  | ATATAAAGCG | CTCGGCTGTA | GAGGTCTAGC | 950  |
|    | CCGTGTGGAT  | ATGTTTTTAC | AAGATAACGG | CCGCATTGTA | CTGAACGAAG | 1000 |
| 25 | TCAATACTCT  | GCCCGGTTTC | ACGTCATACA | GTCGTTATCC | CCGTATGATG | 1050 |
|    | GCCGCTGCAG  | GTATTGCACT | TCCCGAACTG | ATTGACCGCT | TGATCGTATT | 1100 |
|    | AGCGTTAAAG  | GGGTGATAAG | CATGGAAATA | GGATTTACTT | TTTTAGATGA | 1150 |
|    | AATAGTACAC  | GGTGTTCGTT | GGGACGCTAA | ATATGCCACT | TGGGATAATT | 1200 |
| 30 | TCACCGGAAA  | ACCGGTTGAC | GATTATAAGT | AA         |            | 1232 |

2) INFORMATION FOR SEQ ID NO: 1055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 50 | TACCGAGCAA | GCGTTGCGTG | ATACCGTTGA | AAAAACCATT | AAAAACTGTT | 50  |
|    | TGGATTTTGA | AAGGAGACAG | GAGCATGAAT | AGAATAAAAG | TTGCAATACT | 100 |
|    | GTTTGGGGGT | TGCTCAGAGG | AGCATGACGT | ATCGGTAAAA | TCTGCAATAG | 150 |
|    | AGATAGCCGC | TAACATTAAT | AAAGAAAAAT | ACGAGCCGTT | ATACATTGGA | 200 |
|    | ATTACGAAAT | CTGGTGTATG | GAAAATGTGC | GAAAAACCTT | GCGCGGAATG | 250 |
|    | GGAAAACGAC | AATTGCTATT | CAGCTGTACT | CTCGCCGGAT | AAAAAAATGC | 300 |
| 55 | ACGGATTACT | TGTTAAAAAG | AACCATGAAT | ATGAAATCAA | CCATGTTGAT | 350 |
|    | GTAGCATTTT | CAGCTTTGCA | TGGCAAGTCA | GGTGAAGATG | GATCCATACA | 400 |
|    | AGGTCTGTTT | GAATTGTCCG | GTATCCCTTT | TGTAGGCTGC | GATATTCAAA | 450 |
|    | GCTCAGCAAT | TTGTATGGAC | AAATCGTTGA | CATACATCGT | TGCGAAAAAT | 500 |
|    | GCTGGGATAG | CTACTCCCGC | CTTTTGGGTT | ATTAATAAAG | ATGATAGGCC | 550 |
| 60 | GGTGGCAGCT | ACGTTTACCT | ATCCTGTTTT | TGTTAAGCCG | GCGCGTTCAG | 600 |

|    |            |            |            |             |            |      |
|----|------------|------------|------------|-------------|------------|------|
|    | GCTCATCCTT | CGGTGTGAAA | AAAGTCAATA | GCGCGGACGA  | ATTGGACTAC | 650  |
|    | GCAATTGAAT | CGGCAAGACA | ATATGACAGC | AAAATCTTAA  | TTGAGCAGGC | 700  |
|    | TGTTTCGGGC | TGTGAGGTCG | GTTGTGCGGT | ATTGGGAAAC  | AGTGCCGCGT | 750  |
|    | TAGCTGTTGG | CGAGGTGGAC | CAAATCAGGC | TGCAGTACGG  | AATCTTTCGT | 800  |
| 5  | ATTCATCAGG | AAGTCGAGCC | GGAAAAAGGC | TCTGAAAACG  | CAGTTATAAC | 850  |
|    | CGTTCCCGCA | GACCTTTCAG | CAGAGGAGCG | AGGACGGATA  | CAGGAAACGG | 900  |
|    | CAAAAAAAAT | ATATAAAGCG | CTCGGCTGTA | GAGGTCTAGC  | CCGTGTGGAT | 950  |
|    | ATGTTTTTAC | AAGATAACGG | CCGCATTGTA | CTGAACGAAG  | TCAATACTCT | 1000 |
|    | GCCCGGTTTC | ACGTCATACA | GTCGTTATCC | CCGTATGATG  | GCCGCTGCAG | 1050 |
| 10 | GTATTGCACT | TCCCGAACTG | ATTGACCGCT | TGATCGTATT  | AGCGTTAAAG | 1100 |
|    | GGGTGATAAG | CATGGAAATA | GGATTTACTT | TTTGTAGATGA | AATAGTACAC | 1150 |
|    | GGTGTTCGTT | GGGACGCTAA | ATATGCCACT | TGGGATAATT  | TCACCGGAAA | 1200 |
|    | ACCGGTTGAC | GGTTAGAA   |            |             |            | 1218 |

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## 2) INFORMATION FOR SEQ ID NO: 1056

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1265 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: R688
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056

|    |             |            |            |             |            |      |
|----|-------------|------------|------------|-------------|------------|------|
|    | AATCACACCG  | CATACGGCCT | ATTATACCGA | GCAAGCGTTG  | CGTGATACCG | 50   |
|    | TTGAAAAAAC  | CATTAAAAAC | TGTTTGGATT | TTGAAAGGAG  | ACAGGAGCAT | 100  |
| 35 | GAATAGAATA  | AAAGTTGCAA | TACTGTTTGG | GGGTTGCTCA  | GAGGAGCATG | 150  |
|    | ACGTATCGGT  | AAAATCTGCA | ATAGAGATAG | CCGTAACAT   | TAATAAAGAA | 200  |
|    | AAATACGAGC  | CGTTATACAT | TGGAATTACG | AAATCTGGTG  | TATGGAAAAT | 250  |
|    | GTGCGAAAAA  | CCTTGCGCGG | AATGGGAAAA | CGACAATTGC  | TATTCAGCTG | 300  |
|    | TACTCTCGCC  | GGATAAAAAA | ATGCACGGAT | TACTTGTTAA  | AAAGAACCAT | 350  |
| 40 | GAATATGAAA  | TCAACCATGT | TGATGTAGCA | TTTTTCAGCTT | TGCATGGCAA | 400  |
|    | GTCAGGTGAA  | GATGGATCCA | TACAAGGTCT | GTTTGAATTG  | TCCGGTATCC | 450  |
|    | CTTTTGTAGG  | CTGCGATATT | CAAAGCTCAG | CAATTTGTAT  | GGACAAATCG | 500  |
|    | TTGACATACA  | TCGTTGCGAA | AAATGCTGGG | ATAGCTACTC  | CCGCCTTTTG | 550  |
|    | GGTTATTAAT  | AAAGATGATA | GGCCGGTGCG | AGCTACGTTT  | ACCTATCCTG | 600  |
| 45 | TTTTTGTTAA  | GCCGGCGCGT | TCAGGCTCAT | CCTTCGGTGT  | GAAAAAAGTC | 650  |
|    | AATAGCGCGG  | ACGAATTGGA | CTACGCAATT | GAATCGGCAA  | GACAATATGA | 700  |
|    | CAGCAAAATC  | TTAATTGAGC | AGGCTGTTTC | GGGCTGTGAG  | GTCGGTTGTG | 750  |
|    | CGGTATTGGG  | AAACAGTGCC | GCGTTAGCTG | TTGGCGAGGT  | GGACCAAATC | 800  |
|    | AGGCTGCAGT  | ACGGAATCTT | TCGTATTCAT | CAGGAAGTCG  | AGCCGGAAAA | 850  |
| 50 | AGGCTCTGAA  | AACGCAGTTA | TAACCGTTCC | CGCAGACCTT  | TCAGCAGAGG | 900  |
|    | AGCGAGGACG  | GATACAGGAA | ACGGCAAAAA | AAATATATAA  | AGCGCTCGGC | 950  |
|    | TGTAGAGGTC  | TAGCCCGTGT | GGATATGTTT | TTACAAGATA  | ACGGCCGCAT | 1000 |
|    | TGTACTGAAC  | GAAGTCAATA | CTCTGCCCGG | TTTCACGTCA  | TACAGTCGTT | 1050 |
|    | ATCCCCGTAT  | GATGGCCGCT | GCAGGTATTG | CACTTCCCGA  | ACTGATTGAC | 1100 |
| 55 | CGCTTGATCG  | TATTAGCGTT | AAAGGGGTGA | TAAGCATGGA  | AATAGGATTT | 1150 |
|    | ACTTTTTTTAG | ATGAAATAGT | ACACGGTGTT | CGTTGGGACG  | CTAAATATGC | 1200 |
|    | CACTTGGGAT  | AATTTACCG  | GAAAACCGGT | TGACGGTTAT  | GAAGTAAATC | 1250 |
|    | GCATTGTAGG  | GACAT      |            |             |            | 1265 |

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## 2) INFORMATION FOR SEQ ID NO: 1057

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*  
 (B) STRAIN: R689

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057

|             |            |             |            |            |      |
|-------------|------------|-------------|------------|------------|------|
| TCACACCGCA  | TACGGCCTAT | TATACCGAGC  | AAGCGTTGCG | TGATACCGTT | 50   |
| GAAAAAACCA  | TTAAAAACTG | TTTGGATTTT  | GAAAGGAGAC | AGGAGCATGA | 100  |
| ATAGAATAAA  | AGTTGCAATA | CTGTTTGGGG  | GTTGCTCAGA | GGAGCATGAC | 150  |
| GTATCGGTAA  | AATCTGCAAT | AGAGATAGCC  | GCTAACATTA | ATAAAGAAAA | 200  |
| ATACGAGCCG  | TTATACATTG | GAATTACGAA  | ATCTGGTGTA | TGGAAAATGT | 250  |
| GCGAAAAACC  | TTGCGCGGAA | TGGGAAAACG  | ACAATTGCTA | TTCAGCTGTA | 300  |
| CTCTCGCCGG  | ATAAAAAAAT | GCACGGATTA  | CTTGTTAAAA | AGAACCATGA | 350  |
| ATATGAAATC  | AACCATGTTG | ATGTAGCATT  | TTCAGCTTTG | CATGGCAAGT | 400  |
| CAGGTGAAGA  | TGGATCCATA | CAAGGTCTGT  | TTGAATTGTC | CGGTATCCCT | 450  |
| TTTGTAGGCT  | GCGATATTCA | AAGCTCAGCA  | ATTTGTATGG | ACAAATCGTT | 500  |
| GACATACATC  | GTTGCGAAAA | ATGCTGGGAT  | AGCTACTCCC | GCCTTTTGGG | 550  |
| TTATTAATAA  | AGATGATAGG | CCGGTGGCAG  | CTACGTTTAC | CTATCCTGTT | 600  |
| TTTGTTAAGC  | CGGCGCGTTC | AGGCTCATCC  | TTCGGTGTGA | AAAAAGTCAA | 650  |
| TAGCGCGGAC  | GAATTGGACT | ACGCAATTGA  | ATCGGCAAGA | CAATATGACA | 700  |
| GCAAAATCTT  | AATTGAGCAG | GCTGTTTCGG  | GCTGTGAGGT | CGGTTGTGCG | 750  |
| GTATTGGGAA  | ACAGTGCCGC | GTTAGCTGTT  | GGCGAGGTGG | ACCAAATCAG | 800  |
| GCTGCAGTAC  | GGAATCTTTC | GTATTTCATCA | GGAAGTCGAG | CCGGAAAAAG | 850  |
| GCTCTGAAAA  | CGCAGTTATA | ACCGTTCCCG  | CAGACCTTTC | AGCAGAGGAG | 900  |
| CGAGGACGGA  | TACAGGAAAC | GGCAAAAAAA  | ATATATAAAG | CGCTCGGCTG | 950  |
| TAGAGGTCTA  | GCCCGTGTGG | ATATGTTTTT  | ACAAGATAAC | GGCCGCATTG | 1000 |
| TACTGAACGA  | AGTCAATACT | CTGCCCGGTT  | TCACGTCATA | CAGTCGTTAT | 1050 |
| CCCCGTATGA  | TGGCCGCTGC | AGGTATTGCA  | CTTCCCGAAC | TGATTGACCG | 1100 |
| CTTGATCGTA  | TTAGCGTTAA | AGGGGTGATA  | AGCATGGAAA | TAGGATTTAC | 1150 |
| TTTTTTTAGAT | GAAATAGTAC | ACGGTGTTTCG | TTGGGACGCT | AAATATGCCA | 1200 |
| CTTGGGATAA  | TTTCACCGGA | AAACCGGTTG  | ACGGTTATGA | AGTAAATCGC | 1250 |
| ATTGTAGGGA  | CATACGAAT  |             |            |            | 1269 |

## 2) INFORMATION FOR SEQ ID NO: 1058

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*  
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058

|    |            |            |            |            |             |      |
|----|------------|------------|------------|------------|-------------|------|
|    | CAAATTTTCT | TTTCTTTTCC | TAGGTACACT | GAATGTAACC | TTAAAAGAAA  | 50   |
|    | AAAGGAAAGG | AAGAAAATGA | TGAAAAAAAT | TGCCGTTTTA | TTTGGAGGGA  | 100  |
| 5  | ATTCTCCAGA | ATACTCAGTG | TCACTAACCT | CAGCAGCAAG | TGTGATCCAA  | 150  |
|    | GCTATTAACC | CGCTGAAATA | TGAAGTAATG | ACCATTGGCA | TCGCACCAAC  | 200  |
|    | AATGGATTGG | TATTGGTATC | AAGGAAACCT | CGCGAATGTT | CGCAATGATA  | 250  |
|    | CTTGGCTAGA | AGATCACAAA | AACTGTCACC | AGCTGACTTT | TTCTAGCCAA  | 300  |
|    | GGATTTATAT | TAGGAGAAAA | ACGAATCGTC | CCTGATGTCC | TCTTTCCAGT  | 350  |
| 10 | CTTGCAATGG | AAGTATGGCG | AGGATGGCTG | TATCCAAGGA | CTGCTTGAAC  | 400  |
|    | TAATGAACCT | GCCTTATGTT | GGTTGCCATG | TCGCTGCCTC | CGCATTATGT  | 450  |
|    | ATGAACAAAT | GGCTCTTGCA | TCAACTTGCT | GATACCATGG | GAATCGCTAG  | 500  |
|    | TGCTCCCACT | TTGCTTTTAT | CCCGCTATGA | AAACGATCCT | GCCACAATCG  | 550  |
|    | ATCGTTTTAT | TCAAGACCAT | GGATTCCCAG | TCTTTATCAA | GCCGAATGAA  | 600  |
| 15 | GCCGGTTCTT | CAAAAGGGAT | CACAAAAGTA | ACTGACAAAA | CAGCGCTCCA  | 650  |
|    | ATCTGCATTA | ACGACTGCTT | TTGCTTACGG | TTCTACTGTG | TTGATCCAAA  | 700  |
|    | AGGCGATAGC | GGGTATTGAA | ATTGGCTGCG | GCATCTTAGG | AAATGAGCAA  | 750  |
|    | TTGACGATTG | GTGCTTGTGA | TGCGATTTC  | CTTGTCGACG | GTTTTTTTGA  | 800  |
|    | TTTTGAAGAG | AAATACCAAT | TAATCAGCGC | CACGATCACT | GTCCCAGCAC  | 850  |
| 20 | CATTGCCTCT | CGCGCTTGAA | TCACAGATCA | AGGAGCAGGC | ACAGCTGCTT  | 900  |
|    | TATCGAAACT | TGGGATTGAC | GGGTCTGGCT | CGAATCGATT | TTTTTCGTCAC | 950  |
|    | CAATCAAGGA | CGGATTTTAT | TAAACGAAAT | CAACACCATG | CCGGGATTTA  | 1000 |
|    | CTGGGCACTC | CCGCTACCCA | GCTATGATGG | CGGAAGTCGG | GTTATCCTAC  | 1050 |
|    | GAAATATTAG | TAGAGCAATT | GATTGCACTG | GCAGAGGAGG | ACAAACGATG  | 1100 |
| 25 | AACACATTAC | AATTGATCAA | TAAAAACCAT | CCATTGAAAA | AAAATCAAGA  | 1150 |
|    | GCCCCCGCAC | TTAGTGCTA  |            |            |             | 1169 |

30 2) INFORMATION FOR SEQ ID NO: 1059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 bases  
 (B) TYPE: Nucleic acid  
 35 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*  
 (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 45 | CAAATTTTCT | TTTCTTTTCC | TAGGTACACT | GAATGTAACC | TTAAAAGAAA | 50  |
|    | AAAGGAAAGG | AAGAAAATGA | TGAAAAAAAT | TGCCGTTTTA | TTTGGAGGGA | 100 |
|    | ATTCTCCAGA | ATACTCAGTG | TCACTAGCCT | CAGCAGCAAG | TGTGATCCAA | 150 |
|    | GCTATTGACC | CGCTGAAATA | TGAAGTAATG | ACCATTGGCA | TCGCACCAAC | 200 |
| 50 | AATGGATTGG | TATTGGTATC | AAGGAAACCT | CGCGAATGTT | CGCAATGATA | 250 |
|    | CTTGGCTAGA | AGATCACAAA | AACTGTCACC | AGCTGACTTT | TTCTAGCCAA | 300 |
|    | GGATTTATAT | TAGGAGAAAA | ACGAATCGTC | CCTGATGTCC | TCTTTCCAGT | 350 |
|    | CTTGCAATGG | AAGTATGGCG | AGGATGGCTG | TATCCAAGGA | CTGCTTGAAC | 400 |
|    | TAATGAACCT | GCCTTATGTT | GGTTGCCATG | TCGCTGCCTC | CGCATTATGT | 450 |
| 55 | ATGAACAAAT | GGCTCTTGCA | TCAACTTGCT | GATACCATGG | GAATCGCTAG | 500 |
|    | TGCTCCCACT | TTGCTTTTAT | CCCGCTATGA | AAACGATCCT | GCCACAATCG | 550 |
|    | ATCGTTTTAT | TCAAGACCAT | GGATTCCCAG | TCTTTATCAA | GCCGAATGAA | 600 |
|    | GCCGGTTCTT | CAAAAGGGAT | CACAAAAGTA | ACTGACAAAA | CAGCGCTCCA | 650 |
|    | ATCTGCATTA | ACGACTGCTT | TTGCTTACGG | TTCTACTGTG | TTGATCCAAA | 700 |
| 60 | AGGCGATAGC | GGGTATTGAA | ATTGGCTGCG | GCATCTTAGG | AAATGAGCAA | 750 |

|   |            |            |            |            |            |      |
|---|------------|------------|------------|------------|------------|------|
|   | TTGACGATTG | GTGCTTGTGA | TGCGATTTCT | CTTGTCGACG | GTTTTTTTGA | 800  |
|   | TTTTGAAGAG | AAATACCAAT | TAATCAGCGC | CACGATCACT | GTCCCAGCAC | 850  |
|   | CATTGCCTCT | CGCGCTTGAA | TCACAGATCA | AGGAGCAGGC | ACAGCTGCTT | 900  |
|   | TATCGAAACT | TGGGATTGAC | GGGTCTGGCT | CGAATCGATT | TTTTCGTCAC | 950  |
| 5 | CAATCAAGGA | GCGATTTATT | TAAACGAAAT | CAACACCATG | CCGGGATTTA | 1000 |
|   | CTGGGCACTC | CCGCTACCCA | GCTATGATGG | CGGAAGTCGG | GTTATCCTAC | 1050 |
|   | GAAATATTAG | TAGAGCAATT | GATTGCACTG | GCAGAGGAGG | ACAAACGATG | 1100 |
|   | AACACATTAC | AATTGATCAA | TAAAACCAT  | CCATTGAAAA | AAAATCAAGA | 1150 |
|   | CCCCCGCAC  | TTAGTG     |            |            |            | 1166 |

10

## 2) INFORMATION FOR SEQ ID NO: 1060

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1028 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*  
 (B) STRAIN: ATCC 25788

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | AACATGAAAA | AAATCGCCTT | ATTTTTGGAG | GCAATTCACC | GGAATACACC | 50   |
| 30 | GTTTCTTTAG | CTTCAGCAAC | TAGCGCAATC | GAAGCACTCC | AATCATCTCC | 100  |
|    | CTATGACTAC | GACCTCTCTT | TGATCGGGAT | CGCCCCAGAT | GCTATGGATT | 150  |
|    | GGTACTTGTA | TACAGGAGAA | CTGGAAAACA | TCCGACAAGA | CACGTGGTTG | 200  |
|    | TTGGATACGA | AACATAAACA | GAAAATACAG | CCGCTATTTC | AAGGAAACGG | 250  |
|    | CTTTTGGCTA | AGTGAAGAGC | AGCAAACGTT | GGTACCTGAT | GTTTATTTC  | 300  |
| 35 | CCATTATGCA | TGGCAAATAC | GGGGAAGATG | GCAGTATCCA | AGGATTGTTT | 350  |
|    | GAATTGATGA | AGCTGCCTTA | TGTAGGCTGC | GGGGTGGCAG | GTTCTGCCTT | 400  |
|    | ATGTATGAAC | AAATGGCTGC | TGCATCAAGC | TGCAGCAGCC | ATTGGCGTAC | 450  |
|    | AAAGTGCTCC | TACGATTCTC | TTGACAAATC | AAGCCAACCA | GCAAGAACAA | 500  |
|    | ATCGAAGCTT | TTATCCAGAC | CCATGGCTTC | CCAGTTTTCT | TTAAGCCTAA | 550  |
| 40 | TGAAGCGGGC | TCCTCAAAAG | GGATCACTAA | AGTCACCTGC | GTTGAAGAAA | 600  |
|    | TCGCTTCTGC | CTTAAAAGAA | GCCTTTACTT | ATTGTTCCGC | AGTGCTCCTA | 650  |
|    | CAAAAAAATA | TTGCCGGTGT | TGAGATCGGT | TGCGGTATTT | TGGGCAACGA | 700  |
|    | CTCTTTGACT | GTCGGTGCTT | GTGACGCCAT | TTCATTAGTA | GACGGCTTTT | 750  |
|    | TCGATTTTGA | AGAAAAGTAC | CAGCTGATCA | GCGCCAAAAT | CACCGTCCCT | 800  |
| 45 | GCGCCATTGC | CTGAAACGAT | TGAAACCAAG | GTCAAAGAAC | AAGCTCAGCT | 850  |
|    | GCTCTATCGT | AGTCTTGGTC | TTAAAGGTCT | TGCTCGCATC | GACTTTTTTG | 900  |
|    | TCACGGAGCG | AGGAGAACTA | TACTTGAATG | AAATCAATAC | TATGCCGGGC | 950  |
|    | TTTACGAGTC | ACTCCCGCTA | TCCTGCCATG | ATGGCAGCGG | TCGGCTTATC | 1000 |
|    | CTATCAAGAA | CTACTACAAA | AACTGCTT   |            |            | 1028 |

50

## 2) INFORMATION FOR SEQ ID NO: 1061

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061

```

10  AATATGAAAA AAATCGCCTT ATTTTGGAG GCAATTCACC GGAGTACGCC      50
    GTTCTTTAG CCTCAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC      100
    CGATGACTAT GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT      150
    GGTATTTGTA TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG      200
    TTGGATACGA AACATAAACA GAAAATCCAG CCGCTTTTGT AAGGAAACGG      250
    CTTTTGGCTA AGTGAAGAGC AACAAACGTT GGTTCCTGAT GTTTTATTTT      300
15  CCATTATGCA TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT      350
    GAATTGATGA AACTACCTTA TGTAGGCTGC GGGGTGGCAG CCTCTGCCTT      400
    ATGTATGAAC AAATGGCTGC TGCATCAAGC AGCAGAAGCG ATTGGCGTAC      450
    AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGATCAA      500
    ATCGAAGCTT TTATCCAGAC CCATGGCTTT CCGGTTTTTT TTAAGCCTAA      550
20  TGAAGCGGGC TCCTCAAAGG GGATCACTAA AGTCACCTGC GTTGAAGAAA      600
    TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTTTACG AGTGCTCCTA      650
    CAAAAAATAA TTGCCGGTGT TGAGATCGGT TCGGGTATTT TGGGCAACGA      700
    CTCTTTGACT GTCGGTGCTT GTGACGCTAT TTCATTAGTA GACGGCTTTT      750
    TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAGAT CACCGTTCCT      800
25  GCACCATTCG CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT      850
    GCTCTATCGT AGTCTTTGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTG      900
    TCACGGATCA AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC      950
    TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGA TCGGCTTATC     1000
30  CTATCAAGAA CTACTACAAA AACTGCTTGT      1030

```

2) INFORMATION FOR SEQ ID NO: 1062

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1031 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062

```

50  AAACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
    CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
    CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
    TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
    TGTGATGATG GAAACATAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
    GGCTTTTGGC TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTTTATT      300
55  TCCCATATAT CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
    TTGAATTGAT GAAGCTGCCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
    TTATGTATGA ACAAATGGCT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
    ACAAAGTGCT CCTACGATTC TCTTGACAAA TCAAGCCAAC CAGCAAGAAC      500
    AAATCGAAGC TTTTATCCAG ACCCATGGCT TCCCAGTTTT CTTTAAGCCT      550
60  AATGAAGCGG GCTCCTCAAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600

```



```

AATCGCTTCT GCCTTAAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC 650
TACAAAAAAA TATTGCCGGT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC 700
GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATTTCATTAG TAGACGGCTT 750
TTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCGTCC 800
5 CTGCGCCATT GCCTGAAACG ATTGAAACCA AGGTCAAAGA ACAAGCTCAG 850
CTGCTCTATC GTAGTCTTGG TCTTAAAGGT CTTGCTCGCA TCGACTTTTT 900
TGTCACGGAG CGAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG 950
GCTTTACGAG TCACTCCCGC TATCCTGCCA TGATGGCAGC GGTCGGCTTA 1000
TCCTATCAAG AACTACTACA AAAACTGCTT G 1031
10

```

## 2) INFORMATION FOR SEQ ID NO: 1063

```

15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1030 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
20
    (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Enterococcus casseliflavus
25 (B) STRAIN: R775

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063

```

AACATGAAAA AAATCGCCAT TATTTTTTGA GGCAATTCAC CGGAATACAC 50
30 CGTTTCTTTA GCTTCAGCAA CTAGCGCAAT CGAAGCACTC CAATCATCTC 100
CCTATGACTA CGACCTCTCT TTGATCGGGA TCGCCCCAGA TGCTATGGAT 150
TGGTACTTGT ATACAGGAGA ACTGGA AAC ATCCGACAAG ACACGTGGTT 200
GTTGGATACG AAACATAAAC AGAAAATACA GCCGCTATTT GAAGGAAACG 250
GCTTTTGGCT AAGTGAAGAG CAGCAAACGT TAGTACCTGA TATTTTATTT 300
35 CCCATTATGC ATGGCAAATA CGGGGAAGAT GGCAGTATCC AAGGATTGTT 350
TGAATTGATG AAACATACCTT ATGTAGGTTG CGGGGTGGCA GGTCTGCCT 400
TATGTATGAA CAAATGGCTG CTGCATCAAG CTGCAGCAGC CATTGGCGTA 450
CAAAGTGCTC CTACGATTCT CTTGACAAAT CAAGCCAACC AGCAAGAACA 500
AATCGAAGCT TTTATCCAGA CCCATGGCTT CCCAGTTTTC TTTAAGCCTA 550
40 ATGAAGCGGG CTCTTCAAAA GGGATCACTA AAGTCACCTG CGTTGAAGAA 600
ATCGCTTCTG CCTTAAAAAA AGCCTTTACT TATTGTTCCG CAGTGCTCCT 650
ACAAAAAAT ATTGCCGGTG TTGAGATCGG TTGCGGTATT TTGGGCAACG 700
ACTCTTTGAC TGTCGGTGCT TGTGACGCCA TTTCATTAGT AGACGGCTTT 750
TTCGATTTTG AAGAAAAGTA CCAGCTGATC AGCGCCAAA TCACCGTCCC 800
45 TGCGCCATTG CCTGAAACGA TTGAAACCAA GGTCAAAGAA CAAGCTCAGC 850
TGCTCTATCG TAGTCTTGGT CTTAAAGGTC TTGCTCGCAT CGACTTTTTT 900
GTCACGGATC AAGGAGAACT ATACTTGAAT GAAATCAATA CTATGCCGGG 950
CTTTACGAGT CACTCCCGTT ATCCTGCCAT GATGGCAGCG GTCGGCTTAT 1000
CCTATCAAGA ACTACTACAA AAACTGCTTG 1030
50

```

## 2) INFORMATION FOR SEQ ID NO: 1064

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1032 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064

```

10  AACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
    CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
    CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
    TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
    TGTGATGATG GAAACAGAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
    GGCTTTTGGT TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTTATT      300
15  TCCCATTATG CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
    TTGAATTGAT GAAGCTACCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
    TTATGTATGA ACAAATGGTT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
    ACAAAGTGCT CCTACGATTC TCTTGACAAA TCACGCCAAC CAGCAAGAAC      500
    AAATCGAAGC TTTTATCCAG ACCCATGGCT TTCCAGTTTT CTTTAAGCCT      550
20  AATGAAGCGG GTTCCTCAAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600
    AATCGCTTCT GCCTTAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC      650
    TACAAAAAAA TATTGCCGGT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC      700
    GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATTTCAATTAG TAGACGGCTT      750
    TTTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCCTCC      800
25  CTGCGCCATT GCCTGAAACG ATTGAAACTA AGGTCAAAGA ACAAGCTCAG      850
    CTGCTCTATC GTAGTCTTGG ACTTAAAGGT CTTGCTCGCA TCGACTTTTT      900
    TGTACGGGAT CAAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG      950
    GCTTTACGAG TCACTCCCGC TATCCTGCCA TGATGGCAGC GGTCTGGGTTA     1000
30  TCCTATCAAG AACTACTACA AAAACTACTT GT                                1032

```

## 2) INFORMATION FOR SEQ ID NO: 1065

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1034 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065

```

50  AAAAAACATGA AAAAAATCGC CATTATTTT GGAGGCAATT CACCGGAATA      50
    CACCGTTTCT TTAGCTTCAG CAACTAGCGC AATCGAAGCA CTCCAATCAT      100
    CTCCCTATGA CTACGACCTC TCTTTGATCG GGATCGCCCC AGATGCTATG      150
    GATTGGTACT TGTATACAGG AGAACTGGAA AACATCCGAC AAGACACGTG      200
    GTTGTTGGAT ACGAAACATA AACAGAAAAT ACAGCCGCTA TTCGAAGGAA      250
    ACGGCTTTTG GCTAAGTGAA GAGCAGCAAA CGTTGGTACC TGATGTTTTA      300
55  TTTECCATTA TGCATGGCAA ATACGGGGAA GATGGCAGTA TCCAAGGATT      350
    GTTTGAATTG ATGAAGCTGC CTTATGTAGG CTGCGGGGTG GCAAGTTCTG      400
    CCTTATGTAT GAACAAATGG CTGCTGCATC AAGCTGCAGC AGCCATTGGC      450
    GTACAAAGTG CTCCTACGAT TCTCTTGACA AATCAAGCCA ACCAGCAAGA      500
    ACAAATCGAA GCTTTTATCC AGACCCATGG CTTTCCAGTT TTCTTTAAGC      550
60  CTAATGAAGC GGGCTCCTCA AAAGGGATCA CTAAAGTCAC CTGCGTTGAA      600

```

|    |            |            |             |             |            |      |
|----|------------|------------|-------------|-------------|------------|------|
|    | GAAATCGCTT | CTGCCTTAAA | AGAAGCCTTT  | ACTTATTGTT  | CCGCAGTGCT | 650  |
|    | CCTACAAAAA | AATATTGCCG | GTGTTGAGAT  | CGGTTGCGGT  | ATTTTGGGCA | 700  |
|    | ACGACTCTTT | GACTGTCGGT | GCTTGTGACG  | CCATTTTCATT | AGTAGACGGC | 750  |
|    | TTTTTCGATT | TTGAAGAAAA | GTACCAGCTG  | ATCAGCGCCA  | AAATCACCGT | 800  |
| 5  | CCCTGCGCCA | TTGCCTGAAA | CGATTGAAAC  | CAAGGTCAAA  | GAACAAGCTC | 850  |
|    | AGCTGCTCTA | TCGTAGTCTT | GGTCTTAAAG  | GTCTTGCTCG  | CATCGACTTT | 900  |
|    | TTTGTACCGG | ATCAAGGAGA | ACTATACTTG  | AATGAAATCA  | ATACTATGCC | 950  |
|    | GGGCTTTACG | AGTCACTCCC | GCTATCCTGC  | CATGATGGCA  | GCGGTCGGCT | 1000 |
| 10 | TATCCTATCA | AGAACTACTA | CAAAAACCTGC | TTGT        |            | 1034 |

## 2) INFORMATION FOR SEQ ID NO: 1066

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1012 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*  
 (B) STRAIN: R760

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | CATGAAAAAA | ATCGCCATTA | TTTTTGGAGG | CAATTCACCG | GAATACACCG | 50   |
| 30 | TTTCTTTAGC | CTCAGCAACT | AGCGCAATCG | AAGCACTCCA | ATCATCTCCC | 100  |
|    | TATGATTACG | ACCTCTCTTT | GATCGGGATC | GCCCCAGATG | CTATGGATTG | 150  |
|    | GTACTTGTAT | ACAGGAGAAC | TGGAAAACAT | CCGACAAGAC | ACGTGGTTGT | 200  |
|    | TGGATACGAA | ACATACACAG | AAAATCCAGC | CACTTTTTGA | AGGAAACGGC | 250  |
|    | TTTTGGATAA | GTGAAGCGCA | GCAAACGTTG | GTACCTGATG | TTTTATTTCC | 300  |
| 35 | CATTATGCAT | GGTAAATACG | GGGAAGATGG | CAGTATCCAA | GGATTGTTTG | 350  |
|    | AATTGATGAA | GCTGCCTTAT | GTAGGCTGTG | GGGTGGCAGC | CTCTGCCTTA | 400  |
|    | TGTATGAACA | AATGGTTATT | GCATCAAGCA | GCAGCAGCGA | TTGGCGTACA | 450  |
|    | AAGCGCTCCT | ACGATTCTCT | TGACAAATCA | AGCCAACCAG | CAAAGACAAA | 500  |
|    | TCGAAGCCTT | TATCCAGACC | CATGGCTTTC | CAGTTTTCTT | TAAGCCTAAT | 550  |
| 40 | GAAGCGGGCT | CCTCAAAAGG | GATCACAAAA | GTAACCTGTG | TTGAAGAAAT | 600  |
|    | CGCTCCTGCC | TTGAAGGAAG | CCTTCGCTTA | TTGTTCCGCA | GTGCTCTTAC | 650  |
|    | AAAAAAATAT | CGCTGGCGTT | GAGATTGGTT | GCGGTATCTT | AGGCAACGAC | 700  |
|    | TCTTTGACTG | TCGGTGCTTG | TGACGCTATT | TCATTAGTAG | ACGGCTTTTT | 750  |
|    | CGATTTTGAA | GAAAAGTACC | AGTTGATCAG | CGCCAAAATC | ACCGTTCCTG | 800  |
| 45 | CGCCATTGCC | TGAAACGATT | GAAACCAAAG | TCAAAGAACA | AGCTCAGCTG | 850  |
|    | CTCTATCACA | GTCTTGCTCT | TAAAGGACTT | GCTCGCATCG | ACTTTTTTGT | 900  |
|    | CACGGATCAA | GGAGAACTAT | ACTTGAATGA | AATCAATACT | ATGCCGGGCT | 950  |
|    | TTACGAGTCA | CTCCCGCTAT | CCTGCCATGA | TGGCAGCGGT | CGGCTTATCC | 1000 |
| 50 | TATCAAGAAT | TA         |            |            |            | 1012 |

## 2) INFORMATION FOR SEQ ID NO: 1067

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067

```

10 CTTACGCTTT ATCGATTAGA CACGGGNAGC TTGTCCAATG GGRAGCCGAT 50
   TTGATTTTAT GGATGAACGC TCTCATCATG CGGCAAATGG AATATCATGC 100
   AATGAAGCGC AAAATCGCAG ACGTTTGCGC TCCATCATGG AAAACAGTGG 150
   GTTTGAAGCA TATAGCCTCG AATGGTGGCA CTATGTATTA AGAGACGAAC 200
   CATACCCCAA TAGCTATTTT GATTTCCCGG TTAAATAAAC TTTTAACCGT 250
   TGCACGGACA AACTATATAA GCTAACTCTT TCGGCAGGAA ACCCGACGTA 300
15 TGTAAGTGGT TCTTAGGGAA TTTATATATA GTAGATAGTA TTGAAGATGT 350
   AAGGCAGAGC GATATTGCGG TCATTATCTG CGTGCGCTGC GGCAAGATAG 400
   CCTGATAATA AGACTGATCG CATAGAGGGG TGGTATTTCA CACCGCCCAT 450
   TGTCAACAGG CAGTTCAGCC TCGTTAAATT CAGCATGGGT ATCACTTATG 500
   AAAATTTCATC TACATTGGTG ATAATAGTAA ATCCAGTAGG GCGAAATAAT 550
20 TGACTGTAAT TTACGGGGCA AAACGGCACA ATCTCAAACG AGATTGTGCC 600
   GTTTAAGGGG AAGATTCTAG AAATATTTCA TACTTCCAAC TATATAGTTA 650
   AGGAGGAGAC TGAAAATGAA GAAGTTGTTT TTTTATTGT TATTGTTATT 700
   CTTAATATAC TTAGGTTATT G 721

```

25

2) INFORMATION FOR SEQ ID NO: 1068

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 668 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R492

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

```

   ATTTTTAAGG ATGAACGCTC TTCATCATGC GGCAAATGGA ATATCATGCA 50
   ATGAAGCGCA AAATCGCAGA CGTTTGCGCT CCATCATGGA AAACAGTGGG 100
45 TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC TATGTATTAA GAGACGAACC 150
   ATACCCCAAT AGCTATTTTG ATTTCCCGGT TAAATAAACT TTTAACCGTT 200
   GCACGGACAA ACTATATAAG CTAACCTCTT CGGCAGGAAA CCCGACGTAT 250
   GTAAGTGGT CTTAGGGAAT TTATATATAG TAGATAGTAT TGAAGATGTA 300
   AGGCAGAGCG ATATTGCGGT CATTATCTGC GTGCGCTGCG GCAAGATAGC 350
50 CTGATAATAA GACTGATCGC ATAGAGGGGT GGTATTTTAC ACCGCCCAT 400
   GTCAACAGGC AGTTCAGCCT CGTTAAATTC AGCATGGGTA TCACTTATGA 450
   AAATTTCATCT ACATTGGTGA TAATAGTAAA TCCAGTAGGG CGAAATAATT 500
   GACTGTAATT TACGGGGCAA AACGGCACA TCTCAAACGA GATTGTGCCG 550
   TTTAAGGGGA AGATTCTAGA AATATTTTCA ACTTCCAAC ATATAGTTAA 600
55 GGAGGAGACT GAAAATGAAG AAGTTGTTTT TTTTATTGTT ATTGTTATTC 650
   TTAATATACT TAGGTTAT 668

```

60 2) INFORMATION FOR SEQ ID NO: 1069

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: R581

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069

```

15 CGGCAAGTGC CATTGATCTT ACGCTTTATC GATTAGACAC GGGTRAGCTT      50
   GTACCAATGG GAAGCCGATT TGATTTTATG GATGAACGCT CTCATCATGC      100
   GGCAAATGGA ATATCATGCA ATGAAGCGCA AAATCGCAGA CGTTTGCGCT      150
   CCATCATGGA AACACAGTGGG TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC      200
20 TATGTATTAA GAGACGAACC ATACCCCAAT AGCTATTTTG ATTTCCCCGT      250
   TAAATAAACT TTTAACCGTT GCACGGACAA ACTATATAAG CTAACCTCTT      300
   CGGCAGGAAA CCCGACGTAT GTAAC TGGT CTTAGGGAAT TTATATATAG      350
   TAGATAGTAT TGAAGATGTA AGGCAGAGCG ATATTGCGGT CATTATCTGC      400
   GTGCGCTGCG GCAAGATAGC CTGATAATAA GACTGATCGC ATAGAGGGGT      450
25 GGTATTTTAC ACCGCCCAT GTCAACAGGC AGTTCAGCCT CGTTAAATTC      500
   AGCATGGGTA TCACTTATGA AAATTCATCT ACATTGGTGA TAATAGTAAA      550
   TCCAGTAGGG CGAAATAATT GACTGTAATT TACGGGGCAA AACGGCACAA      600
   TCTCAAACGA GATTGTGCCG TTTAAGGGGA AGATTCTAGA AATATTTCAT      650
   ACTTCCAAC TATATAGTTAA GGAGGAGACT GAAAATGAAG AAGTTGTTTT      700
30 TTTTATTGTT ATTGTTATTC TTAATATACT TAGGTTATGA CTACGTTAAT      750
   GAAANCCTGA                                     760

```

## 2) INFORMATION FOR SEQ ID NO: 1070

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*  
 (B) STRAIN: R610

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070

```

50 AAAAGGAATA CGGGGCTTTC AAAAATCCAA GCCATAACCC GCGGGCAAGT      50
   GCCATTTGAT TCTTACGCTT TAATCGATTA GACACGGGTA AGCTTGTAACC      100
   AATGGGGAAC CGATTTGATT TTAATGNATG AACGCTCTTC ATCATGCGGC      150
   AAATGGAATA TCATGCAATG AAGCGCAAAA TCGCAGACGT TTGCGCTCCA      200
55 TCATGGAAAA CAGTGGGTTT GAAGCATATA GCCTCGAATG GTGGCACTAT      250
   GTATTAAGAG ACGAACCATA CCCC AATAGC TATTTTGATT TCCCCGTTAA      300
   ATAACTTTT AACCGTTGCA CGGACAAACT ATATAAGCTA ACTCTTTCGG      350
   CAGGAAACCC GACGTATGTA ACTGGTTCTT AGGGAATTTA TATATAGTAG      400
   ATAGTATTGA AGATGTAAGG CAGAGCGATA TTGCGGTCAT TATCTGCGTG      450
60 CGCTGCGGCA AGATAGCCTG ATAATAAGAC TGATCGCATA GAGGGGTGGT      500

```

|              |            |            |            |            |     |
|--------------|------------|------------|------------|------------|-----|
| ATTTACACACC  | GCCCATTGTC | AACAGGCAGT | TCAGCCTCGT | TAAATTCAGC | 550 |
| ATGGGTATCA   | CTTATGAAAA | TTCATCTACA | TTGGTGATAA | TAGTAAATCC | 600 |
| AGTAGGGCGA   | AATAATTGAC | TGTAATTTAC | GGGGCAAAAC | GGCACAATCT | 650 |
| CAAACGAGAT   | TGTGCCGTTT | AAGGGGAAGA | TTCTAGAAAT | ATTTCATACT | 700 |
| 5 TCCAACTATA | TAGTTAAGGA | GGAGACTGAA | AATGAAGAAG | TTGTTTTTTT | 750 |
| TTATTGTTAT   | TGTTATTCTT | AATATACTTA | GGTTATGACT | ACGTTAATGA | 800 |
| A            |            |            |            |            | 801 |

10

## 2) INFORMATION FOR SEQ ID NO: 1071

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 711 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*  
(B) STRAIN: R684

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071

|               |            |             |            |            |     |
|---------------|------------|-------------|------------|------------|-----|
| TTGTACCAAT    | GGGGAGCCGA | TTTGATTTTA  | TGGATGAACG | CTCTCATCAT | 50  |
| GCGGCAAATG    | GAATATCATG | CAATGAAGCG  | CAAAATCGCA | GACGTTTGCG | 100 |
| CTCCATCATG    | GAAACAGTG  | GGTTTGAAGC  | ATATAGCCTC | GAATGGTGGC | 150 |
| 30 ACTATGTATT | AAGAGACGAA | CCATACCCCA  | ATAGCTATTT | TGATTTCCCC | 200 |
| GTTAAATAAA    | CTTTTAACCG | TTGCACGGAC  | AAACTATATA | AGCTAACTCT | 250 |
| TTCGGCAGGA    | AACCCGACGT | ATGTAAC TGG | TTCTTAGGGA | ATTTATATAT | 300 |
| AGTAGATAGT    | ATTGAAGATG | TAAGGCAGAG  | CGATATTGCG | GTCATTATCT | 350 |
| GCGTGCGCTG    | CGGCAAGATA | GCCTGATAAT  | AAGACTGATC | GCATAGAGGG | 400 |
| 35 GTGGTATTTT | ACACCGCCCA | TTGTCAACAG  | GCAGTTCAGC | CTCGTTAAAT | 450 |
| TCAGCATGGG    | TATCACTTAT | GAAAATTCAT  | CTACATTGGT | GATAATAGTA | 500 |
| AATCCAGTAG    | GGCGAAATAA | TTGACTGTAA  | TTTACGGGGC | AAAACGGCAC | 550 |
| AATCTCAAAC    | GAGATTGTGC | CGTTTAAGGG  | GAAGATTCTA | GAAATATTTT | 600 |
| ATACTTCCAA    | CTATATAGTT | AAGGAGGAGA  | CTGAAAATGA | AGAAGTTGTT | 650 |
| 40 TTTTTTATTG | TTATTGTTAT | TCTTAATATA  | CTTAGGTTAT | GACTACGTTA | 700 |
| ATGAAGCACT    | G          |             |            |            | 711 |

## 45 2) INFORMATION FOR SEQ ID NO: 1072

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 751 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
(B) STRAIN: R688

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072

60

|    |            |             |            |            |             |     |
|----|------------|-------------|------------|------------|-------------|-----|
|    | GCCATTGATC | TTACGCTTTA  | TCGATTAGAC | ACGGGTNAGC | TTGTACCAAT  | 50  |
|    | GGGGAGCCGA | TTTGATTTTA  | TGGATGAACG | CTCTCATCAT | GCGGCAAATG  | 100 |
|    | GAATATCATG | CAATGAAGCG  | CAAAATCGCA | GACGTTTGCG | CTCCATCATG  | 150 |
|    | GAAAACAGTG | GGTTTGAAGC  | ATATAGCCTC | GAATGGTGGC | ACTATGTATT  | 200 |
| 5  | AAGAGACGAA | CCATACCCCA  | ATAGCTATTT | TGATTTCCCC | GTTAAATAAA  | 250 |
|    | CTTTTAACCG | TTGCACGGAC  | AAACTATATA | AGCTAACTCT | TTCGGCAGGA  | 300 |
|    | AACCCGACGT | ATGTAACCTG  | TTCTTAGGGA | ATTTATATAT | AGTAGATAGT  | 350 |
|    | ATTGAAGATG | TAAGGCAGAG  | CGATATTGCG | GTCATTATCT | GCGTGCGCTG  | 400 |
|    | CGGCAAGATA | GCCTGATAAT  | AAGACTGATC | GCATAGAGGG | GTGGTATTTC  | 450 |
| 10 | ACACCGCCCA | TTGTCAACAG  | GCAGTTCAGC | CTCGTTAAAT | TCAGCATGGG  | 500 |
|    | TATCACTTAT | GAAAATTTCAT | CTACATTGGT | GATAATAGTA | AATCCAGTAG  | 550 |
|    | GGCGAAATAA | TTGACTGTAA  | TTTACGGGGC | AAAACGGCAC | AATCTCAAAC  | 600 |
|    | GAGATTGTGC | CGTTTAAGGG  | GAAGATTCTA | GAAATATTTT | ATACTTCCAA  | 650 |
|    | CTATATAGTT | AAGGAGGAGA  | CTGAAAATGA | AGAAGTTGTT | TTTTTTTATTG | 700 |
| 15 | TTATTGTTAT | TCTTAATATA  | CTTAGGTTAT | GACTACGTTA | ATGAAGCACT  | 750 |
|    | G          |             |            |            |             | 751 |

## 20 2) INFORMATION FOR SEQ ID NO: 1073

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*  
 (B) STRAIN: R689

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 35 | ATTTGATTTT | ATGGATGAAC | GCTCTCATCA | TGCGGCAAAT | GGAATATCAT | 50  |
|    | GCAATGAAGC | GCAAAATCGC | AGACGTTTGC | GCTCCATCAT | GGAAAACAGT | 100 |
|    | GGGTTTGAAG | CATATAGCCT | CGAATGGTGG | CACTATGTAT | TAAGAGACGA | 150 |
|    | ACCATACCCC | AATAGCTATT | TTGATTTCCC | CGTTAAATAA | ACTTTTAACC | 200 |
| 40 | GTTGCACGGA | CAAACTATAT | AAGCTAACTC | TTTCGGCAGG | AAACCCGACG | 250 |
|    | TATGTAACTG | GTTCTTAGGG | AATTTATATA | TAGTAGATAG | TATTGAAGAT | 300 |
|    | GTAAGGCAGA | GCGATATTGC | GGTCATTATC | TGCGTGCGCT | GCGGCAAGAT | 350 |
|    | AGCCTGATAA | TAAGACTGAT | CGCATAGAGG | GGTGGTATTT | CACACCGCCC | 400 |
|    | ATTGTCAACA | GGCAGTTCAG | CCTCGTTAAA | TTCAGCATGG | GTATCACTTA | 450 |
| 45 | TGAAAATTCA | TCTACATTGG | TGATAATAGT | AAATCCAGTA | GGGCGAAATA | 500 |
|    | ATTGACTGTA | ATTTACGGGG | CAAAACGGCA | CAATCTCAA  | CGAGATTGTG | 550 |
|    | CCGTTTAAGG | GGAAGATTCT | AGAAATATTT | CATACTTCCA | ACTATATAGT | 600 |
|    | TAAGGAGGAG | ACTGAAAATG | AAGAAGTTGT | TTTTTTTATT | GTTATTGTTA | 650 |
| 50 | TTCTTAATAT | ACTTAGGTTA | TGACTACGTT | AATGA      |            | 685 |

## 2) INFORMATION FOR SEQ ID NO: 1074

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATCGATTAGA | CACGGGTGAG | CTTGTACCAA | TGGGGAGCCG | ATTTGATTTT | 50  |
| 10 | ATGGATGAAC | GCTCTCATCA | TGCGGCAAAT | GGAATATCAT | GCAATGAAGC | 100 |
|    | GCAAAATCGC | AGACGTTTGC | GCTCCATCAT | GGAAAACAGT | GGGTTTGAAG | 150 |
|    | CATATAGCCT | CGAATGGTGG | CACTATGTAT | TAAGAGACGA | ACCATACCCC | 200 |
|    | AATAGCTATT | TTGATTTCCC | CGTTAAATAA | ACTTTTAACC | GTTGCACGGA | 250 |
|    | CAAACTATAT | AAGCTAACTC | TTTCGGCAGG | AAACCCGACG | TATGTAACTG | 300 |
| 15 | GTTCTTAGGG | AATTTATATA | TAGTAGATAG | TATTGAAGAT | GTAAGGCAGA | 350 |
|    | GCGATATTGC | GGTCATTATC | TGCGTGCGCT | GCGGCAAGAT | AGCCTGATAA | 400 |
|    | TAAGACTGAT | CGCATAGAGG | GGTGGTATTT | CACACCGCCC | ATTGTCAACA | 450 |
|    | GGCAGTTCAG | CCTCGTTAAA | TTCAGCATGG | GTATCACTTA | TGAAAATTCA | 500 |
|    | TCTACATTGG | TGATAATAGT | AAATCCAGTA | GGGCGAAATA | ATTGACTGTA | 550 |
| 20 | ATTTACGGGG | CAAAACGGCA | CAATCTCAAA | CGAGATTGTG | CCGTTTAAGG | 600 |
|    | GGAAGATTCT | AGAAATATTT | CATACTTCCA | ACTATATAGT | TAAGGAGGAG | 650 |
|    | ACTGAAAATG | AAGAAGTTGT | TTTTTTTATT | GTTATTGTTA | TTCTTAATAT | 700 |
|    | ACTTAGGTTA | TGACTACGTT | AATGAAGCAC | TG         |            | 732 |

25

2) INFORMATION FOR SEQ ID NO: 1075

(i) SEQUENCE CHARACTERISTICS:

|    |                          |
|----|--------------------------|
| 30 | (A) LENGTH: 670 bases    |
|    | (B) TYPE: Nucleic acid   |
|    | (C) STRANDEDNESS: Double |
|    | (D) TOPOLOGY: Linear     |

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R691

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | TCTCATCATG | CGGCAAATGG | AATATCATGC | AATGAAGCGC  | AAAATCGCAG | 50  |
|    | ACGTTTGC   | TCCATCATGG | AAAACAGTGG | GTTTGAAGCA  | TATAGCCTCG | 100 |
| 45 | AATGGTGGCA | CTATGTATTA | AGAGACGAAC | CATACCCCAA  | TAGCTATTTT | 150 |
|    | GATTTCCCCG | TTAAATAAAC | TTTTAACCGT | TGCACGGACA  | AACTATATAA | 200 |
|    | GCTAACTCTT | TCGGCAGGAA | ACCCGACGTA | TGTAACCTGGT | TCTTAGGGAA | 250 |
|    | TTTATATATA | GTAGATAGTA | TTGAAGATGT | AAGGCAGAGC  | GATATTGCGG | 300 |
|    | TCATTATCTG | CGTGCGCTGC | GGCAAGATAG | CCTGATAATA  | AGACTGATCG | 350 |
| 50 | CATAGAGGGG | TGGTATTTCA | CACCGCCCAT | TGTCAACAGG  | CAGTTCAGCC | 400 |
|    | TCGTAAATTT | CAGCATGGGT | ATCACTTATG | AAAATTCATC  | TACATTGGTG | 450 |
|    | ATAATAGTAA | ATCCAGTAGG | GCGAAATAAT | TGACTGTAAT  | TTACGGGGCA | 500 |
|    | AAACGGCACA | ATCTCAAACG | AGATTGTGCC | GTTTAAGGGG  | AAGATTCTAG | 550 |
|    | AAATATTTCA | TACTTCCAAC | TATATAGTTA | AGGAGGAGAC  | TGAAAATGAA | 600 |
| 55 | GAAGTTGTTT | TTTTTATTGT | TATTGTTATT | CTTAATATAC  | TTAGGTTATG | 650 |
|    | ACTACGTAA  | TGAAGCACTG |            |             |            | 670 |

60 2) INFORMATION FOR SEQ ID NO: 1076



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (B) STRAIN: DG131/3 serotype OX3:H8  
 (C) ACCESSION NUMBER: Z36901

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076

```

ATGAAAATAA TAATTTT TAG AGTGCTAACT TTTTCTTTG TTATCTTTTC      50
TGTTAATGTG GTTGCGAAGG AATTACCTT AGATTCTCG ACAGCAAAGA      100
CGTATGTAGA TTCGCTGAAT GTCATTCGCT CTGCAATAGG TACTCCATTA      150
20 CAGACTATTT CATCAGGAGG TACGTCTTTA CTGATGATTG ATAGTGGCAC      200
AGGGGATAAT TTGTTTGCAG TTGATGTCAG AGGGATAGAT CCAGAGGAAG      250
GGCGGTTTAA TAATCTACGG CTTATTGTTG AACGAAATAA TTTATATGTG      300
ACAGGATTTG TTAACAGGAC AAATAATGTT TTTTATCGCT TTGCTGATTT      350
TTCACATGTT ACCTTTCCTG GTACAACTGC GGTTACATTG TCTGGTGACA      400
25 GTAGCTATAC CACGTTACAG CGTGTTGCGG GGATCAGTCG TACGGGGATG      450
CAGATAAATC GCCATTCGTT GACTACTTCT TATCTGGATT TAATGTCGCA      500
TAGCGGAACC TCACTGACGC AGTCTGTGGC AAGAGCGATG TTACGGTTTG      550
TTACTGTGAC AGCTGAAGCT TTACGTTTTC GGCAAATTCA GAGGGGATTT      600
CGTACAACAC TTGATGATCT CAGTGGGCGT TCTTATGTAA TGACTGCTGA      650
30 AGATGTTGAT CTTACGTTGA ACTGGGGAAG GTTGAGTAGT GTCCTGCCTG      700
ACTATCATGG ACAAGACTCT GTTCGTGTTG GAAGAATTTC TTTTGGAAGT      750
GTTAATGCAA TTCTGGGTAG CGTGGCATT AACTGAATT GTCATCATCA      800
TGCATCGCGA GTTGCCAGAA TTGTACCTAA TGAGTTTCCT TCTATGTGCC      850
CGGTAGATGG AAGAGTGCGT GGGATTACGC ACAATAAAAT ATTGTGGGAC      900
35 TCATCCACTC TGGGGGCAAT TTTGATACGC AGGGCTATTA GCAGTTGA      948

```

## 2) INFORMATION FOR SEQ ID NO: 1077

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (B) STRAIN: 94C serotype O48:H21  
 (C) ACCESSION NUMBER: extracted from Z37725

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077

```

CACCTGTATA TGAAGTGTAT ATTATTTAAA TGGGTACTGT GCCTGTTACT      50
GGGTTTTTCT TCGGTATCCT ATTCCCGGGA GTTTACGATA GACTTTTCGA      100
CCCAACAAAG TTATGTCTCT TCGTTAAATA GTATACGGAC AGAGATATCG      150
ACCCCTCTTG AACATATATC TCAGGGGACC ACATCGGTGT CTGTTATTAA      200
60 CCACACCCCA CCGGGCAGTT ATTTTGCTGT GGATATACGA GGGCTTGATG      250

```

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | TCTATCAGGC | GCGTTTTGAC | CATCTTCGGC | TGATTATTGA | GCAAAATAAT | 300  |
|    | TTATATGTGG | CCGGGTTCGT | TAATACGGCA | ACAAATACTT | TCTACCGTTT | 350  |
|    | TTCAGATTTT | ACACATATAT | CAGTGCCCGA | TGTGACAACG | GTTTCCATGA | 400  |
|    | CAACGGACAG | CAGTTATACC | ACTCTGCAAC | GTGTCGCAGC | GCTGGAACGT | 450  |
| 5  | TCCGGAATGC | AAATCAGTCG | TCACTCACTG | GTTTCATCAT | ATCTGGCGTT | 500  |
|    | AATGGAGTTC | AGTGGTAATA | CAATGACCAG | AGATGCATCC | AGAGCAGTTC | 550  |
|    | TGCGTTTTGT | CACTGTCACA | GCAGAAGCCT | TACGCTTCAG | GCAGATACAG | 600  |
|    | AGAGAATTTT | GTCAGGCACT | GTCTGAAACT | GCTCCTGTGT | ATACCATGAC | 650  |
|    | GCCGGGAGAC | GTGGACCTCA | CTCTGAACTG | GGGGCGAATC | AGCAATGTGC | 700  |
| 10 | TTCCGGAGTA | TCGGGGAGAG | GATGGTGTCA | GAGTGGGGAG | AATATCCTTT | 750  |
|    | AATAATATAT | CAGCGATACT | GGGTACTGTG | GCCGTTATAC | TGAATTGCCA | 800  |
|    | TCATCAGGGG | GCGCGTTCTG | TTCGCGCCGT | GAATGAAGAG | AGTCAACCAG | 850  |
|    | AATGTCAGAT | AACTGGCGAC | AGGCCCGTTA | TAAAAATAAA | CAATACATTA | 900  |
|    | TGGGAAAGTA | ATACAGCTGC | AGCGTTTCTG | AACAGAAAGT | CACAGTTTTT | 950  |
| 15 | ATATACAACG | GGTAAATAAA | GGAGTTAAGT | ATGAAGAAGA | TGTTTATGGC | 1000 |
|    | GGTTTTATTT | GCATTAGTTT | CTGTTAATGC | AATGGCGGCG | GATTGTGCTA | 1050 |
|    | AAGGTAAAAT | TGAGTTTTTC | AAGTATAATG | AGGATGACAC | ATTTACAGTG | 1100 |
|    | AAGGTTGACG | GGAAAGAATA | CTGGACCAGT | CGCTGGAATC | TGCAACCGTT | 1150 |
|    | ACTGCAAAGT | GCTCAGCTGA | CAGGAATGAC | TGTCACAATC | AAATCCAGTA | 1200 |
| 20 | CCTGTGAATC | AGGCTCCGGA | TTTGCTGAAG | TGCAGTTTAA | TAATGACTGA | 1250 |
|    | GGCATAACC  |            |            |            |            | 1259 |

## 25 2) INFORMATION FOR SEQ ID NO: 1078

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078

AGTTCTGCGT TTTGTCACTG TC

22

40

## 2) INFORMATION FOR SEQ ID NO: 1079

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 19 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079

CGGAAGCACA TTGCTGATT

19

55

## 2) INFORMATION FOR SEQ ID NO: 1080

## (i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 25 bases

(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080

10 TATAGCTACT GTCACCAGAC AATGT

25

2) INFORMATION FOR SEQ ID NO: 1081

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081

25 ATGTCAGAGG GATAGATCCA

20

2) INFORMATION FOR SEQ ID NO: 1082

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082

40

TTGARCRAAA TAATTTATAT GTG

23

45 2) INFORMATION FOR SEQ ID NO: 1083

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083

TGATGATGRC AATTCAGTAT

20

60

## 2) INFORMATION FOR SEQ ID NO: 1084

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084

CCACGCCGCT TTGCTGATTT TTCACATGTT ACCGCGTGG

39

## 2) INFORMATION FOR SEQ ID NO: 1085

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085

CCACGCCACT GTCTGAAACT GCTCCTGTGC GTGG

34

## 2) INFORMATION FOR SEQ ID NO: 1086

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086

CTACTCCCGC CTTTTGGGTT

20

## 2) INFORMATION FOR SEQ ID NO: 1087

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087

5 2) INFORMATION FOR SEQ ID NO: 1088

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088

TGCCGTTTCC TGTATCCGTC

20

20

2) INFORMATION FOR SEQ ID NO: 1089

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089

ATCCACACGG GCTAGACCTC

20

35

2) INFORMATION FOR SEQ ID NO: 1090

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090

AATAGCGCGG ACGAATTGGA C

21

50

2) INFORMATION FOR SEQ ID NO: 1091

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091

5 AACGCGGCAC TGTTTCCCAA

20

## 2) INFORMATION FOR SEQ ID NO: 1092

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092

20

TCGGCAAGAC AATATGACAG C

21

## 2) INFORMATION FOR SEQ ID NO: 1093

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
- (B) STRAIN: CSsa-165

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093

40

|            |             |            |            |            |     |
|------------|-------------|------------|------------|------------|-----|
| TAACGGGCGT | CTCGATAGAA  | AAACACGTGA | AAATCCCAAT | GATTATAAAC | 50  |
| AATCAATATA | CGATTTTGCT  | GAAGCTGTAA | CAAAAGGTAT | TAAGGAACAA | 100 |
| ACAAATAAAA | ATTAATAGGC  | AACTTAACCA | GAATCGTTAA | AACTATATGA | 150 |
| CGATTCTGGT | TTTTTAAATT  | CAAAAAGTTT | TCTAAAAAAT | TTACCTGCTT | 200 |
| TTTTAAAGTA | TAGGTATAAA  | ATACAATTGA | TTAAAATAGT | AAAGGAAATG | 250 |
| AATCATGAAA | CAATTAACCTA | AGCCTTTATA | CTTTTACCTA | TTACTTTTTA | 300 |
| TTACAACAAC | ACTGATTGGC  | GCGTTACTAT | TATATTTGCC | AATCACAGGT | 350 |
| AAACATCCTA | TTGATTTTGT  | GGACGCCCGT | T          |            | 381 |

50

## 2) INFORMATION FOR SEQ ID NO: 1094

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094

GGTAAACAG GTACTTCTAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1095

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095

CGATAGAAGC AGCAGGACAA

20

2) INFORMATION FOR SEQ ID NO: 1096

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096

CTGATGGATG CGGAAGATAC

20

2) INFORMATION FOR SEQ ID NO: 1097

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097

TCYTCAAAAG GGATCACWAA AGTMAC

26

2) INFORMATION FOR SEQ ID NO: 1098

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098

TCTTCAAAAT CGAAAAAGCC GTC

23

2) INFORMATION FOR SEQ ID NO: 1099

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099

TCAAAAGGGA TCACWAAAGT MAC

23

2) INFORMATION FOR SEQ ID NO: 1100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100

GTAAAKCCCG GCATRGTRTT GATTTC

26

2) INFORMATION FOR SEQ ID NO: 1101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101

GACGGYTTTT TYGATTTTGA AGA

23

2) INFORMATION FOR SEQ ID NO: 1102



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102

AAAAARTCGA TKCGAGCMAG ACC

## 2) INFORMATION FOR SEQ ID NO: 1103

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103

ATCCCGCTAT GAAAACGATC

## 2) INFORMATION FOR SEQ ID NO: 1104

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104

GGATCAACAC AGTAGAACCG

## 2) INFORMATION FOR SEQ ID NO: 1105

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105

CTCCTACGAT TCTCTTGAYA AATCA

## 2) INFORMATION FOR SEQ ID NO: 1106

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106

CAACCGATCT CAACACCGGC AAT

23

## 2) INFORMATION FOR SEQ ID NO: 1107

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107

CTCATTTGAC TTCCTCCTTT GCT

23

## 2) INFORMATION FOR SEQ ID NO: 1108

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108

GTAAGAATCG GAAAAGCGGA AGG

23

## 2) INFORMATION FOR SEQ ID NO: 1109

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109

ACATCGTGAT CGCTAAAAGG AGC

23

2) INFORMATION FOR SEQ ID NO: 1110

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110

ACGAGAAAGA CAACAGGAAG ACC

23

2) INFORMATION FOR SEQ ID NO: 1111

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111

CTTTTCCGG CTCGWYTTCC TGATG

25

2) INFORMATION FOR SEQ ID NO: 1112

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112

GGCTGYGATA TTCAAAGCTC

20

2) INFORMATION FOR SEQ ID NO: 1113

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113

ACCGACCTCA CAGCCCGAAA

20

10

2) INFORMATION FOR SEQ ID NO: 1114

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114

TCWGAGCCTT TTTCCGGCTC G

21

25

2) INFORMATION FOR SEQ ID NO: 1115

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115

40

TTTCGGGCTG TGAGGTCGGB TGHGCG

26

2) INFORMATION FOR SEQ ID NO: 1116

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116

55

TTTCGGGCTG TGAGGTCGGB TGHGCGG

27

60 2) INFORMATION FOR SEQ ID NO: 1117

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 801 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Enterococcus faecium*  
(B) STRAIN: 94  
(C) ACCESSION NUMBER: U94526

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117

15 AAATTCGATC CGCACTACAT CGGAATTACA AAAAACGGTG TATGGAAGCT 50  
ATGCAAGAAG CCATGTACGG AATGGGAAGC CGACAGTCTC CCCGCCATAC 100  
TCTCCCCGGA TAGGAAAACG CATGGGCTGC TTGTCATGAA AGAAAGCGAA 150  
20 TACGAAACAC GCGGTATTGA TGTGGCTTTC CCGGTTTTGC ATGGCAAATG 200  
CGGGGAGGAT GGTGCGATAC AGGGGCTGTT TGTATTGTCT GGTATCCCCT 250  
ATGTGGGCTG TGATATTCAA AGCTCCGCAG CTTGCATGGA CAAATCACTG 300  
GCCTACATTC TTACAAAAAA TGCGGGCATC GCCGTTCCCG AATTTCAAAT 350  
GATTGATAAA GGTGACAAGC CGGAGGCGGG TGCGCTTACC TACCCTGTCT 400  
25 TTGTGAAGCC GGCACGGTCA GGTTCGTCCT TTGGCGTAAC CAAAGTAAAC 450  
GGTACGGAAG AACTTAACGC TGCGATAGAA GCGGCAGGAC AATATGATGG 500  
AAAAATCTTA ATTGAGCAAG CGATTTTCGGG CTGTGAGGTC GGGTGTGCGG 550  
TCATGGGGAA CGAGGATGAT TTGATTGTCG GCGAAGTGGA TCAAATCCGG 600  
CTGAGCCACG GTATCTTCCG CATCCATCAG GAAAACGAGC CGGAAAAAGG 650  
30 CTCAGAAAAT GCGATGATTA CAGTTCCTCG AGACATTCCG GTCGAGGAAC 700  
GAAATCGGGT GCAGGAAACG GCAAAGAAAG TATATCGGGT GCTTGGATGC 750  
AGAGGGCTTG CCCGTGTTGA TCTTTTTTTT CAGGAGGATG GCGGCATCGT 800  
T 801

35

## 2) INFORMATION FOR SEQ ID NO: 1118

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118

TTTTTCWGAGC CTTTTTCCGG CTCG

50 24

## 2) INFORMATION FOR SEQ ID NO: 1119

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119

5 TTTCGGGCTG TGAGGTCGGB TGHGC

25

2) INFORMATION FOR SEQ ID NO: 1120

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120

20

TTTCGGGCTG TGAGGTCGGB TGHG

24

2) INFORMATION FOR SEQ ID NO: 1121

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121

35

TGTTTGWATT GTCYGGYATC CC

22

2) INFORMATION FOR SEQ ID NO: 1122

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

45

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122

50

TGGTGCATTG CTACGTGG

18

2) INFORMATION FOR SEQ ID NO: 1123

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

60

(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123

TTTCGGGCTG TGAGGTCGGB TG

22

2) INFORMATION FOR SEQ ID NO: 1124

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124

25 GATTTGRTCC ACYTCGCCRA CA

22

2) INFORMATION FOR SEQ ID NO: 1125

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125

40

ACTCACAAC TGGGATGGATG

20

2) INFORMATION FOR SEQ ID NO: 1126

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126

55

TTATGGTTGT GCTGGTTGAG G

21

60

## 2) INFORMATION FOR SEQ ID NO: 1127

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127

KCAAAYGCCA TTTCAAGTAA

20

## 2) INFORMATION FOR SEQ ID NO: 1128

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128

GACGACYTTA TKGATATACA

20

## 2) INFORMATION FOR SEQ ID NO: 1129

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129

ATGATGACHG AMATGATGAA AAC

23

## 2) INFORMATION FOR SEQ ID NO: 1130

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130



5 2) INFORMATION FOR SEQ ID NO: 1131

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131

CATCTGGAGC TACRTARCCA GT

22

20

2) INFORMATION FOR SEQ ID NO: 1132

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132

AGTGAAAARA TGGCTGCTGC

20

35

2) INFORMATION FOR SEQ ID NO: 1133

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133

CATCAAGAAC ACTGGCTAYG TAG

23

50

2) INFORMATION FOR SEQ ID NO: 1134

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134

5 CTAGATAGAG CTAAAACCTT CCT

23

2) INFORMATION FOR SEQ ID NO: 1135

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135

CATTATGCAA ACGCCATTTC AAG

23

2) INFORMATION FOR SEQ ID NO: 1136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136

ACTTGTCCAC GTTSGATRTC T

21

2) INFORMATION FOR SEQ ID NO: 1137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137

AATTAATGGC TGCWGTTGAY GAA

23

2) INFORMATION FOR SEQ ID NO: 1138

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1032 bases

628

- (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*  
 (C) ACCESSION NUMBER: M75132

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138

|    |             |             |            |            |             |      |
|----|-------------|-------------|------------|------------|-------------|------|
|    | ATGAAAAAAA  | TTGCCGTTTT  | ATTTGGAGGG | AATTCTCCAG | AATACTCAGT  | 50   |
|    | GTCAC TAACC | TCAGCAGCAA  | GTGTGATCCA | AGCTATTGAC | CCGCTGAAAT  | 100  |
| 15 | ATGAAGTAAT  | GACCATTTGGC | ATCGCACCAA | CAATGGATTG | GTATTGGTAT  | 150  |
|    | CAAGGAAACC  | TCGCGAATGT  | TCGCAATGAT | ACTTGGCTAG | AAGATCACAA  | 200  |
|    | AAACTGTCAC  | CAGCTGACTT  | TTTCTAGCCA | AGGATTTATA | TTAGGAGAAA  | 250  |
|    | AACGAATCGT  | CCCTGATGTC  | CTCTTTCCAG | TCTTGCATGG | GAAGTATGGC  | 300  |
|    | GAGGATGGCT  | GTATCCAAGG  | ACTGCTTGAA | CTAATGAACC | TGCCTTATGT  | 350  |
| 20 | TGGTTGCCAT  | GTGCTGCCT   | CGCATTATG  | TATGAACAAA | TGGCTCTTGC  | 400  |
|    | ATCAACTTGC  | TGATACCAT   | CGAATCGCTA | GTGCTCCAC  | TTTGCTTTTA  | 450  |
|    | TCCCGCTATG  | AAAACGATCC  | TGCCACAATC | GATCGTTTTA | TTCAAGACCA  | 500  |
|    | TGGATTCCCG  | ATCTTTATCA  | AGCCGAATGA | AGCCGGTTCT | TCAAAGGGA   | 550  |
|    | TCACAAAAGT  | AACTGACAAA  | ACAGCGCTCC | AATCTGCATT | AACGACTGCT  | 600  |
| 25 | TTTGCTTACG  | GTTCTACTGT  | GTTGATCCAA | AAGGCGATAG | CGGGTATTGA  | 650  |
|    | AATTGGCTGC  | GGCATCTTAG  | GAAATGAGCA | ATTGACGATT | GGTGCTTG TG | 700  |
|    | ATGCGATTTT  | TCTTGTCGAC  | GGTTTTTTTG | ATTTTGAAGA | GAAATACCAA  | 750  |
|    | TTAATCAGCG  | CCACGATCAC  | TGTCCCAGCA | CCATTGCCTC | TCGCGCTTGA  | 800  |
|    | ATCACAGATC  | AAGGAGCAGG  | CACAGCTGCT | TTATCGAAAC | TTGGGATTGA  | 850  |
| 30 | CGGGTCTGGC  | TCGAATCGAT  | TTTTTCGTCA | CCAATCAAGG | AGCGATTTAT  | 900  |
|    | TTAAACGAAA  | TCAACACCAT  | GCCGGGATTT | ACTGGGCACT | CCCGCTACCC  | 950  |
|    | AGCTATGATG  | GCGGAAGTCG  | GGTTATCCTA | CGAAATATTA | GTAGAGCAAT  | 1000 |
|    | TGATTGCACT  | GGCAGAGGAG  | GACAAACGAT | GA         |             | 1032 |

35

2) INFORMATION FOR SEQ ID NO: 1139

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1768 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: BM4147  
 50 (C) ACCESSION NUMBER: X56895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | GATATCGTTA | CGCTTCATGT | GCCGCTCAAT | ACGGATACGC | ACTATATTAT  | 50  |
| 55 | CAGCCACGAA | CAAATACAGA | GAATGAAGCA | AGGAGCATT  | CTTATCAATA  | 100 |
|    | CTGGGCGCGG | TCCACTTGTA | GATACCTATG | AGTTGGTTAA | AGCATTAGAA  | 150 |
|    | AACGGGAAAC | TGGGCGGTGC | CGCATTGGAT | GTATTGGAAG | GAGAGGAAGA  | 200 |
|    | GTTTTTCTAC | TCTGATTGCA | CCCAAAAACC | AATTGATAAT | CAATTTT TAC | 250 |
|    | TTAAACTTCA | AAGAATGCCT | AACGTGATAA | TCACACCGCA | TACGGCCTAT  | 300 |
| 60 | TATACCGAGC | AAGCGTTGCG | TGATACCGTT | GAAAAAACCA | TTAAAACTG   | 350 |

|    |             |            |            |            |            |      |
|----|-------------|------------|------------|------------|------------|------|
|    | TTTGGATTTT  | GAAAGGAGAC | AGGAGCATGA | ATAGAATAAA | AGTTGCAATA | 400  |
|    | CTGTTTGGGG  | GTTGCTCAGA | GGAGCATGAC | GTATCGGTAA | AATCTGCAAT | 450  |
|    | AGAGATAGCC  | GCTAACATTA | ATAAAGAAAA | ATACGAGCCG | TTATACATTG | 500  |
|    | GAATTACGAA  | ATCTGGTGTA | TGGAAAATGT | GCGAAAAACC | TTGCGCGGAA | 550  |
| 5  | TGGGAAAACG  | ACAATTGCTA | TTCAGCTGTA | CTCTCGCCGG | ATAAAAAAAT | 600  |
|    | GCACGGATTA  | CTTGTTAAAA | AGAACCATGA | ATATGAAATC | AACCATGTTG | 650  |
|    | ATGTAGCATT  | TTCAGCTTTG | CATGGCAAGT | CAGGTGAAGA | TGGATCCATA | 700  |
|    | CAAGGTCTGT  | TTGAATTGTC | CGGTATCCCT | TTTGTAGGCT | GCGATATTCA | 750  |
|    | AAGCTCAGCA  | ATTTGTATGG | ACAAATCGTT | GACATACATC | GTTGCGAAAA | 800  |
| 10 | ATGCTGGGAT  | AGCTACTCCC | GCCTTTTGGG | TTATTAATAA | AGATGATAGG | 850  |
|    | CCGGTGGCAG  | CTACGTTTAC | CTATCCTGTT | TTTGTTAAGC | CGGCGCGTTC | 900  |
|    | AGGCTCATCC  | TTCGGTGTGA | AAAAAGTCAA | TAGCGCGGAC | GAATTGGACT | 950  |
|    | ACGCAATTGA  | ATCGGCAAGA | CAATATGACA | GCAAAATCTT | AATTGAGCAG | 1000 |
|    | GCTGTTTCGG  | GCTGTGAGGT | CGGTTGTGCG | GTATTGGGAA | ACAGTGCCGC | 1050 |
| 15 | GTTAGTTGTT  | GGCGAGGTGG | ACCAAATCAG | GCTGCAGTAC | GGAATCTTTC | 1100 |
|    | GTATTCATCA  | GGAAGTCGAG | CCGGAAAAAG | GCTCTGAAAA | CGCAGTTATA | 1150 |
|    | ACCGTTCCCG  | CAGACCTTTC | AGCAGAGGAG | CGAGGACGGA | TACAGGAAAC | 1200 |
|    | GGCAAAAAAA  | ATATATAAAG | CGCTCGGCTG | TAGAGGTCTA | GCCCGTGTGG | 1250 |
|    | ATATGTTTTT  | ACAAGATAAC | GGCCGCATTG | TACTGAACGA | AGTCAATACT | 1300 |
| 20 | CTGCCCGGTT  | TCACGTCATA | CAGTCGTTAT | CCCCGTATGA | TGGCCGCTGC | 1350 |
|    | AGGTATTGCA  | CTTCCCGAAC | TGATTGACCG | CTTGATCGTA | TTAGCGTTAA | 1400 |
|    | AGGGGTGATA  | AGCATGGAAA | TAGGATTTAC | TTTTTTAGAT | GAAATAGTAC | 1450 |
|    | ACGGTGTTTCG | TTGGGACGCT | AAATATGCCA | CTTGGGATAA | TTTCACCGGA | 1500 |
|    | AAACCGGTTG  | ACGGTTATGA | AGTAAATCGC | ATTGTAGGGA | CATACGAGTT | 1550 |
| 25 | GGCTGAATCG  | CTTTTGAAGG | CAAAAGAACT | GGCTGCTACC | CAAGGGTACG | 1600 |
|    | GATTGCTTCT  | ATGGGACGGT | TACCGTCCTA | AGCGTGCTGT | AAACTGTTTT | 1650 |
|    | ATGCAATGGG  | CTGCACAGCC | GGAAAATAAC | CTGACAAAGG | AAAGTTATTA | 1700 |
|    | TCCCAATATT  | GACCGAACTG | AGATGATTTT | AAAAGGATAC | GTGGCTTCAA | 1750 |
|    | AATCAAGCCA  | TAGCCGCG   |            |            |            | 1768 |
| 30 |             |            |            |            |            |      |

## 2) INFORMATION FOR SEQ ID NO: 1140

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1086 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus casseliflavus*
- 45 (C) ACCESSION NUMBER: L29638
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140

|    |             |             |            |            |            |     |
|----|-------------|-------------|------------|------------|------------|-----|
|    | GTAAGAATCG  | GAAAAGCGGA  | AGGAAGAAAA | ACATGAAAAA | AATCGCCATT | 50  |
| 50 | ATTTTTGGAG  | GCAATTCACC  | GGAATACACC | GTTTCTTTAG | CTTCAGCAAC | 100 |
|    | TAGCGCAATC  | GAAGCACTCC  | AATCATCTCC | CTATGACTAC | GACCTCTCTT | 150 |
|    | TGATCGGGAT  | CGCCCCAGAT  | GCTATGGATT | GGTACTTGTA | TACAGGAGAA | 200 |
|    | CTGGAAAAACA | TCCGACAAGA  | CACGTGGTTG | TTGGATACGA | AACATAAACA | 250 |
|    | GAAAATACAG  | CCGCTATTTC  | AAGGAAACGG | CTTTTGGCTA | AGTGAAGAGC | 300 |
| 55 | AGCAAACGTT  | GGTACCTGAT  | GTTTTATTTC | CCATTATGCA | TGGCAAATAC | 350 |
|    | GGGGAAGATG  | GCAGTATCCA  | AGGATTGTTT | GAATTGATGA | AGCTGCCTTA | 400 |
|    | TGTAGGCTGC  | GGGGTGGCAG  | GTTCTGCCTT | ATGTATGAAC | AAATGGCTGC | 450 |
|    | TGCATCAAGC  | TGCAGCAGCC  | ATTGGCGTAC | AAAGTGCTCC | TACGATTCTC | 500 |
|    | TTGACAAATC  | AAGCCAACCA  | GCAAGAACAA | ATCGAAGCTT | TTATCCAGAC | 550 |
| 60 | CCATGGCTTC  | CCAGTTTTTCT | TTAAGCCTAA | TGAAGCGGGC | TCCTCAAAAG | 600 |

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | GGATCACTAA | AGTCACCTGC | GTTGAAGAAA | TCGCTTCTGC | CTTAAAAGAA | 650  |
|    | GCCTTTACTT | ATTGTTCCGC | AGTGCTCCTA | CAAAAAAATA | TTGCCGGTGT | 700  |
|    | TGAGATCGGT | TGCGGTATTT | TGGGCAACGA | CTCTTTGACT | GTCGGTGCTT | 750  |
|    | GTGACGCCAT | TTCATTAGTA | GACGGCTTTT | TCGATTTTGA | AGAAAAGTAC | 800  |
| 5  | CAGCTGATCA | GCGCCAAAAT | CACCGTCCCT | GCGCCATTGC | CTGAAACGAT | 850  |
|    | TGAAACCAAG | GTCAAAGAAC | AAGCTCAGCT | GCTCTATCGT | AGTCTTGCTC | 900  |
|    | TTAAAGGTCT | TGCTCGCATC | GACTTTTTTG | TCACGGAGCG | AGGAGAACTA | 950  |
|    | TACTTGAATG | AAATCAATAC | TATGCCGGGC | TTTACGAGTC | ACTCCCGCTA | 1000 |
|    | TCCTGCCATG | ATGGCAGCGG | TCGGCTTATC | CTATCAAGAA | CTACTACAAA | 1050 |
| 10 | AACTGCTTGT | CTTAGCAAAG | GAGGAAGTCA | AATGAG     |            | 1086 |

## 2) INFORMATION FOR SEQ ID NO: 1141

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3946 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 25 (B) STRAIN: BM4147  
 (C) ACCESSION NUMBER: extracted from M97297

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141

|    |             |            |            |            |             |      |
|----|-------------|------------|------------|------------|-------------|------|
| 30 | ATGAATAACA  | TCGGCATTAC | TGTTTATGGA | TGTGAGCAGG | ATGAGGCAGA  | 50   |
|    | TGCATTCCAT  | GCTCTTTCGC | CTCGCTTTGG | CGTTATGGCA | ACGATAATTA  | 100  |
|    | ACGCCAACGT  | GTCGGAATCC | AACGCCAAAT | CCGCGCCTTT | CAATCAATGT  | 150  |
|    | ATCAGTGTGG  | GACATAAATC | AGAGATTTCC | GCCTCTATTC | TTCTTGCGCT  | 200  |
|    | GAAGAGAGCC  | GGTGTGAAAT | ATATTTCTAC | CCGAAGCATC | GGCTGCAATC  | 250  |
| 35 | ATATAGATAC  | AACGTCTGCT | AAGAGAATTG | GCATCACTGT | CGACAATGTG  | 300  |
|    | GCGTACTCGC  | CGGATAGCGT | TGCCGATTAT | ACTATGATGC | TAATTTCTTAT | 350  |
|    | GGCAGTACGC  | AACGTAAAAT | CGATTGTGCG | CTCTGTGGAA | AAACATGATT  | 400  |
|    | TCAGGTTTGA  | CAGCGACCGT | GGCAAGGTAC | TCAGCGACAT | GACAGTTGGT  | 450  |
|    | GTGGTGGGAA  | CGGGCCAGAT | AGGCAAAGCG | GTTATTGAGC | GGCTGCGAGG  | 500  |
| 40 | ATTTGGATGT  | AAAGTGTGG  | CTTATAGTCG | CAGCCGAAGT | ATAGAGGTAA  | 550  |
|    | ACTATGTACC  | GTTTGATGAG | TTGCTGCAAA | ATAGCGATAT | CGTTACGCTT  | 600  |
|    | CATGTGCCGC  | TCAATACGGA | TACGCACTAT | ATTATCAGCC | ACGAACAAAT  | 650  |
|    | ACAGAGAATG  | AAGCAAGGAG | CATTTCTTAT | CAATACTGGG | CGCGGTCCAC  | 700  |
|    | TTGTAGATAC  | CTATGAGTTG | GTTAAAGCAT | TAGAAAACGG | GAAACTGGGC  | 750  |
| 45 | GGTGCCGCAT  | TGGATGTATT | GGAAGGAGAG | GAAGAGTTTT | TCTACTCTGA  | 800  |
|    | TTGCACCCAA  | AAACCAATTG | ATAATCAATT | TTTACTTAAA | CTTCAAAGAA  | 850  |
|    | TGCCTAACGT  | GATAATCACA | CCGCATACGG | CCTATTATAC | CGAGCAAGCG  | 900  |
|    | TTGCGTGATA  | CCGTTGAAAA | AACCAATAAA | AACTGTTTGG | ATTTTGAAAG  | 950  |
|    | GAGACAGGAG  | CATGAATAGA | ATAAAAGTTG | CAATACTGTT | TGGGGGTTGC  | 1000 |
| 50 | TCAGAGGAGC  | ATGACGTATC | GGTAAAATCT | GCAATAGAGA | TAGCCGCTAA  | 1050 |
|    | CATTAATAAA  | GAAAAATACG | AGCCGTTATA | CATTGGAATT | ACGAAATCTG  | 1100 |
|    | GTGTATGGAA  | AATGTGCGAA | AAACCTTGCG | CGGAATGGGA | AAACGACAAT  | 1150 |
|    | TGCTATTTCAG | CTGTACTCTC | GCCGGATAAA | AAAATGCACG | GATTACTTGT  | 1200 |
|    | TAAAAAGAAC  | CATGAATATG | AAATCAACCA | TGTTGATGTA | GCATTTTCAG  | 1250 |
| 55 | CTTTGCATGG  | CAAGTCAGGT | GAAGATGGAT | CCATACAAGG | TCTGTTTGAA  | 1300 |
|    | TTGTCCGGTA  | TCCCTTTTGT | AGGCTGCGAT | ATTCAAAGCT | CAGCAATTTG  | 1350 |
|    | TATGGACAAA  | TCGTTGACAT | ACATCGTTGC | GAAAAATGCT | GGGATAGCTA  | 1400 |
|    | CTCCCGCCTT  | TTGGGTTATT | AATAAAGATG | ATAGGCCGGT | GGCAGCTACG  | 1450 |
|    | TTTACCTATC  | CTGTTTTTGT | TAAGCCGGCG | CGTTCAGGCT | CATCCTTCGG  | 1500 |
| 60 | TGTGAAAAAA  | GTCAATAGCG | CGGACGAATT | GGACTACGCA | ATTGAATCGG  | 1550 |

|    |            |             |            |             |            |      |
|----|------------|-------------|------------|-------------|------------|------|
|    | CAAGACAATA | TGACAGCAAA  | ATCTTAATTG | AGCAGGCTGT  | TTCGGGCTGT | 1600 |
|    | GAGGTCGGTT | GTGCGGTATT  | GGGAAACAGT | GCCGCGTTAG  | TTGTTGGCGA | 1650 |
|    | GGTGGACCAA | ATCAGGCTGC  | AGTACGGAAT | CTTTCGTATT  | CATCAGGAAG | 1700 |
|    | TCGAGCCGGA | AAAAGGCTCT  | GAAAACGCAG | TTATAACCGT  | TCCCGCAGAC | 1750 |
| 5  | CTTTCAGCAG | AGGAGCGAGG  | ACGGATACAG | GAAACGGCAA  | AAAAAATATA | 1800 |
|    | TAAAGCGCTC | GGCTGTAGAG  | GTCTAGCCCC | TGTGGATATG  | TTTTTACAAG | 1850 |
|    | ATAACGGCCG | CATTGTACTG  | AACGAAGTCA | ATACTCTGCC  | CGGTTTCACG | 1900 |
|    | TCATACAGTC | GTTATCCCCG  | TATGATGGCC | GCTGCAGGTA  | TTGCACTTCC | 1950 |
|    | CGAACTGATT | GACCGCTTGA  | TCGTATTAGC | GTTAAAGGGG  | TGATAAGCAT | 2000 |
| 10 | GGAAATAGGA | TTTACTTTTT  | TAGATGAAAT | AGTACACGGT  | GTTCGTTGGG | 2050 |
|    | ACGCTAAATA | TGCCACTTGG  | GATAATTTCA | CCGGAAAACC  | GGTTGACGGT | 2100 |
|    | TATGAAGTAA | ATCGCATTGT  | AGGGACATAC | GAGTTGGCTG  | AATCGCTTTT | 2150 |
|    | GAAGGCAAAA | GAAGTGGCTG  | CTACCCAAGG | GTACGGATTG  | CTTCTATGGG | 2200 |
|    | ACGGTTACCG | TCCTAAGCGT  | GCTGTAAACT | GTTTTATGCA  | ATGGGCTGCA | 2250 |
| 15 | CAGCCGGAAA | ATAACCTGAC  | AAAGGAAAGT | TATTATCCCA  | ATATTGACCG | 2300 |
|    | AACTGAGATG | ATTTCAAAAAG | GATACGTGGC | TTCAAAAATCA | AGCCATAGCC | 2350 |
|    | GCGGCAGTGC | CATTGATCTT  | ACGCTTTATC | GATTAGACAC  | GGGTGAGCTT | 2400 |
|    | GTACCAATGG | GGAGCCGATT  | TGATTTTATG | GATGAACGCT  | CTCATCATGC | 2450 |
|    | GGCAAATGGA | ATATCATGCA  | ATGAAGCGCA | AAATCGCAGA  | CGTTTGCGCT | 2500 |
| 20 | CCATCATGGA | AAACAGTGGG  | TTTGAAGCAT | ATAGCCTCGA  | ATGGTGGCAC | 2550 |
|    | TATGTATTAA | GAGACGAACC  | ATACCCCAAT | AGCTATTTTG  | ATTTCCCCGT | 2600 |
|    | TAAATAAACT | TTTAACCGTT  | GCACGGACAA | ACTATATAAG  | CTAACTCTTT | 2650 |
|    | CGGCAGGAAA | CCCGACGTAT  | GTAACGGTT  | CTTAGGGAAT  | TTATATATAG | 2700 |
|    | TAGATAGTAT | TGAAGATGTA  | AGGCAGAGCG | ATATTGCGGT  | CATTATCTGC | 2750 |
| 25 | GTGCGCTGCG | GCAAGATAGC  | CTGATAATAA | GACTGATCGC  | ATAGAGGGGT | 2800 |
|    | GGTATTTTAC | ACCGCCCAT   | GTCAACAGGC | AGTTCAGCCT  | CGTTAAATTC | 2850 |
|    | AGCATGGGTA | TCACCTTATGA | AAATTCATCT | ACATTGGTGA  | TAATAGTAAA | 2900 |
|    | TCCAGTAGGG | CGAAATAAAT  | GACTGTAAAT | TACGGGGCAA  | AACGGCACAA | 2950 |
|    | TCTCAAACGA | GATTGTGCCG  | TTTAAGGGGA | AGATTCTAGA  | AATATTTTAT | 3000 |
| 30 | ACTTCCAAC  | ATATAGTTAA  | GGAGGAGACT | GAAAATGAAG  | AAGTTGTTTT | 3050 |
|    | TTTTATTGTT | ATTGTTATTC  | TTAATATACT | TAGGTTATGA  | CTACGTTAAT | 3100 |
|    | GAAGCACTGT | TTTCTCAGGA  | AAAAGTCGAA | TTTCAAAATT  | ATGATCAAAA | 3150 |
|    | TCCCAAAGAA | CATTTAGAAA  | ATAGTGGGAC | TTCTGAAAAT  | ACCCAAGAGA | 3200 |
|    | AAACAATTAC | AGAAGAACAG  | GTTTATCAAG | GAAATCTGCT  | ATTAATCAAT | 3250 |
| 35 | AGTAAATATC | CTGTTCCGCA  | AGAAAGTGTG | AAGTCAGATA  | TCGTGAATTT | 3300 |
|    | ATCTAAACAT | GACGAATTAA  | TAAATGGATA | CGGGTTGCTT  | GATAGTAATA | 3350 |
|    | TTTATATGTC | AAAAGAAATA  | GCACAAAAT  | TTTCAGAGAT  | GGTCAATGAT | 3400 |
|    | GCTGTAAAGG | GTGGCGTTAG  | TCATTTTATT | ATTAATAGTG  | GCTATCGAGA | 3450 |
|    | CTTTGATGAG | CAAAGTGTGC  | TTTACCAAGA | AATGGGGGCT  | GAGTATGCCT | 3500 |
| 40 | TACCAGCAGG | TTATAGTGAG  | CATAATTCAG | GTTTATCACT  | AGATGTAGGA | 3550 |
|    | TCAAGCTTGA | CGAAAATGGA  | ACGAGCCCCT | GAAGGAAAGT  | GGATAGAAGA | 3600 |
|    | AAATGCTTGG | AAATACGGGT  | TCATTTTACG | TTATCCAGAG  | GACAAAACAG | 3650 |
|    | AGTTAACAGG | AATTCAATAT  | GAACCATGGC | ATATTCGCTA  | TGTTGGTTTA | 3700 |
|    | CCACATAGTG | CGATTATGAA  | AGAAAAGAAT | TTCGTTCTCG  | AGGAATATAT | 3750 |
| 45 | GGATTACCTA | AAAGAAGAAA  | AAACCATTTC | TGTTAGTGTA  | AATGGGGAAA | 3800 |
|    | AATATGAGAT | CTTTTATTAT  | CCTGTTACTA | AAAATACCAC  | CATTCATGTG | 3850 |
|    | CCGACTAATC | TTCGTTATGA  | GATATCAGGA | AACAATATAG  | ACGGTGTAAT | 3900 |
|    | TGTGACAGTG | TTTCCCGGAT  | CAACACATAC | TAATTCAAGG  | AGGTAA     | 3946 |

50

## 2) INFORMATION FOR SEQ ID NO: 1142.

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 25 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142

GATCCTCTAA ATGATTCTCA GGTGG

25

2) INFORMATION FOR SEQ ID NO: 1143

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143

CAATTAGCTT AGCAATAGGT GTTGG

25

2) INFORMATION FOR SEQ ID NO: 1144

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144

TGTYTTCCAA GGTTTCAGCTC

20

2) INFORMATION FOR SEQ ID NO: 1145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145

AACATATTKG GTTGATAGGT

20

2) INFORMATION FOR SEQ ID NO: 1146

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146

GGGATTACCT ATGCCAATAT GAT

23

10

2) INFORMATION FOR SEQ ID NO: 1147

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147

AGCTGTGTTA GCVCGAACAT CTTG

24

25

2) INFORMATION FOR SEQ ID NO: 1148

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148

40

GACTTTGT TT GCGTGATAT

20

2) INFORMATION FOR SEQ ID NO: 1149

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149

55

TCCYACWATT TCTTTTGTGWG

20

60 2) INFORMATION FOR SEQ ID NO: 1150



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150

TGATAATCAC ACCGCATACG

20

2) INFORMATION FOR SEQ ID NO: 1151

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151

TGCTGTCATA TTGTCTTGCC

20

2) INFORMATION FOR SEQ ID NO: 1152

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152

ATAAAGATGA TAGGCCGGTG

20

2) INFORMATION FOR SEQ ID NO: 1153

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153

CTCGTATGTC CCTACAATGC

20

## 2) INFORMATION FOR SEQ ID NO: 1154

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154

GTTTGAAGCA TATAGCCTCG

20

## 2) INFORMATION FOR SEQ ID NO: 1155

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155

CAGTGCTTCA TTAACGTAGT C

21

## 2) INFORMATION FOR SEQ ID NO: 1156

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156

GTTGAAATGC ATCACGAACA ATT

23

## 2) INFORMATION FOR SEQ ID NO: 1157

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157

AAGAACGTTT CAGTTAAGGA AAT

23

5

2) INFORMATION FOR SEQ ID NO: 1158

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158

20 AAGAGGTAAT GTCTGTGGT

19

2) INFORMATION FOR SEQ ID NO: 1159

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159

35

TGAAGGTTTG CCAGGTGA

18

40 2) INFORMATION FOR SEQ ID NO: 1160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1160

50

CGTTTCTGTT AAAGAAATTA GAAG

24

55

2) INFORMATION FOR SEQ ID NO: 1161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid

60

637

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161

TCCAGGTGAT AACGTTGG

18

2) INFORMATION FOR SEQ ID NO: 1162

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162

CAAGTCCGTG GAAATGCA

18

2) INFORMATION FOR SEQ ID NO: 1163

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1163

GTTGGTTTCA ACGTTAAGAA C

21

2) INFORMATION FOR SEQ ID NO: 1164

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164

GGTTTCAACG TCAAGAAC

18

2) INFORMATION FOR SEQ ID NO: 1165

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165

GGTTTCAACG TGAAGAAC

## 2) INFORMATION FOR SEQ ID NO: 1166

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166

ACGTTAAGAA TGTTTCTGTC AA

## 2) INFORMATION FOR SEQ ID NO: 1167

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167

GTTGGTTTCA ACGT

## 2) INFORMATION FOR SEQ ID NO: 1168

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168

GAACAATTGG TTGAAGGTGT

## 2) INFORMATION FOR SEQ ID NO: 1169

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: SP-665  
 (C) ACCESSION NUMBER: AF139883

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169

|    |            |            |            |            |             |      |
|----|------------|------------|------------|------------|-------------|------|
| 20 | ATGAACAAAC | CAACGATTCT | GCGCCTAATC | AAGTATCTGA | GCATTAGCTT  | 50   |
|    | CTTAAGCTTG | GTTATCGCAG | CCATTGTCTT | AGGCGGAGGA | GTTTTTTTCT  | 100  |
|    | ACTACGTTAG | CAAGGCTCCT | AGCCTATCCG | AGAGTAAACT | AGTTGCAACA  | 150  |
|    | ACTTCTAGTA | AAATCTACGA | CAATAAAAAT | CAACTCATTG | CTGACTTGGG  | 200  |
| 25 | TTCTGAACGC | CGCGTCAATG | CCCAAGCTAA | TGATATTCCC | ACAGATTTGG  | 250  |
|    | TTAAGGCAAT | CGTTTCTATC | GAAGACCATC | GCTTCTTCGA | CCACAGGGGG  | 300  |
|    | ATTGATTCCA | TCCGTATCCT | GGGAGCTTTC | TTGCGCAATC | TGCAAAGTAA  | 350  |
|    | TTCCCTCCAA | GGTGGATCAA | CTCTCACCCA | ACAGTTGATT | AAGTTGACTT  | 400  |
|    | ACTTTTCAAC | CTCGACTTCC | GACCAGACTA | TTTCTCGTAA | GGCTCAGGAA  | 450  |
| 30 | GCTTGGTTAG | CGATTTCAGT | AGAACAAAAA | GCAACCAAAC | AGGAAATCTT  | 500  |
|    | GACCTACTAT | ATAAATAAGG | TCTACATGTC | TAATGGCAAC | TATGGAATGC  | 550  |
|    | AGACAGCAGC | TCAAAACTAC | TATGGTAAAG | ACCTCAATAA | TTTAAGTTTA  | 600  |
|    | CCTCAGTTAG | CCTTGCTGGC | TGGAATGCCT | CAGGCACCAA | ACCAATATGA  | 650  |
|    | CCCTGATTCA | CATCCAGAAG | CAGCCCAAGA | CCGCCGAAAC | TTGGTCTTAT  | 700  |
| 35 | CTGAAATGAA | AAATCAAGGT | TACATCTCTG | CTGAACAGTA | TGAGAAAGCA  | 750  |
|    | GTCAATACAC | CAATTACTGA | TGGACTACAA | AGTCTCAAAT | CAGCAAGTAA  | 800  |
|    | TTACCCTGCT | TACATGGATA | ATTACCTCAA | GGAGGTCATC | AATCAAGTAG  | 850  |
|    | AACAAGAAAC | TGGCTATAAC | CTTCTAACTA | CTGGGATGGA | TGTTTACACA  | 900  |
|    | AATGTAGACC | AAGAAGCTCA | AAAACATCTG | TGGGATATCT | ACAACTCCGA  | 950  |
| 40 | TCAATACGTC | TCTTACCCTG | ACGATGATTT | GCAAGTCGCA | TCTACGGTCG  | 1000 |
|    | TAGATGTTTC | AAATGGTAAA | GTCATCGCCC | AACCTGGAGC | TCGTCACCAA  | 1050 |
|    | GCAAGTAAAC | TTTCATTTGG | TACCAACCAA | GCTGTGGAAA | CCAATCGTGA  | 1100 |
|    | CTGGGGTTCT | GCTATGAAAC | CAATCACCGA | TTATGCACCT | GCCATAGAAT  | 1150 |
|    | ACGGTGTTTA | TGATTCCACT | GCAACTATGG | TTAATGATAT | TCCTTATAAC  | 1200 |
| 45 | TATCCGGGAA | CAAGCACACC | TGTCTACAAC | TGGGATAGAG | CATATTTTCGG | 1250 |
|    | TAATATTACT | CTGCAATATG | CTCTTCAACA | ATCACGAAAT | GTCACAGCCG  | 1300 |
|    | TTGAGACTTT | GAATAAGGTC | GGTCTAGATA | GAGCTAAAAC | CTTCCTTAAT  | 1350 |
|    | GGTCTTGTTA | TCGACTATCC | AAGCATGCAT | TATGCAAACG | CCATTTCAAG  | 1400 |
|    | TAATACAACA | GAATCTAATA | AACAATACGG | AGCAAGTAGT | GAAAAAATGG  | 1450 |
| 50 | CTGCTGCTTA | TGCTGCCTTT | GCAAATGGTG | GCACTTACTA | TAAACCAATG  | 1500 |
|    | TATATCCATA | AAGTCGTCTT | CAGTGATGGA | AGTAAAAAAG | AGTTCTCTAA  | 1550 |
|    | TGTCGGAAC  | CGTGCCATGA | AGGAAACGAC | AGCCTATATG | ATGACCGACA  | 1600 |
|    | TGATGAAAAC | AGTCTTGACT | TATGGAAC   | GGCGTGGAGC | CTATCTTCCT  | 1650 |
|    | TGGCTTCCTC | AAGCTGGTAA | AACAGGAACC | TCTAACTATA | CAGATGAGGA  | 1700 |
| 55 | AGTTGAAAAC | CACATCAAGA | ACACTGGCTA | TGTAGCTCCA | GATGAAATGT  | 1750 |
|    | TTGTTGGTTA | TACTCGTAAG | TATTCTATGG | CTGTATGGAC | AGGTTATTCTG | 1800 |
|    | AATCGTTTAA | CTCCTATCGT | TGGAGATGGT | TTCTAGTTG  | CAGCTAAAGT  | 1850 |
|    | TTATCGCTCA | ATGATAACGT | ATCTATCAGA | AGATACTCAT | CCAGAAGACT  | 1900 |
|    | GGACGATGCC | AGACGGACTT | TTCAGAAACG | GGGAATTTGT | ATTCAAAAAT  | 1950 |
| 60 | GGAGCTCGCC | CAATATGGAC | TGAACCCTCT | ACTCAACAAT | CCTCAACAGC  | 2000 |

|            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------|
| TGAAAGTTCA | AGCTCATCAT | CAGATAGTTC | AACTTCACAG | TCTAGCTCAA | 2050 |
| CCACTCCAAG | CACAAATAAT | AGTACGACTA | CCAATCCTAA | CAATAATACG | 2100 |
| CAACAATCAA | ATACAACCCC | TGATCAACAA | AATCAGAATC | CTCAACCAGC | 2150 |
| ACAACCATAA |            |            |            |            | 2160 |

5

## 2) INFORMATION FOR SEQ ID NO: 1170

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170

20 ACGAATTGGA CTACGCAATT

20

## 2) INFORMATION FOR SEQ ID NO: 1171

25

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171

35

ACGAGGATGA TTTGATTGTC

20

## 40 2) INFORMATION FOR SEQ ID NO: 1172

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1560 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
(B) STRAIN: 64147  
(C) ACCESSION NUMBER: X13136

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| GATCCTCTAA    | ATGATTCTCA | GGTGGCTGTT | ATTGCCTCTA | TTTCAAAGGA | 50  |
| GATGCCTGGC    | ATTAGTATTT | CTACTTCTTG | GGATAGAAAG | GTTTTGGAAA | 100 |
| CTTCCCTTTC    | TTCTATAGTT | GGGAGTGTAT | CCAGTGAAAA | AGCTGGTCTC | 150 |
| 60 CCAGCGGAAG | AAGCAGAAGC | CTATCTTAA  | AAAGGCTATT | CTCTAAATGA | 200 |

641

|    |             |            |            |             |            |      |
|----|-------------|------------|------------|-------------|------------|------|
|    | CCGTGTAGGA  | ACCTCCTATT | TGGAAAAGCA | ATATGAAGAG  | ACCTTACAAG | 250  |
|    | GAAAACGCTC  | GGTAAAAGAA | ATCCATCTGG | ACAAATATGG  | CAACATGGAA | 300  |
|    | AGCGTGGATA  | CAATTGAGGA | AGGTAGTAAG | GGAAACAATA  | TCAAGCTGAC | 350  |
|    | CATTGATTTG  | GCCTTCCAAG | ATAGCGTGGA | TGCTTTGCTG  | AAAAGTTATT | 400  |
| 5  | TCAATTGAGA  | GTTGGGAAAT | GGTGGAGCCA | AGTATTCTGA  | AGGTGTCTAT | 450  |
|    | GCAGTCGCC   | TTAACCCAAA | AACAGGTGCT | GTTTGTCTA   | TGTCAGGAAT | 500  |
|    | TAAACATGAC  | TTGAAAACAG | GAGAGTTGAC | GCCGGATTCC  | TTGGGAACGG | 550  |
|    | TAACCAATGT  | CTTTGTCCCA | GGTTCGGTTG | TCAAAGCAGC  | GACCATCAGC | 600  |
|    | TCTGGTTGGG  | AAAATGGAGT | CTTGTGAGGA | AATCAGACCT  | TGACAGACCA | 650  |
| 10 | GTCCATTGTC  | TTTCAAGGTT | CAGCTCCAAT | TAATTCTTGG  | TATCCTGCCT | 700  |
|    | TTTCTAGACC  | AATGCCGATT | ACGGCGGTTT | AGGCTCTAGA  | GTATTCATCC | 750  |
|    | AATGCTTATA  | TGGTCCAAAC | AGCCCTAGGT | CTTATGGGGC  | AGACCTATCA | 800  |
|    | ACCCAATATG  | TTTGTGCGCA | CCAGCAATCT | AGAGTCTGCT  | ATGGGGAAAT | 850  |
|    | TGCGTTCAAC  | CTTTGGTGAA | TATGGTTTGG | GTTCTGCGAC  | CGGAATTGAC | 900  |
| 15 | CTACCAGATG  | AATCTACTGG | ATTTGTTCCC | AAAGAGTATA  | GCTTTGCTAA | 950  |
|    | TTTCATTACC  | AATGCCTTTG | GGCAGTTTGA | TAACCTATACG | CCGATGCAGT | 1000 |
|    | TGGCTCAGTA  | TGTAGCAACT | ATTGCAAATG | ATGGTGTTTCG | TGTGGCTCCT | 1050 |
|    | CGTATTGTTG  | AAGGCATTTA | TGGTAATAAT | GATAAGGGAG  | GACTGGGTGA | 1100 |
|    | CTTGATTTCAG | CAACTGCAAC | CGACAGAGAT | GAATAAGGTC  | AATATATCCG | 1150 |
| 20 | ACTCCGATAT  | GAGCATCTTG | CACCAAGGTT | TTTATCAGGT  | TGCCCATGGT | 1200 |
|    | ACTAGTGAAT  | TGACAACTGG | ACGTGCCTTT | TCAAATGGCG  | CCTTGGTATC | 1250 |
|    | CATTAGCGGA  | AAAACAGGTA | CAGCCGAAAG | CTATGTGGCA  | GATGGTCAGC | 1300 |
|    | AAGCAACCAA  | TACCAATGCG | GTGGCCTATG | CCCCATCTGA  | TAATCCCCAA | 1350 |
|    | ATCGCTGTAG  | CTGTTGTCTT | CCCTCATAAC | ACCAACCTTA  | CAAATGGTGT | 1400 |
| 25 | CGGACCTTCC  | ATTGCGCGCG | ATATTATCAA | CCTCTATAAC  | CAACATCATC | 1450 |
|    | CAATGAATTA  | GAAAGGAACA | TATGCTTTAT | CCAACACCTA  | TTGCTAAGCT | 1500 |
|    | AATTGACAGT  | TATTCGAAGT | TACCGGGTAT | CGGGATTAAG  | ACGGCTACCC | 1550 |
|    | GTTTGGCCTT  |            |            |             |            | 1560 |

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## 2) INFORMATION FOR SEQ ID NO: 1173

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2007 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 40 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: CS109  
 45 (C) ACCESSION NUMBER: Z49096

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173

|    |            |             |            |            |            |     |
|----|------------|-------------|------------|------------|------------|-----|
|    | GAGTCCCGAT | TGCTGAGGAT  | GCAACCTCCT | ATAATGTCTA | TGCGGTCATT | 50  |
| 50 | GATGAGAACT | ATAAGTCAGC  | AACGGGTAAG | ATTCTTTACG | TAGAAAAAAC | 100 |
|    | ACAATTTAAC | AAGGTTGCAG  | AGGTCTTTCA | TAAGTATCTG | GACATGGAAG | 150 |
|    | AATCCTATGT | AAGAGAGCAA  | CTCTCGCAAC | CTAATCTCAA | GCAAGTTTCC | 200 |
|    | TTTGGAGCAA | AGGGAAATGG  | GATTACCTAT | GCCAATATGA | TGACTATCAA | 250 |
|    | AAAAGAGTTG | GAAACTGCAG  | AGGTCAAGGG | GATTGATTTT | ACAACCAGTC | 300 |
| 55 | CCAATCGTAG | TTATCCAAAC  | GGACAATTTG | CTTCTAGTTT | TATCGGTCTA | 350 |
|    | GCTCAGCTCC | ATGAAAATGA  | AGATGGCAGC | AAGAGCTTGC | TGGGAACCTC | 400 |
|    | TGGAATGGAG | AGTTCCCTTGA | ACAGTATTCT | TGCAGGGACA | GACGGCATTG | 450 |
|    | TTACCTATGA | AAAGGATCGT  | CTGGGCAATA | TTGTACCCGG | AACAGAACTG | 500 |
|    | GTATCGCAAC | AAACTGTGGA  | TGGCAAGGAT | GTTTATACAA | CATTGTCTAG | 550 |
| 60 | TCCGCTACAA | TCTTTCATGG  | AAACTCAGAT | GGATGCCTTT | CTAGAAAAAG | 600 |



|    |            |            |             |            |             |      |
|----|------------|------------|-------------|------------|-------------|------|
|    | TAAAAGGTAA | GTATATGACC | GCGACCTTGG  | TCAGTGCAAA | GACCGGTGAA  | 650  |
|    | ATTCTCGCTA | CCACCCAACG | ACCTACCTTT  | AATGCAGATA | CTAAAGAAGG  | 700  |
|    | AATCACTGAG | GACTTTGTTT | GGCGTGATAT  | TCTTTATCAA | AGTAACTATG  | 750  |
|    | AACCAGGATC | AGCCTTTAAG | GTCATGATGT  | TAGCTTCTTC | TATTGATAAT  | 800  |
| 5  | AATACCTTCC | CAAGTGGAGA | ATACTTCAAT  | AGCAGTGAAT | TCAAAATAGC  | 850  |
|    | GGATGCGACG | ACTCGAGATT | GGGATGTTAA  | TGAGGGTTTG | ACTACTGGTG  | 900  |
|    | GGATGATGAC | TTTCTCACAA | GGTTTCGCTC  | ACTCCAGTAA | TGTTGGAACG  | 950  |
|    | AGTCTACTTG | AACAAAAAAT | GGGAGATGCT  | ACTTG GTTG | ATTATCTAAA  | 1000 |
|    | ACGCTTTAAA | TTTGGGGTTC | CAACTCGCTT  | TGGCTTGACA | GATGAATACG  | 1050 |
| 10 | CTGGTCAACT | TCCAGCTGAT | AATATTGTTA  | GTATTGCTCA | AAGCTCATTT  | 1100 |
|    | GGGCAAGGAA | TTTCAGTGAC | ACAAACACAA  | ATGCTTCGTG | CCTTTACAGC  | 1150 |
|    | TATTGCTAAT | GATGGAGTTA | TGCTGGAGCC  | AAAATTTATA | AGTGCTATTT  | 1200 |
|    | ATGATACTAA | CAATCAGTCT | GTACGTAAGT  | CACAAAAAGA | AATAGTAGGA  | 1250 |
|    | AATCCTGTTT | CCAAAGAGGC | AGCAAGCACA  | ACTCGAAATC | ACATGATCTT  | 1300 |
| 15 | AGTTGGGACG | GACCTCTAT  | ATGGAAGTAT  | GTATAATCAC | TACACAGGAA  | 1350 |
|    | AGCCAATTAT | AACAGTTCCT | GGACAAAATG  | TAGCAGTTAA | ATCCGGTACG  | 1400 |
|    | GCTCAAATCG | CTGATGAGAA | AAATGGAGGA  | TACTTGGTTG | GTTCTACCAA  | 1450 |
|    | TTATATTTTC | TCAGTTGTGA | CTATGAATCC  | TGCTGAAAAT | CCTGATTTTA  | 1500 |
|    | TCTTGATATG | AACGGTTCAA | CAGCCTGAGC  | ATTATTCAGG | TATCCAGTTG  | 1550 |
| 20 | GGAGAATTTG | CCACCCCAAT | CTTGGAGCGG  | GCTTCAGCTA | TGAAAGAATC  | 1600 |
|    | TCTCAATCTT | CAATCTCCAG | CCAAAATTT   | AGATAAAGTT | ACGACAGAAT  | 1650 |
|    | CTTCTTATGC | AATGCCTAGC | ATCAAAGGATA | TTTCACCTGG | TGAGTTGGCG  | 1700 |
|    | GAAGCCTTAC | GCCGAAATAT | TGTGCAACCA  | ATCGTTGTAG | GTA CTGGAAC | 1750 |
|    | AAAGATTAAA | GAGACTTCTG | TAGAAGAAGG  | GACCAATCTT | GCACCAAACC  | 1800 |
| 25 | AACAAGTTCT | CCTTTTATCG | GATAAGGTAG  | AAGAAATTCC | AGACATGTAT  | 1850 |
|    | AGCTGGAAAA | AAGAGACTGC | CGAGACCTTT  | GCTAAATGGT | TGGATATTGA  | 1900 |
|    | ACTGGAATTT | GAAGGTTTCA | GTTCCGTTGT  | TCAGAAGCAA | GATGTTTCGGA | 1950 |
|    | CTAATACAGC | TATCAAAAAC | ATTAAAAAAA  | TTAAATTAAC | TTTAGGAGAC  | 2000 |
| 30 | TAATATG    |            |             |            |             | 2007 |

## 2) INFORMATION FOR SEQ ID NO: 1174

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174

45 GAACGTGGTG AAGTTCGC

18

## 2) INFORMATION FOR SEQ ID NO: 1175

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175

60

5 2) INFORMATION FOR SEQ ID NO: 1176

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 19 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176

TACTGGTGTA GAAATGTTC

19

20 2) INFORMATION FOR SEQ ID NO: 1177

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177

GCTCAACAAG TTCCAGATTA

20

35 2) INFORMATION FOR SEQ ID NO: 1178

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 2456 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus  
(B) STRAIN: NCTC8325  
50 (C) ACCESSION NUMBER: X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| ATGAACTGAT    | TATACTTAAC | ATTAAAAAAG | ATGATAACAC | CTTCTACACC | 50  |
| 55 TCCATATCAC | AAAAAATTAT | AACATTATTT | TGACATAAAT | ACTACATTTG | 100 |
| TAATATACTA    | CAAATGTAGT | CTTATATAAG | GAGGATATTG | ATGAAAAAGA | 150 |
| TAAAAATTGT    | TCCACTTATT | TTAATAGTTG | TAGTTGTCGG | GTTTGGTATA | 200 |
| TATTTTATG     | CTTCAAAAGA | TAAAGAAATT | AATAATACTA | TTGATGCAAT | 250 |
| TGAAGATAAA    | AATTTCAAAC | AAGTTTATAA | AGATAGCAGT | TATATTTCTA | 300 |
| 60 AAAGCGATAA | TGGTGAAGTA | GAAATGACTG | AACGTCCGAT | AAAAATATAT | 350 |

|    |          |       |      |      |      |      |      |      |     |      |     |     |      |      |
|----|----------|-------|------|------|------|------|------|------|-----|------|-----|-----|------|------|
|    | AATAGTTT | AG    | CGT  | TAA  | AG   | TATA | AA   | CATT | CAG | GAT  | CG  | TAA | AAAA | 400  |
|    | AGTATCT  | AA    | ATA  | AAAA | AA   | CAG  | TAG  | AT   | GC  | TCA  | AT  | ATA | AAAA | 450  |
|    | ACTACGG  | TAA   | CATT | GAT  | CG   | AA   | CG   | TT   | CA  | AT   | T   | TT  | GT   | 500  |
|    | GGTATGT  | GGA   | AG   | TTAG | ATT  | GG   | AT   | CA   | TAG | GC   | GT  | CA  | TAT  | 550  |
| 5  | GAAAGAC  | CAA   | AG   | CATA | CATA | TT   | GAAA | AT   | TT  | AAA  | AT  | CAG | AA   | 600  |
|    | TTTTAG   | ACCG  | AA   | CA   | AT   | GT   | GA   | AT   | TG  | CC   | CA  | AT  | AC   | 650  |
|    | TTAGGC   | ATCG  | TT   | CC   | AA   | AG   | AA   | AG   | AT  | TATA | AA  | GC  | AT   | 700  |
|    | TAAAGA   | ACTA  | AG   | TAT  | TT   | CT   | GA   | CT   | TAT | AT   | CA  | AC  | AA   | 750  |
|    | TTGGGT   | TACAA | GAT  | GAT  | AC   | CT   | TC   | GT   | TT  | CC   | ACT | TT  | AA   | 800  |
| 10 | GATGAAT  | ATT   | TA   | AG   | TG   | AT   | TT   | TA   | CT  | CT   | TA  | CT  | TA   | 850  |
|    | AACAGAA  | AGT   | CG   | TA   | ACT  | AT   | CT   | CT   | AG  | AA   | AA  | AG  | CT   | 900  |
|    | GTTATGT  | TGG   | TCC  | CA   | TT   | AA   | TCT  | G    | A   | AG   | AA  | T   | AA   | 950  |
|    | GGCTATA  | AAAG  | AT   | GAT  | GC   | AG   | TAT  | TG   | G   | T    | AA  | AA  | AA   | 1000 |
|    | CGATAAA  | AAAG  | CT   | CC   | A    | CA   | TG   | CT   | AA  | AG   | AT  | GC  | T    | 1050 |
| 15 | ATAATAG  | CAA   | TAC  | AT   | CG   | CA   | CAT  | AT   | T   | AA   | TA  | TA  | GA   | 1100 |
|    | GGCAAAG  | ATA   | TT   | CA   | ACT  | AA   | TAT  | TG   | AT  | GC   | T   | AA  | AA   | 1150 |
|    | TAACAAC  | ATG   | AAAA | AT   | G    | AT   | TG   | GC   | T   | CA   | AG  | CT  | AT   | 1200 |
|    | CAGGTGA  | ATT   | ATT  | AG   | CA   | CT   | G    | T    | AA  | GC   | AC  | AC  | CT   | 1250 |
|    | TTTATGT  | ATG   | GC   | AT   | G    | AG   | T    | AA   | TA  | TA   | TA  | TA  | TA   | 1300 |
| 20 | AAAAGA   | AAC   | CT   | G    | CT   | CA   | CA   | AG   | T   | CC   | AG  | AT  | TA   | 1350 |
|    | CTCAAAA  | AT    | TT   | AA   | C    | AG   | CA   | AT   | G   | T    | TG  | G   | AT   | 1400 |
|    | GATAAAA  | CAA   | G    | T    | T    | AA   | AA   | CG   | AT  | TG   | G   | CA  | AA   | 1450 |
|    | TTGGGG   | TGGT  | TAC  | A    | AC   | G    | TT   | CA   | AG  | AT   | TA  | TA  | TA   | 1500 |
|    | ACTTAAA  | ACA   | AG   | CA   | AT   | AG   | AA   | TC   | AT  | CA   | GA  | TA  | TA   | 1550 |
| 25 | GCACTCG  | AAT   | TAG  | G    | C    | AG   | T    | AA   | TT  | TG   | AA  | AA  | AA   | 1600 |
|    | TGTTGGT  | GAA   | GAT  | ATA  | CC   | AA   | GT   | G    | AT  | T    | AT  | CC  | AT   | 1650 |
|    | CAAACAAA | AAA   | TT   | T    | AG   | ATA  | AT   | G    | AA  | T    | AT  | T   | AT   | 1700 |
|    | CAAGGTG  | AAA   | TAC  | T    | G    | AT   | T    | AA   | CCC | AG   | T   | AC  | AG   | 1750 |
|    | ATTAGAA  | AA    | AAT  | G    | G    | CA   | TA   | TT   | AA  | CG   | CA  | CC  | AT   | 1800 |
| 30 | AAAACAA  | AGT   | TT   | G    | G    | A    | G    | AA   | AA  | AA   | AA  | TA  | TA   | 1850 |
|    | TTAAATG  | ATG   | GT   | AT   | G    | CA   | CA   | AG   | T   | CG   | TA  | AA  | TA   | 1900 |
|    | TTATAG   | AT    | T    | AT   | G    | CA   | AA   | CT   | TA  | AT   | TG  | G   | CA   | 1950 |
|    | AAATGAA  | ACA   | AG   | G    | A    | G    | AA   | AG   | T   | G    | G   | CA  | CA   | 2000 |
|    | GATAAAG  | ATA   | AT   | CC   | AA   | AC   | AT   | G    | AT  | TG   | G   | CT  | AT   | 2050 |
| 35 | AGATAAG  | GGA   | AT   | G    | G    | CT   | AG   | CT   | AA  | TC   | AG  | GT  | AT   | 2100 |
|    | ATGAGCT  | ATA   | TG   | AG   | AA   | CG   | GT   | AA   | TA  | AA   | AA  | AT  | TA   | 2150 |
|    | AACAGTG  | AAG   | CA   | AT   | CC   | G    | T    | AA   | CG  | AT   | TG  | GT  | GC   | 2200 |
|    | TATTAAT  | AAG   | TG   | CT   | G    | T    | T    | ACT  | T   | AA   | AT  | TT  | TC   | 2250 |
|    | TTGTATG  | TG    | AA   | AG   | TG   | AC   | AC   | CC   | AT  | TT   | T   | CT  | TT   | 2300 |
| 40 | TTTCTT   | AT    | TT   | CT   | T    | CT   | AG   | CG   | AT  | AA   | CG  | TA  | CA   | 2350 |
|    | AGTTTAA  | TAA   | AT   | TT   | AA   | CG   | TT   | AT   | T   | CA   | TT  | TG  | TC   | 2400 |
|    | TCCGTAT  | TTA   | C    | T    | T    | CT   | CT   | CC   | CA  | T    | AA  | TT  | AA   | 2450 |
|    | GCATGC   |       |      |      |      |      |      |      |     |      |     |     |      | 2456 |

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## 2) INFORMATION FOR SEQ ID NO: 1179

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 20 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## 55 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179

ATTTGGTGAC GGGTGACTTT

60

20

## 2) INFORMATION FOR SEQ ID NO: 1180

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180

15 TCCACCGTTG CCAATCGCA

19

## 2) INFORMATION FOR SEQ ID NO: 1181

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181

30 AGCAGCTTAC TAGATGCCGT

20

## 2) INFORMATION FOR SEQ ID NO: 1182

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
40 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182

AACTGCAAGA GATCCTTTGG

20

## 2) INFORMATION FOR SEQ ID NO: 1183

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2535 bases  
(B) TYPE: Nucleic acid  
55 (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: 175  
 (C) ACCESSION NUMBER: M18729

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## (xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1183

|    |            |             |             |             |             |      |
|----|------------|-------------|-------------|-------------|-------------|------|
|    | ATGGCGATAG | AAAAGCTATC  | ACCCGGCATG  | CAACAGTATG  | TGGATATTAA  | 50   |
| 10 | AAAGCAATAT | CCAGATGCTT  | TTTTGCTCTT  | TCGGATGGGT  | GATTTTTTATG | 100  |
|    | AATTATTTTA | TGAGGATGCG  | GTCAATGCTG  | CGCAGATTCT  | GGAAATTTCC  | 150  |
|    | TTAACGAGTC | GCAACAAGAA  | TGCCGACAAT  | CCGATCCCTA  | TGGCGGGTGT  | 200  |
|    | TCCCTATCAT | TCTGCCCAAC  | AGTATATCGA  | TGTCTTGATT  | GAGCAGGGTT  | 250  |
|    | ATAAGGTGGC | TATCGCAGAG  | CAGATGGAAG  | ATCCTAAACA  | AGCAGTTGGG  | 300  |
| 15 | GTTGTAAAC  | GAGAGGTTGT  | TCAGGTCATT  | ACGCCAGGGA  | CAGTGGTCTGA | 350  |
|    | TAGCAGTAAG | CCGGACAGTC  | AGAATAATTT  | TTTGGTTTCC  | ATAGACCGCG  | 400  |
|    | AAGGCAATCA | ATTTGGCCTA  | GCTTATATGG  | ATTTGGTGAC  | GGGTGACTTT  | 450  |
|    | TATGTGACAG | GTCTTTTGA   | TTTCACGCTG  | GTTTGTGGGG  | AAATCCGTAA  | 500  |
|    | CCTCAAGGCT | CGAGAAGTGG  | TGTTGGGTTA  | TGACTTGTCT  | GAGGAAGAAG  | 550  |
| 20 | AACAAATCCT | CAGCCGCCAG  | ATGAATCTGG  | TACTCTCTTA  | TGAAAAAGAA  | 600  |
|    | AGCTTTGAAG | ACCTTCATTT  | ATTGGATTG   | CGATTGGCAA  | CGGTGGAGCA  | 650  |
|    | AACGGCATCT | AGTAAGCTGC  | TCCAGTATGT  | TCATCGGACT  | CAGATGAGGG  | 700  |
|    | AATTGAACCA | CCTCAAACCT  | GTTATCCGCT  | ACGAAATTAA  | GGATTTCTTG  | 750  |
|    | CAGATGGATT | ATGCGACCAA  | GGCTAGTCTG  | GATTTGGTTG  | AGAATGCTCG  | 800  |
| 25 | CTCAGGTAAG | AAACAAGGCA  | GTCTTTTCTG  | GCTTTTGGAT  | GAAACCAAAA  | 850  |
|    | CGGCTATGGG | GATGCGTCTC  | TTGCGTTCTT  | GGATTCATCG  | CCCCTTGATT  | 900  |
|    | GATAAGGAAC | GAATCGTCCA  | ACGTCAAGAA  | GTAGTGCAGG  | TCTTTCTCGA  | 950  |
|    | CCATTTCTTT | GAGCGTAGTG  | ACTTGACAGA  | CAGTCTCAAG  | GGTGTTTTATG | 1000 |
|    | ACATTGAGCG | CTTGGCTAGT  | CGTGTTTCTT  | TTGGCAAAAC  | CAATCCAAAG  | 1050 |
| 30 | GATCTCTTGC | AGTTGGCGAC  | TACCTTGTCT  | AGTGTGCCAC  | GGATTCGTGC  | 1100 |
|    | GATTTTAGAA | GGGATGGAGC  | AACCTACTCT  | AGCCTATCTC  | ATCGCACAAAC | 1150 |
|    | TGGATGCAAT | CCCTGAGTTG  | GAGAGTTTGA  | TTAGCGCAGC  | GATTGCTCCT  | 1200 |
|    | GAAGCTCCTC | ATGTGATTAC  | AGATGGGGGA  | ATTATCCGGA  | CTGGATTTGA  | 1250 |
|    | TGAGACTTTA | GACAAGTATC  | GTTGCGTTCT  | CAGAGAAGGG  | ACTAGCTGGA  | 1300 |
| 35 | TTGCTGAGAT | TGAGGCTAAG  | GAGCGAGAAA  | ACTCTGGTAT  | CAGCAGCTC   | 1350 |
|    | AAGATTGACT | ACAATAAAAA  | GGATGGCTAC  | TATTTTCATG  | TGACCAATTG  | 1400 |
|    | GCAACTGGGA | AATGTGCCAG  | CCCACTTTTT  | CCGCAAGGCG  | ACGCTGAAAA  | 1450 |
|    | ACTCAGAACG | CTTTGGAACC  | GAAGAATTAG  | CCCGTATCGA  | GGGAGATATG  | 1500 |
|    | CTTGAGGCGC | GTGAGAAGTC  | AGCCAACCTC  | GAATACGAAA  | TATTTATGCG  | 1550 |
| 40 | CATTCGTGAA | GAGGTCGGCA  | AGTACATCCA  | GCGTTTACAA  | GCTCTAGCCC  | 1600 |
|    | AAGGAATTGC | GACGGTTGAT  | GTCTTACAGA  | GTCTGGCGGT  | TGTGGCTGAA  | 1650 |
|    | ACCCAGCATT | TGATTTCGACC | TGAGTTTGGT  | GACGATTCAC  | AAATTGATAT  | 1700 |
|    | CCGGAAAGGG | CGCCATGCTG  | TCGTTGAAAA  | GGTTATGGGG  | GCTCAGACCT  | 1750 |
|    | ATATTCCAAA | TACGATTTCAG | ATGGCAGAAG  | ATACCAAGTAT | TCAATTGGTT  | 1800 |
| 45 | ACAGGGCCAA | ACATGAGTGG  | GAAGTCTACC  | TATATGCGTC  | AGTTAGCCAT  | 1850 |
|    | GACGGCGGTT | ATGGCCCAGC  | TGGGTTCCCTA | TGTTCCCTGCT | GAAAGCGCCC  | 1900 |
|    | ATTTACCGAT | TTTTGATGCG  | ATTTTTACCC  | GTATCGGAGC  | AGCAGATGAC  | 1950 |
|    | TTGGTTTTCG | GTCAGTCAAC  | CTTTATGGTG  | GAGATGATGG  | AGGCCAATAA  | 2000 |
|    | TGCCATTTTC | CATGCGACCA  | AGAACTCTCT  | CATTCTCTTT  | GATGAATTGG  | 2050 |
| 50 | GACGTGGAAC | TGCAACTTAT  | GACGGGATGG  | CTCTTGCTCA  | GTCCATCATC  | 2100 |
|    | GAATATATCC | ATGAGCACAT  | CGGAGCTAAG  | ACCTCTTTTG  | CGACCCACTA  | 2150 |
|    | CCATGAGTTG | ACTAGTCTGG  | AGTCTAGTTT  | ACAACACTTG  | GTCAATGTCC  | 2200 |
|    | ACGTGGCAAC | TTTGGAGCAG  | GATGGGCAGG  | TCACCTTCCT  | TCACAAGATT  | 2250 |
|    | GAACCGGGAC | CAGCTGATAA  | ATCCTACGGT  | ATCCATGTTG  | CCAAGATTGC  | 2300 |
| 55 | TGGCTTGCCA | GCAGACCTTT  | TAGCAAGGGC  | GGATAAGATT  | TTGACTCAGC  | 2350 |
|    | TAGAGAATCA | AGGAACAGAG  | AGTCCTCCTC  | CCATGAGACA  | AACTAGTGCT  | 2400 |
|    | GTCACTGAAC | AGATTTCACT  | CTTTGATAGG  | GCAGAAGAGC  | ATCCTATCCT  | 2450 |
|    | AGCAGAATTA | GCTAAACTGG  | ATGTGTATAA  | TATGACACCT  | ATGCAGGTTA  | 2500 |
| 60 | TGAATGTCTT | AGTAGAGTTA  | AAACAGAAAC  | TATAA       |             | 2535 |

## 2) INFORMATION FOR SEQ ID NO: 1184

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: StrR-05

## (xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1184

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | TGACGGGTGA | CTTTTATGTG | ACAGGTCTTT | TGGATTTCAC | GCTGGTTTGT  | 50  |
|    | GGGGAAATCC | GTAACCTCAA | GGCTCGAGAA | GTGGTGTTGG | GTTATGACTT  | 100 |
| 20 | GTCTGAGGAA | GAAGAACAAA | TCCTCAGCCG | CCAGATGAAT | CTGGTACTCT  | 150 |
|    | CTTATGAAAA | AGAAAGCTTT | GAAGACCTTC | ATTTATTGGA | TTTGCGATTG  | 200 |
|    | GCAACGGTGG | AGCAAACGGC | ATCTAGTAAG | CTGCTCCAGT | ATGTTTCATCG | 250 |
|    | GACTCAGATG | AGGGAATTGA | ACCACCTCAA | ACCTGTTATC | CGATACGAAA  | 300 |
|    | TTAAGGATTT | CTTGCAGATG | GATTATGCGA | CCAAGGCTAG | TCTGGATTTG  | 350 |
| 25 | GTTGAGAATG | CTCGCTCAGG | TAAGAAACAA | GGCAGTCTTT | TCTGGCTTTT  | 400 |
|    | GGATGAAACC | AAAACGGCTA | TGGGGATGCG | TCTCTTGCGT | TCTTGGATTC  | 450 |
|    | ATCGCCCCTT | GATTGATAAG | GAACGAATCG | TCCAACGTCA | AGAAGTAGTG  | 500 |
|    | CAGGTCTTTC | TCGACCATTT | CTTTGAGCGT | AGTGACTTGA | CAGACAGTCT  | 550 |
|    | CAAGGGTGTT | TATGACATTG | AGCGCTTGCG | TAGTCGTGTT | TCTTTTGGCA  | 600 |
| 30 | AAACCAATCC | AAAGGATCTC | TTG        |            |             | 623 |

## 2) INFORMATION FOR SEQ ID NO: 1185

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: StrR-06

## (xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1185

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
| 50 | TGACGGGTGA | CTTTTATGTG | ACAGGTCTTT | TGGATTTCAC | GCTGGTTTGT  | 50  |
|    | GGGGAAATCC | GTAACCTCAA | GGCTCGAGAA | GTGGTGTTGG | GTTATGACTT  | 100 |
|    | GTCTGAGGAA | GAAGAACAAA | TCCTCAGCCG | CCAGATGAAT | CTGGTACTCT  | 150 |
|    | CTTATGAAAA | AGAAAGCTTT | GAAGACCTTC | ATTTATTGGA | TTTGCGATTG  | 200 |
|    | GCAACGGTGG | AGCAAACGGC | ATCTAGTAAG | CTGCTCCAGT | ATGTTTCATCG | 250 |
| 55 | GACTCAGATG | AGGGAATTGA | ACCACCTCAA | ACCTGTTATC | CGATACGAAA  | 300 |
|    | TTAAGGATTT | CTTGCAGATG | GATTATGCGA | CCAAGGCTAG | TCTGGATTTG  | 350 |
|    | GTTGAGAATG | CTCGCTCAGG | TAAGAAACAA | GGCAGTCTTT | TCTGGCTTTT  | 400 |
|    | GGATGAAACC | AAAACGGCTA | TGGGGATGCG | TCTCTTGCGT | TCTTGGATTC  | 450 |
|    | ATCGCCCCTT | GATTGATAAG | GAACGAATCG | TCCAACGTCA | AGAAGTAGTG  | 500 |
| 60 | CAGGTCTTTC | TCGACCATTT | CTTTGAGCGT | AGTGACTTGA | CAGACAGTCT  | 550 |

CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600  
 AAACCAATCC AAAGGATCTC T 621

5

## 2) INFORMATION FOR SEQ ID NO: 1186

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 622 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: StrR-11

## 20 (xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1186

25 TGACGGGTGA CTTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50  
 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100  
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150  
 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200  
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCAGT ATGTTTCATCG 250  
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300  
 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTG 350  
 GTTGAGAATG CTCGCTCAGG TAAGAAACAA GGCAGTCTTT TCTGGCTTTT 400  
 30 GGATGAAACC AAAACGGCTA TGGGGATGCG TCTCTTGCGT TCTTGGATTC 450  
 ATCGCCCCTT GATTGATAAG GAACGAATCG TCCAACGTCA AGAAGTAGTG 500  
 CAGGTCTTTC TCGACCATT TTTTGAGCGT AGTGACTTGA CAGACAGTCT 550  
 CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600  
 AAACCAATCC AAAGGATCTC TT 622  
 35

## 2) INFORMATION FOR SEQ ID NO: 1187

## 40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 45 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: StrR-55

## (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1187

55 TGACGGGTGA CTTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50  
 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100  
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150  
 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200  
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCGGT ATGTTTCATCG 250  
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300  
 60 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTG 350

|              |            |            |            |            |     |
|--------------|------------|------------|------------|------------|-----|
| GTTGAGAATG   | CTCGCTCAGG | TAAGAAACAA | GGCAGTCTTT | TCTGGCTTTT | 400 |
| GGATGAAACC   | AAAACGGCTA | TGGGGATGCG | TCTCTTGCGT | TCTTGATTTC | 450 |
| ATCGCCCCCTT  | GATTGATAAG | GAACGAATCG | TCCAACGTCA | AGAAGTAGTG | 500 |
| CAGGTCTTTC   | TCGACCATT  | CTTTGAGCGT | AGTGACTTGA | CAGACAGTCT | 550 |
| 5 CAAGGGTGTT | TATGACATTG | AGCGCTTGCG | TAGTCGTGTT | TCTTTTGGCA | 600 |
| AAACCAATCC   | AAAGGATCTC | TT         |            |            | 622 |

## 10 2) INFORMATION FOR SEQ ID NO: 1188

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*  
 (B) STRAIN: ATCC 35037

## (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1188

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
| 25 | GGGTGACTTT | TATGTAACGG | GGCTATTGGA | TTTCACGTTG | GTTTGTGGGG  | 50  |
|    | AAATTCGCAA | TCTCAAGGCT | AGAGAAGTGG | TGCTGGGTTA | TGACTTGTCT  | 100 |
|    | GAGGAAGAAG | AACAAATCCT | CAGTCGTCAG | ATGAATCTGG | TGCTTTCTTA  | 150 |
|    | TGAGAAGGAA | GGCTTTGAGG | ACCTTCATTT | ACTGGATCCA | CGACTGGCAG  | 200 |
| 30 | CTGTGGAGCA | AGCGGCAGCT | AGTAAGCTCC | TCCAGTATGT | TCACCGGACC  | 250 |
|    | CAGATGCGGG | AATTGAACCA | CCTCAAACCA | GTTATCCGCT | ATGAAATCAA  | 300 |
|    | AGATTTCTTA | CAGATGGACT | ATGCGACCAA | GGCTAGTCTG | GATTTGGTTG  | 350 |
|    | AGAATGCCCG | TTCAGGCAAG | AAGCAAGGCA | GTCTTTTCTG | GCTTTTAGAT  | 400 |
|    | GAAACCAAGA | CGGCTATGGG | AATGCGTCTC | TTGCGTTCTT | GGATTTCATCG | 450 |
| 35 | TCCTTTGATT | GATAAGGAGC | GAATCGTCCA | GCGTCAAGAG | GTGGTGCAGG  | 500 |
|    | TCTTTCTTGA | CCACTTCTTT | GAGCGTAGTG | ATTTAACGGA | CAGTCTTAAG  | 550 |
|    | GGTGTTTATG | ATATCGAACG | CTTGGCTAGT | CGGGTTTCTT | TTGGCAAGA   | 599 |

40

## 2) INFORMATION FOR SEQ ID NO: 1189

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases  
 45 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*  
 (B) STRAIN: ATCC 49456

## 55 (x) SEQUENCE DESCRIPTION: SEQ ID NO: 1189

|              |            |            |            |            |     |
|--------------|------------|------------|------------|------------|-----|
| GGTGACGGGT   | GACTTTTATG | TGACAGGTCT | TTTGGATTTT | ACGCTGGTTT | 50  |
| GTGGGGAAAT   | CCGCAATCTC | AAGGCTCGAG | AAGTGGTGCT | GGGTTATGAC | 100 |
| TTGTCTGAGG   | AAGAAGAACA | GATCCTTAGT | CGTCAGATGA | ATCTGGTACT | 150 |
| 60 TTCTATGAA | AAAGAAGGCT | TTGAAGACCT | TCATTTACTG | GATTCACGAT | 200 |



|   |            |             |            |            |             |     |
|---|------------|-------------|------------|------------|-------------|-----|
|   | TGGCAGCTGT | GGAGCAAGCG  | GCATCTAGTA | AACTGCTTCA | GTATGTTTCAT | 250 |
|   | CGGACTCAGA | TGAGGGAATT  | GAACCACCTC | AAGCCTGTTA | TCCGCTATGA  | 300 |
|   | AATCAAAGAT | TTTTTGCAGA  | TGGATTATGC | GACCAAGGCT | AGTCTGGATT  | 350 |
|   | TGGTTGAGAA | TGCCCCGTTCA | GGCAAGAAGC | AAGGTAGTCT | TTTTTGGCTT  | 400 |
| 5 | TTGGATGAAA | CCAAAACAGC  | TATGGGAATG | CGTCTCTTGC | GGTCTTGGAT  | 450 |
|   | TCATCGCCCC | CTGATTGATA  | AGGAACGAAT | TGTCCAACGC | CAAGAAGTTG  | 500 |
|   | TGCAGGTCTT | TCTCGACCAT  | TTCTTTGAGC | GTAGTGATTT | GACAGACAGT  | 550 |
|   | CTCAAGGGTG | TTTATGACAT  | TGAGCGCTTG | GCTAGTCGTG | TTTCTTTTGG  | 600 |
|   | CAAAACCAAT | CCAAAGGATC  | TCTT       |            |             | 624 |

10

## 2) INFORMATION FOR SEQ ID NO: 1190

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*  
 (B) STRAIN: LSPQ 2583

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | TGACGGGTGA | CTTTCAGGTG | ACTAGTTTAG | AGGACTTTGT | CTTGGTCTGC | 50  |
| 30 | GGGGAAATCC | GCAATTTGAA | AGCTAGGGGA | GTGGTGCTGG | GCTATGCCTT | 100 |
|    | GCCAGAAGCT | GAGGAGCAGG | TTTTGGCTGG | ACAGATGAAC | CTTTTACTGT | 150 |
|    | CCTATGTGGA | GAAGGTTTTG | GAGGATGTTC | AGCTGCTGGG | CGAGGAGCTG | 200 |
|    | TCTCCTATGG | AGCGTCAGGC | AGCAGGGAAA | CTGCTGGAGT | ATGTGCACCG | 250 |
|    | GACCCAGATG | AGGGAGCTCA | GCCATTTGAA | GAAGGCTCAG | CATTATGAAA | 300 |
| 35 | TCAAGGACTT | CCTGCAAATG | GACTATGCCA | CCAAGGCGAG | TCTGGATTTG | 350 |
|    | ACAGAAAATG | CTCGCTCGGG | CAAGAAGCAC | GGCAGTCTTT | ATTGGCTGAT | 400 |
|    | GGACGAGACT | AAGACGGCCA | TGGGCGGCCG | CATGCTGCGC | TCTTGATATC | 450 |
|    | AGCGTCCGCT | GATTGATGAA | GCGCGAATTA | GCCAGCGACA | GAATGTCGTT | 500 |
|    | GAGGTTTTTC | TGGATCATTT | CTTTGAGCGG | AGTGATTTGA | CGGAGAGCCT | 550 |
| 40 | CAAGGGGGTC | TATGATATCG | AGCGGCTGGC | TAGTCGGGTG | TCTTTTGGC  | 599 |

## 2) INFORMATION FOR SEQ ID NO: 1191

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*  
 (B) STRAIN: ATCC 903

55

## (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1191

|    |            |            |            |            |            |    |
|----|------------|------------|------------|------------|------------|----|
| 60 | TGACGGGTGA | CTTTCAGGTG | ACTAGTTTAG | AGGACTTTGC | CCTGGTCTGC | 50 |
|----|------------|------------|------------|------------|------------|----|

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GGGGAAATCC | GTAATTTGAA | GGCTAGGGAA | GTGGTGCTGG | GCTATGCTTT | 100 |
|    | GCCAGAAGCT | GAGGAGCAGG | TCTTGGCTGG | ACAGATGAAT | CTTTTGCTGT | 150 |
|    | CCTATGTACA | GACGGCCTTG | GACGATGTCC | AGCTGCTGGG | CGAGGAACTG | 200 |
|    | TCTCCTATGG | AGCGTCAGGC | AGCGGGGAAA | TTGCTAGAGT | ATGTGCACCG | 250 |
| 5  | GACCCAGATG | AGGGAGCTCA | GCCATTTGAA | GAAGGCCAG  | CATTATGAAA | 300 |
|    | TCAAGGACTT | TCTGCAAATG | GATTATGCTA | CCAAGGCGAG | TCTGGATTTG | 350 |
|    | ACAGAAAATG | CTCGCTCGGG | TAAGAAACAC | GGCAGTCTTT | ATTGGCTGAT | 400 |
|    | GGACGAGACC | AAGACGGCCA | TGGGCGGCCG | TATGCTGCGC | TCTTGGATCC | 450 |
|    | AGCGTCCGTT | GATTGATGAA | GTGCGAATTA | GCCAGCGGCA | GAATGTCGTC | 500 |
| 10 | GAGGTTTTTC | TGGAACATTT | CTTTGAGCGG | AGTGATTTGA | CGGAGAGCCT | 550 |
|    | CAAGGGAGTC | TATGATATCG | AGCGGCTGGC | TAGTCGGGTG | TCTTTTGGCA | 600 |
|    | AGACCAATCC | AAAGGATCTC | TT         |            |            | 622 |

15

## 2) INFORMATION FOR SEQ ID NO: 1192

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192

GGTAAAACAG GAACCTCTAA CT

22

30

## 2) INFORMATION FOR SEQ ID NO: 1193

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193

GGTAAGACAG GTACTTCTAA CT

22

45

## 2) INFORMATION FOR SEQ ID NO: 1194

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194

60

CATTTC AAGT AATACAACAG AATC

24

## 5 2) INFORMATION FOR SEQ ID NO: 1195

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195

CATTTC AAGT AACACAAC TGAATC

24

## 20 2) INFORMATION FOR SEQ ID NO: 1196

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196

GCCATTTC AAGT GTAATACAAC AGAA

24

## 35 2) INFORMATION FOR SEQ ID NO: 1197

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## 45 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197

CAAACGCCAT TTCAAGTAAT ACAAC

25

## 50 2) INFORMATION FOR SEQ ID NO: 1198

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 381 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198

```

AACGGGCGTC TCGATAGAAA AACACGTGAA AATCCCAATG ATTATAAACA      50
10 ATCAATATAC GATTTTGCTG AAGCTGTAAC AAAAGGTATT AAGGAACAAA      100
CAAATAAAAA TTAATAGGCA ACTTAACCAG AATCGTTAAA ACTATATGAC      150
GATTCTGGTT TTTTAAATTC AAAAAGTTTT CTAAAAAATT TACTTGCTTC      200
TTTAAAGTAT AGGTATGAAA TACAATTGAT TAAAATAGTA AAGGAAATGA      250
ATCATGAAAC AATTAATAA GCCTTTATAC TTTTACCTAT TACTTTTTAT      300
15 TACAACAACG CTGATTGGCG CGTTACTATT ATATTTGCCA ATCACAKGTA      350
AACATCCTAT TGATTTTGTG GACGCCCGTT A                          381

```

20 2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

25 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199

GTATTAAAGA AGATATCCAA AAAGC

25

35 2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

40 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200

TCAAAGAAGA AACTAAAAAA GCTGT

25

50 2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201

AACGTAGGTG TCCTTCTTC

19

2) INFORMATION FOR SEQ ID NO: 1202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202

GTGTTGAAAT GTTCCGTAAA CA

22

2) INFORMATION FOR SEQ ID NO: 1203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203

GGIGARMGIG GIAAYGARAT G

21

2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1204

GCIAAYAACI TCIWMYATGC C

21

2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

655

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205

AAYACITCIA WYATGCCIGT

20

2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206

CKISRIGTIG ARTCIGCCA

19

2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207

CCITCITCWC CIGGCATYTC

20

2) INFORMATION FOR SEQ ID NO: 1208

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208

TCAAAAAGTT TTCTAAAAAA TTTAC

25

2) INFORMATION FOR SEQ ID NO: 1209

656

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209

ACGGGCGTCC ACAAATCAA TAGGA

2) INFORMATION FOR SEQ ID NO: 1210

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210

ACCAGCTTGC CCAATACAAA GG

2) INFORMATION FOR SEQ ID NO: 1211

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211

ATTCTTGTA CAGGCTTTGA TCCC

2) INFORMATION FOR SEQ ID NO: 1212

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212

CCICIRGIG GIGAIACIGC WCC

## 2) INFORMATION FOR SEQ ID NO: 1213

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213

AARGGIGGIA CIGCIGCIAT HCCIGG

26

## 2) INFORMATION FOR SEQ ID NO: 1214

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214

GGTAAAACAG GTACCTCTAA CTA

23

## 2) INFORMATION FOR SEQ ID NO: 1215

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
- (B) STRAIN: D471
- (C) ACCESSION NUMBER: X65717

## (xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1215

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| AACAAAATAA | AAGAACTTAC | CTATTTTCCA | TCCAAAATGT | TTAGCAATCA | 50  |
| TCATCTGCAA | GGCAACGTAT | TGCATGGCAT | TGATGTGATG | AGCAACTAAT | 100 |
| ATGTCATTAG | AACGTTGCGT | CAAACTAGCA | TCTAAATAAA | GATCGAAATG | 150 |
| CAGTTATCAA | AAATGCAAGC | TCCTATCGGC | CCTTGTTTTA | ATTATTACTC | 200 |
| ACATTGCCTT | AATGTATTTA | CTTGCTTATT | ATTAACTTTT | TTGCTAAGTT | 250 |
| AGTAGCGTCA | GTTATTCATT | GAAAGGACAT | TATTATGAAA | ATTCTTGTA  | 300 |
| CAGGCTTTGA | TCCCTTTGGC | GGCGAAGCTA | TTAATCCTGC | CCTTGAAGCT | 350 |
| ATCAAGAAAT | TGCCAGCAAC | CATTCATGGA | GCAGAAATCA | AATGTATTGA | 400 |



|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | AGTTCCAACG | GTTTTTCAAA | AATCTGCCGA | TGTGCTCCAG | CAGCATATCG | 450  |
|    | AAAGCTTTCA | ACCTGATGCA | GTCCTTTGTG | TTGGGCAAGC | TGGTGGCCGG | 500  |
|    | ACTGGACTAA | CGCCAGAACG | CGTTGCCATT | AATCAAGACG | ATGCTCGCAT | 550  |
|    | TCCTGATAAC | GAAGGGAATC | AGCCTATTGA | TACACCTATT | CGTGCAGATG | 600  |
| 5  | GTAAAGCAGC | TTATTTTTC  | ACCTTGCCAA | TCAAAGCGAT | GGTTGCTGCC | 650  |
|    | ATTCATCAGG | CTGGGCTTCC | TGCTTCTGTT | TCTAATACAG | CTGGTACCTT | 700  |
|    | TGTTTGCAAT | CATTTGATGT | ATCAAGCCCT | TTACTTAGTG | GATAAATATT | 750  |
|    | GTCCAAATGC | CAAAGCTGGG | TTTATGCATA | TTCCCTTTAT | GATGGAACAG | 800  |
|    | GTTGTTGATA | AACCTAATAC | AGCTGCCATG | AACCTCGATG | ATATTACAAG | 850  |
| 10 | AGGAATTGAG | GCTGCTATTT | TTGCCATTGT | CGATTTCAAA | GATCGTTCGG | 900  |
|    | ATTTAAAACG | TGTAGGGGGC | GCTACTCACT | GACTGTGACG | CTACTAAACC | 950  |
|    | TATTTTAAAA | AAACAGAGAT | ATGAATAAAC | TCTGTTTTTT | TTGTGCTAAA | 1000 |
|    | AATGAAAGAC | CTAGGGAAAC | TTTTCATCGG | TCTTTCTCAA | TTGTCATCTT | 1050 |
|    | AATCTAATAC | TACTTCTAAC | ATCAGCGGGT | ATAGTTTGCC | AGTAATTAAG | 1100 |
| 15 | AAACGTTGTT | GATCTAAATG | AGCAATCCCA | TTCAAACAT  | TAAGGTCAGG | 1150 |
|    | GTAATGGGAC | TTATCAAGAT | TTAAGGCTTT | TAACAAAGGA | CTAATATCAT | 1200 |
|    | AGGTGGCTAC | CACCTTTCCA | GAATCAGGTT | GGAGTTTGAC | AATAGTATTG | 1250 |
|    | GTTTGCCAAA | TATTGGCATA | GAGATAACCA | TCTACATACT | CTAATTCGTT | 1300 |
|    | AAGCATTGAG | ATAGGGACAC | TTTCTATAGC | AACTAGT    |            | 1337 |

## 2) INFORMATION FOR SEQ ID NO: 1216

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216

35 GGTAAGACTG GTACATCAAA CTA

23

## 2) INFORMATION FOR SEQ ID NO: 1217

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217

50

CAAATGCCAT TTCAAGTAAC ACAAC

25

## 55 2) INFORMATION FOR SEQ ID NO: 1218

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218

CAAACGCCAT TTCAAGTAAC ACAAC

25

10

2) INFORMATION FOR SEQ ID NO: 1219

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219

CAAATGCTAT TTCAAGTAAT ACAAC

25

25

2) INFORMATION FOR SEQ ID NO: 1220

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220

CAAACGCCAT TTCAAGTAAT ACGAC

25

40

2) INFORMATION FOR SEQ ID NO: 1221

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221

55 GAYACICCCIG GICAYGTIGA YTT

23

60

2) INFORMATION FOR SEQ ID NO: 1222

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222

ATYGAYACIC CIGGICAYGT IGAYTT

26

2) INFORMATION FOR SEQ ID NO: 1223

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223

AYITCIARRT GIARYTCRCC CATICC

26

2) INFORMATION FOR SEQ ID NO: 1224

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224

CCIGYIHTIY TIGARCCIAT IATG

24

2) INFORMATION FOR SEQ ID NO: 1225

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225

TAICCRAACA TYTCISMIAR IGGIAC

26

## 2) INFORMATION FOR SEQ ID NO: 1226

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
10 (ii) MOLECULE TYPE: DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226  
15 GTIRMRTAIC CRAACATYTC 20

## 2) INFORMATION FOR SEQ ID NO: 1227

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
25 (D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227  
30 GTICCIYTIK CIGARATGTT YGGITA 26

## 2) INFORMATION FOR SEQ ID NO: 1228

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 bases  
(B) TYPE: Nucleic acid  
40 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: DNA  
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228  
GTICCIYTIK CIGARATGTT YGGITAYGC 29

## 2) INFORMATION FOR SEQ ID NO: 1229

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
55 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: DNA  
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229

TCCATYTGIG CIGCICCI GT IATCAT

26

## 5 2) INFORMATION FOR SEQ ID NO: 1230

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2145 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (D) ACCESSION NUMBER: X00415

## (xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1230

20 TGAACGCCTA AAAGATAAAC GAGGAAACAA ATGGCTCGTA CAACACCCAT 50  
 CGCACGCTAC CGTAACATCG GTATCAGTGC GCACATCGAC GCCGGTAAAA 100  
 CCACTACTAC CGAACGTATT CTGTTCTACA CCGGTGTAAA CCATAAAATC 150  
 GGTGAAGTTC ATGACGGCGC TGCAACCATG GACTGGATGG AGCAGGAGCA 200  
 25 GGAACGTGGT ATTACCATCA CTTCCGCTGC GACTACTGCA TTCTGGTCTG 250  
 GTATGGCTAA GCAGTATGAG CCGCATCGCA TCAACATCAT CGACACCCCG 300  
 GGGCACGTTG ACTTCACAAT CGAAGTAGAA CGTTCCATGC GTGTTCTCGA 350  
 TGGTGCGGTA ATGGTTTACT GCGCAGTTGG TGGTGTTCAG CCGCAGTCTG 400  
 AAACCGTATG GCGTCAGGCA AACAAATATA AAGTTCCGCG CATTCGCTTC 450  
 30 GTTAACAAAA TGGACCGCAT GGGTGCGAAC TTCCTGAAAG TTGTTAACCA 500  
 GATCAAAACC CGTCTGGGCG CGAACCCGGT TCCGCTGCAG CTGGCGATTG 550  
 GTGCTGAAGA ACATTTACC GGTGTTGTTG ACCTGGTGAA AATGAAAGCT 600  
 ATCAACTGGA ACGACGCTGA CCAGGGCGTA ACCTTCGAAT ACGAAGATAT 650  
 CCCGGCAGAC ATGGTTGAAC TGGCTAACGA ATGGCACCAG AACCTGATCG 700  
 35 AATCCGCAGC TGAAGCTTCT GAAGAGCTGA TGGAAAAATA CCTGGGTGGT 750  
 GAAGAAGTGA CTGAAGCAGA AATCAAAGGT GCTCTGCGTC AGCGCGTTCT 800  
 GAACAACGAA ATCATCCTGG TAACCTGTGG TTCTGCGTTC AAGAACAAAG 850  
 GTGTTACAGC GATGCTGGAT GCGGTAATTG ATTACCTGCC ATCCCCGGTT 900  
 GACGTACCTG CGATCAACGG TATCCTGGAC GACGGTAAAG ACACTCCGGC 950  
 40 TGAACGTCAC GCAAGTGATG ACGAGCCGTT CTCTGCACTG GCGTTCAAAA 1000  
 TCGCTACCGA CCCGTTTGTT GGTAACCTGA CCTTCTTCCG TGTTTACTCC 1050  
 GGTGTGGTTA ACTCTGGTGA TACCGTACTG AACTCCGTGA AAGCTGCACG 1100  
 TGAGCGTTTC GGTGCTATCG TTCAGATGCA CGCTAACAAA CGTGAAGAGA 1150  
 TCAAAGAAGT TCGCGCGGGC GACATCGCTG CTGCTATCGG TCTGAAAGAC 1200  
 45 GTAACCACTG GTGACACCCT GTGTGACCCG GATGCGCCGA TCATTCTGGA 1250  
 ACGTATGGAA TTCCCTGAGC CGGTAATCTC CATCGCAGTT GAACCGAAAA 1300  
 CCAAAGCTGA CCAGGAAAAA ATGGGTCTGG CTCTGGGCCG TCTGGCTAAA 1350  
 GAAGACCCGT CTTTCCGTGT ATGGACTGAC GAAGAATCTA ACCAGACCAT 1400  
 CATCGCGGGT ATGGGCGAAC TGCACCTCGA CATCATCGTT GACCGTATGA 1450  
 50 AGCGTGAATT CAACGTTGAA GCGAAGCTAG GTAAACCGCA GGTGTGTTAC 1500  
 CGTGAAACTA TCCGCCAGAA AGTTACCGAT GTTGAAGGTA AACACGCGAA 1550  
 ACAGTCTGGT GGTCGTGGTC AGTATGGTCA TGTTGTTATC GACATGTACC 1600  
 CGCTGGAGCC GGGTTCAAAC CCGAAAGGCT ACGAGTTCAT CAACGACATT 1650  
 AAAGGTGGTG TAATCCCTGG CGAATACATC CCGGCCGTTG ATAAAGGTAT 1700  
 55 CCAGGAACAG CTGAAAGCAG GTCCGCTGGC AGGCTACCCG GTAGTAGACA 1750  
 TGGGTATTTC TCTGCACTTC GGTCTTACC ATGACGTTGA CTCCTCTGAA 1800  
 CTGGCGTTTA AACTGGCTGC TTCTATCGCC TTAAAGAAG GCTTTAAGAA 1850  
 AGCGAAACCA GTTCTGCTTG AGCCGATCAT GAAGGTTGAA GTAGAAACTC 1900  
 CGGAAGAGAA CACCGGTGAC GTTATCGGTG ACTTGAGCCG TCGTCGTGGT 1950  
 60 ATGCTCAAAG GTCAGGAATC TGAAGTTACT GGC GTTAAGA TCCACGCTGA 2000

|            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------|
| AGTACCGCTG | TCTGAAATGT | TCGGATACGC | AACTCAGCTG | CGTTCTCTGA | 2050 |
| CCAAAGGTCG | TGCATCATAC | ACTATGGAAT | TCCTGAAGTA | TGATGAAGCG | 2100 |
| CCGAGTAACG | TTGCTCAGGC | CGTAATTGAA | GCCCGTGGTA | AATAA      | 2145 |

5

## 2) INFORMATION FOR SEQ ID NO: 1231

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 37 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231

20 GCGAGCCCGA AGATAAAAAA GAACCTCTGC TGCTCGC 37

## 2) INFORMATION FOR SEQ ID NO: 1232

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232

35 GGAGCCGCGC GATTTTATAA ATGAATGTTG ATAACCGGCT CC 42

## 2) INFORMATION FOR SEQ ID NO: 1233

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233

50 GCGAGCGTTA CTGGTGTAGA AATGTTCCGG CTCGC 35

## 55 2) INFORMATION FOR SEQ ID NO: 1234

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
60 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234

ACTAAATAAA CGCTCATTCG

20

10

2) INFORMATION FOR SEQ ID NO: 1235

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 38 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235

GCGAGCCGAA GTTGAAGTTG TTGGTATTGC TGGCTCGC

38

25

2) INFORMATION FOR SEQ ID NO: 1236

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 34 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236

GCGAGCCGTG GTGAAGTTCG CGTTGGTGGC TCGC

34

40

2) INFORMATION FOR SEQ ID NO: 1237

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 38 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237

55 GCGAGCCGCG AAATCGAAGT TGCTGTATTA GGGCTCGC

38

60

2) INFORMATION FOR SEQ ID NO: 1238

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238

GCGAGCGGCG TTAATTTTGG CACCGAAGAA GAGCTCGC

38

2) INFORMATION FOR SEQ ID NO: 1239

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239

GCGAGCGCAG ACCTTTCAGC AGAGGAGGCT CGC

33

2) INFORMATION FOR SEQ ID NO: 1240

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240

GCGAGCCGGC AAGACAATAT GACAGCAAAA TCGCTCGC

38

2) INFORMATION FOR SEQ ID NO: 1241

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241

GCGAGCGGGG AACGAGGATG ATTTGATTGG CTCGC

35



## 2) INFORMATION FOR SEQ ID NO: 1242

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 600 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Enterococcus faecium*  
 (E) STRAIN: BM4147-1  
 (F) ACCESSION NUMBER: U39790
- 15 (xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1242

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 20 | TTCTTAGAGA | CATTGAATAT | GCCTTATGTC | GGCGCAGGCG | TATTGACCAG | 50  |
|    | TGCATGTGCC | ATGGATAAAA | TCATGACCAA | GTATATTTTA | CAAGCTGCTG | 100 |
|    | GTGTGCCGCA | AGTTCCTTAT | GTACCAGTAC | TTAAGAATCA | ATGGAAAGAA | 150 |
|    | AATCCTAAAA | AAGTATTTGA | TCAATGTGAA | GGTTCTTTGC | TTTATCCGAT | 200 |
|    | GTTTGTCAAA | CCTGCGAATA | TGGGTTCTAG | TGTCGGCATT | ACAAAGGCAG | 250 |
| 25 | AAAACCGAGA | AGAGCTGCAA | AATGCTTTAG | CAACAGCCTA | TCAGTATGAT | 300 |
|    | TCTCGAGCAA | TCGTTGAACA | AGGAATTGAA | GCGCGCGAAA | TCGAAGTTGC | 350 |
|    | TGTATTAGGA | AATGAAGATG | TTCGGACGAC | TTTGCCTGGC | GAAGTCGTAA | 400 |
|    | AAGACGTAGC | ATTCTATGAT | TATGAAGCCA | AATATATCAA | TAATAAAATC | 450 |
|    | GAAATGCAGA | TTCCAGCCGA | AGTGCCGGAA | GAAGTTTATC | AAAAAGCGCA | 500 |
| 30 | AGAGTACGCG | AAGTTAGCTT | ACACGATGTT | AGGTGGAAGC | GGATTGAGCC | 550 |
|    | GGTGCGATTT | CTTTTTGACA | AATAAAAATG | AATTATTCCT | GAATGAATTA | 600 |

## 35 2) INFORMATION FOR SEQ ID NO: 1243

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2275 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Enterococcus faecalis*  
 (C) ACCESSION NUMBER: M38386

## 50 (xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1243

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 50 | GGTACCAAAG | AAAAAAACGA | ACGCCACAAC | CAACAGCCTC | TAAAGCAACA | 50  |
|    | CCTGCTTCTG | AAATTGAGGG | AGATTTAGCA | AATGTCAATG | AGATTCTTTT | 100 |
|    | GGTTCACGAT | GATCGTGTCG | GGTCAGCAAC | GATGGGAATG | AAAGTCTTAG | 150 |
|    | AAGAAATTTT | AGATAAAGAG | AAAATTTCAA | TGCCGATTCG | AAAAATTAAT | 200 |
| 55 | ATTAATGAAT | TAACCAACA  | AACACAGGCT | TTAATTGTCA | CAAAAGCTGA | 250 |
|    | ACTAACGGAA | CAAGCACGTA | AAAAGCACC  | GAAAGCGACA | CACTTATCAG | 300 |
|    | TAAAAAGTTA | TGGTTAATCC | CCAAAAATAT | GAAACAGTGG | GTTTCGCTCT | 350 |
|    | TAAAAGAAAG | TGCCTAGAGA | GGAAGAAAAC | AATGGAAAAT | CTTACGAATA | 400 |
|    | TTTCAATTGA | ATTAAATCAA | CAGTTTAATA | CAAAAGAAGA | AGCTATTTCG | 450 |
| 60 | TTTTCCGGCC | AGAAACTAGT | CGAGGCAGGC | TGTGTTGAGC | CCGCTTATAT | 500 |

|    |            |             |             |              |            |      |
|----|------------|-------------|-------------|--------------|------------|------|
|    | CGAAGCAATG | ATTGAAAGAG  | ACCAATTGCT  | ATCTGCCCCAT  | ATGGGGAATT | 550  |
|    | TTATTGCCAT | TCCTCATGGA  | ACAGAAAGAAG | CCAAAAAATT   | AGTGAAAAAA | 600  |
|    | TCAGGAATCT | GTGTAGTGCA  | AGTCCCAGAG  | GGCGTTAATT   | TTGGCACCGA | 650  |
|    | AGAAGATGAA | AAAATTGCTA  | CCGTATTATT  | TGGGATTGCC   | GGAGTCGGTG | 700  |
| 5  | AAGAACATTT | GCAATTAGTC  | CAACAAATTG  | CACTTTATTG   | TAGTGATATG | 750  |
|    | GATAACGTGG | TGCAACTTGC  | CGATGCATTA  | AGTAAAGAAG   | AAATAACAGA | 800  |
|    | AAATTTAGCC | ATTGCTTAAA  | GGAGAGAATA  | AGAATGAACG   | CAGTACATTT | 850  |
|    | TGGAGCAGGA | AATATTGGAC  | GCGGCTTTAT  | TGGCGAAATT   | TTAGCTAAAA | 900  |
|    | CGGGTTTCAT | ATTACCGTTT  | GTGGATGTTA  | ATGGAAACCA   | TCATCAAGCG | 950  |
| 10 | TTAAAAGAAC | GTAAAAGTTA  | TACAATTGAA  | TTGGCCGATG   | CCTCACATCA | 1000 |
|    | ACAAATTAAC | GTTGAAAATG  | TGACCGGGTT  | AAATAACATG   | ACAGAACCAG | 1050 |
|    | AAAAAGTAGT | AGAAGCAATT  | GCGGAAGCCG  | ATTTAGTCAC   | GACGGCAATT | 1100 |
|    | GGTCCTAATA | TTTTACCAAG  | AATTGCTGAA  | TTAATTGCTC   | AAGGAATTGA | 1150 |
|    | TGCACGTGCC | GAAGCAAATT  | GTCAAAACGG  | CCCGCTGGAT   | ATTATCGCTT | 1200 |
| 15 | GTGAAAATAT | GATTGGTGGT  | TCAACCTTTT  | TAGCAGAAGA   | AGTGGCCATA | 1250 |
|    | ATATTTGAAA | AACCCAGCTT  | ATCTGAACAA  | TGGATTGGTT   | TTCTTGATGC | 1300 |
|    | GGCAGTTGAT | CGGATTGTTC  | CATTACAAAA  | ACATAAAGAT   | CCACTTTTTG | 1350 |
|    | TTCAAGTTGA | GCCTTTTTGT  | GAATGGGTCA  | TTGATGATAC   | CAACCGAAAA | 1400 |
|    | GCCAAAGAGA | TTCAGTTAGA  | AGGCGTCATT  | ACTTGTCGAT   | TAGAGCCGTA | 1450 |
| 20 | TATTGAACGA | AAATTATTTA  | GTGTAACCAG  | TGGCCATGCT   | ACAGTTGCCT | 1500 |
|    | ATACAGGGGC | GTTGTTAGGC  | TATCAAACCA  | TTGACGAAGC   | GATGCAGGAC | 1550 |
|    | GCCTTAGTGG | TAGCGCAACT  | CAAAATCAGT  | TTGCAGGAAA   | CCGGTAAACT | 1600 |
|    | TTTAGTGGCC | AAATGGAATT  | TTGATGAACA  | AGAACATGCA   | GCCTATATTG | 1650 |
|    | AAAAAATTAT | CAACCGTTTC  | CAAAATAAAT  | ATATTTTCAGA  | TGCTATTACA | 1700 |
| 25 | CGTGTAGCAC | GGACACCAAT  | CAGAAAATTA  | GGTGCACGCAAG | AACGGTTTAT | 1750 |
|    | TCGACCAATC | CGTGAATTAC  | AGGAACGCAA  | TCTAGTGTCTG  | GCCGCATTTA | 1800 |
|    | TAGCAATGAT | TGGTATTGTC  | TTTAATTATC  | ATGATCCAGA   | AGATGAACAA | 1850 |
|    | AGCCGTCAAT | TACAGGAAAT  | GCTTGACCAA  | GAAAGTGTTG   | ATACAGTGGA | 1900 |
|    | TCGCTGAAGT | AACGGGCATT  | GAAGATCCAG  | AAACGGTTAA   | AAATATTAAA | 1950 |
| 30 | CAAAACGTAG | AACCTGCTATG | CGCGACCACA  | AGTAGCATAA   | TTAACAAAAT | 2000 |
|    | CCTTCTACCA | AGATACTTCA  | CATTTCTTAA  | TTAAAGAAAA   | AACAACCGCG | 2050 |
|    | CCTCACCTGA | GCCGACCCCC  | AAAAGTTAGA  | CCTAGAAATC   | TAACTTTGG  | 2100 |
|    | AGGTTTTTTT | GTATGGCAAA  | ATACAGTTTT  | GAAATTTAAA   | CTTAAACTTG | 2150 |
|    | TTCATGACTA | CTTATATGGT  | CAAGGAGGTC  | TAAGGTTTCT   | CGCAAAGAAG | 2200 |
| 35 | TATGGGTTTA | AAGATAGTCT  | CAAATAAGCA  | AATGGATAAA   | TGCCTATAAA | 2250 |
|    | GAACTTGGTG | AAGAAGGGGG  | GATCC       |              |            | 2275 |

40 2) INFORMATION FOR SEQ ID NO: 1244

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 442 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*  
(B) STRAIN: ATCC 25923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 55 | GATCAATCTT | TGTCGGTACA | CGATATTCTT | CACGACTAAA | TAAACGCTCA | 50  |
|    | TTGCGGATTT | TATAAATGAA | TGTTGATAAC | AATGTTGTAT | TATCTACTGA | 100 |
|    | AATCTCATT  | CGTTGCATCG | GAAACATTGT | GTTCTGTATG | TAAAAGCCGT | 150 |
|    | CTTGATAATC | TTTAGTAGTA | CCGAAGCTGG | TCATACGAGA | GTTATATTTT | 200 |
| 60 | CCAGCCAAAA | CGATATTTTT | ATAATCATT  | CGTGAAAAAG | GTTTCCCTTC | 250 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATTATCACAC | AAATATTTTA | GCTTTTCAGT | TTCTATATCA | ACTGTAGCTT | 300 |
| CTTTATCCAT | ACGTTGAATA | ATTGTACGAT | TCTGACGCAC | CATCTTTTGC | 350 |
| ACACCTTTAA | TGTTATTTGT | TTTAAAAGCA | TGAATAAGTT | TTTCAACACA | 400 |
| ACGATGTGAA | TCTTCTAAGA | AGTCACCGTA | AAATGAAGGA | TC         | 442 |

## 2) INFORMATION FOR SEQ ID NO: 1245

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*  
 (B) STRAIN: CIP 9444

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245

|            |            |            |             |            |     |
|------------|------------|------------|-------------|------------|-----|
| GATGGCGGAA | AGCTACCAGA | AATCTACAAC | GCCCTTACGG  | TAAAACAGAG | 50  |
| CAACGAAAAC | GGAACAAGCA | TTAACTTAAC | ATTTGAAGTT  | GCACTTCATT | 100 |
| TAGGTGATGA | CACAGTTCGT | ACAGTTGCAA | TGTCTTCCAC  | AGATGGACTT | 150 |
| GTTCGTGGCA | CAGAAGTAGA | AGATACTGGT | AAAGCAATCT  | CTGTACCAGT | 200 |
| TGGTGATGCA | ACACTTGGTC | GTGTATTTAA | CGTATTAGGT  | GATGCAATTG | 250 |
| ACTTAGATGG | TGAGGTTCTT | GCGGATGTAC | GTCGTGATCC  | AATTCACCGT | 300 |
| CAAGCACCTG | CATTCGAAGA | ATTATCTACT | AAAGTAGAAA  | TTCTTGAAAC | 350 |
| TGGTATTAAA | GTAGTAGACT | TACTTGCTCC | TTACATTAAG  | GGTGGTAAGA | 400 |
| TCGGTCTATT | CGGTGGTGCC | GGTGTAGGTA | AAACGGTATT  | AATTCAGGAA | 450 |
| TTAATCAATA | ACATCGCACA | AGAACACGGT | GGTATCTCTG  | TATTCGCTGG | 500 |
| TGTAGGTGAG | CGTACTCGTG | AGGGTAATGA | CTTATAACCAC | GAAATGAGCG | 550 |
| ATTCTGGCGT | AATTAAGAAA | ACTGCGATGG | TATTCGGACA  | AATGAACGAG | 600 |
| CCACCTGGAG | CACGTCAACG | TGTTGCGTTA | ACAGGTTTAA  | CAATGGCTGA | 650 |
| GCATTTCCGT | GATGAGCAAG | GACAAGATGT | ACTTCTGTTC  | ATCGATAATA | 700 |
| TCTTCCGTTT | CACGCAAGCA | GGTTCTGAAG | TATCTGCCCT  | TCTTGCCCGT | 750 |
| ATGCCATCTG | CGGTAGGTTA | CCAACCAACA | CTTGCAACAG  | AAATGGGTCA | 800 |
| ATTACAAGAG | CGTATTACAT | CTACAAATAA | AGGGTCTATC  | ACGTC      | 845 |

## 2) INFORMATION FOR SEQ ID NO: 1246

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*  
 (B) STRAIN: ATCC 11986

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246

|            |            |            |            |            |    |
|------------|------------|------------|------------|------------|----|
| TGCACTTCAT | TTAGGTGATG | ACACAGTTCG | TACAGTTGCA | ATGTCTTCCA | 50 |
|------------|------------|------------|------------|------------|----|

|    |            |             |            |            |            |     |
|----|------------|-------------|------------|------------|------------|-----|
|    | CAGATGGACT | TGTTTCGTGGC | ACAGAAGTAG | AAGATACTGG | TAAAGCAATC | 100 |
|    | TCTGTACCA  | TTGGTGATGT  | AACACTTGGT | CGTGTATTTA | ACGTATTAGG | 150 |
|    | TGATGCAATT | GACTTAGATG  | GTGATGTTCC | TGCGGATGTA | CGTCGTGATC | 200 |
|    | CAATTCACCG | TCAAGCGCCT  | GCATTCGAAG | AGTTATCTAC | TAAAGTAGAA | 250 |
| 5  | ATTCTTGAAA | CTGGTATTAA  | AGTAGTAGAC | TTACTTGCTC | CTTACATTAA | 300 |
|    | GGGTGGTAAG | ATTGGTCTAT  | TCGGTGGTGC | CGGCGTAGGT | AAAACAGTAT | 350 |
|    | TAATTCAGGA | ATTAATTAAT  | AACATCGCAC | AAGAGCACGG | TGGTATCTCT | 400 |
|    | GTATTCGCTG | GTGTAGGTGA  | GCGTACTCGT | GAAGGTAACG | ACTTATACCA | 450 |
|    | CGAAATGAGC | GATTCTGGCG  | TAATTAAGAA | AACTGCGATG | GTATTCGGAC | 500 |
| 10 | AAATGAACGA | GCCACCTGGA  | GCACGTCAAC | GTGTTGCATT | AACAGGTTTA | 550 |
|    | ACAATGGCTG | AACATTTCCG  | TGATGAGCAA | GGACAAGACG | TACTATTGTT | 600 |
|    | CATCGATAAC | ATCTTCCGTT  | TCACGCAAGC | GGGTTCTGAA | GTATCTGCCC | 650 |
|    | TTCTTG     |             |            |            |            | 656 |

15

## 2) INFORMATION FOR SEQ ID NO: 1247

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 791 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*  
 (B) STRAIN: ATCC 10792

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247

|    |             |            |             |             |             |             |     |
|----|-------------|------------|-------------|-------------|-------------|-------------|-----|
|    | CGAAACGGA   | AGTATTA    | ACTTA       | TAACATTTGA  | AGTTGCACTT  | CATTTAGGTTG | 50  |
|    | ATGATACAGT  | TCGTACAGTT | GCGATGTCTT  | CCACAGATGG  | ACTTGTTTCGT |             | 100 |
| 35 | GGCACAGAAG  | TAGAAGATAC | TGGTAAACCA  | ATCTCTGTAC  | CAGTTGGTGA  |             | 150 |
|    | TGTAACACTT  | GGTCGCGTAT | TTAACGTATT  | AGGTGATGCA  | ATTGACTTAG  |             | 200 |
|    | ATGGTGAGGT  | TCCTGCAGAT | GTACATCGTG  | ATCCAATTCA  | CCGTCAAGCA  |             | 250 |
|    | CCTGCATTTCG | AAGAATTATC | TACTAAAGTA  | GAAATTCTTG  | AAACTGGTAT  |             | 300 |
|    | TAAAGTAGTA  | GACTTACTTG | CTCCTTACAT  | TAAGGGTGGT  | AAGATCGGCC  |             | 350 |
| 40 | TATTCGGTGG  | TGCCGGCGTA | GGTAAACAG   | TATTAATTCA  | GGAATTAATT  |             | 400 |
|    | AACAACATCG  | CACAAGAGCA | CGGTGGTATC  | TCTGTATTTCG | CTGGTGTAGG  |             | 450 |
|    | TGAGCGTACT  | CGTGAGGGTA | ATGACTTATA  | CCACGAAATG  | AGCGATTCTG  |             | 500 |
|    | GCGTAATCAA  | GAAAACTGCG | ATGGTATTTCG | GACAAATGAA  | CGAGCCACCT  |             | 550 |
|    | GGAGCACGTC  | AACGTGTTGC | ATTAACAGGT  | TTAACAATGG  | CTGAGCATTT  |             | 600 |
| 45 | CCGTGATGAG  | CAAGGACAAG | ACGTACTTCT  | GTTTCATCGAT | AACATCTTCC  |             | 650 |
|    | GTTTCACGCA  | AGCGGGTTCT | GAAGTATCTG  | CCCTTCTTGG  | TCGTATGCCA  |             | 700 |
|    | TCTGCGGTAG  | GTTACCAACC | AACACTTGCA  | ACAGAAATGG  | GTCAATTACA  |             | 750 |
|    | AGAGCGTATT  | ACATCTACAA | ATAAAGGGTC  | TATCACGTCT  | A           |             | 791 |

50

## 2) INFORMATION FOR SEQ ID NO: 1248

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*  
 (B) STRAIN: BGSC 4AC1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248

|    |            |             |             |            |             |     |
|----|------------|-------------|-------------|------------|-------------|-----|
| 15 | ATCTACAATG | CCCTTACGGT  | AAAACAAAGC  | AACGAAAACG | GAAGCATGAA  | 50  |
|    | CTTAACATTT | GAAGTTGCAC  | TTCATTTAGG  | TGATGATACA | GTTCGTACAG  | 100 |
|    | TTGCGATGTC | TTCCACAGAT  | GGACTTGTTT  | GTGGCACAGA | AGTAGAAGAT  | 150 |
|    | ACTGGTAAAG | CAATCTCTGT  | ACCAAGTTGGT | GATGCAACAC | TTGGACGTGT  | 200 |
|    | ATTCAACGTA | TTAGGTGATG  | CAATTGACTT  | AGATGGTGAA | CTTCCTGCGG  | 250 |
| 20 | ATGTACACCG | TGATCCAATT  | CACCGTCAAG  | CACCTGCATT | CGAAGAATTA  | 300 |
|    | TCTACTAAAG | TAGAAATTCT  | TGAAACTGGT  | ATTAAAGTAG | TAGACTTACT  | 350 |
|    | TGCTCCTTAC | ATTAAGGGTG  | GTAAGATCGG  | CCTATTCGGT | GGTGCCGGCG  | 400 |
|    | TAGGTAAAAC | AGTATTAATT  | CAGGAGTTAA  | TCAATAACAT | CGCACAAAGAG | 450 |
|    | CACGGTGGTA | TCTCTGTATT  | CGCTGGTGTA  | GGTGAGCGTA | CTCGTGAGGG  | 500 |
| 25 | TAATGACTTA | TACCACGAAA  | TGAGCGATTC  | TGGCGTAATC | AAGAAAACCTG | 550 |
|    | CGATGGTATT | CGGACAAATG  | AACGAGCCAC  | CTGGAGCACG | TCAACGTGTT  | 600 |
|    | GCATTAACAG | GTTTAACAAT  | GGCTGAGCAT  | TTCCGTGATG | AGCAAGGACA  | 650 |
|    | AGACGTACTT | CTGTTTCATCG | ATAACATCTT  | CCGTTTCACG | CAAGCGGGTT  | 700 |
|    | CTGAAGTATC | TGCCCTTCTT  | GGTCGTATGC  | CATCTGCGGT | AGGTTACCAA  | 750 |
| 30 | CCAACACTTG | CAACAGAAAT  | GGGTCAATTA  | CAAGAGCGTA | TTACATCTAC  | 800 |
|    | AAATAAAGGG | TCTATCACGT  | CTATC       |            |             | 825 |

## 35 2) INFORMATION FOR SEQ ID NO: 1249

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*  
 (B) STRAIN: HER 1236

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 50 | ATCTACAACG | CCCTTACGGT | AAAACAAAGC | AACGAAAACG | GAAGTATTAA | 50  |
|    | CTTAACATTT | GAAGTTGCAC | TTCATTTAGG | TGATGATACA | GTTCGTACAG | 100 |
|    | TTGCGATGTC | TTCCACAGAT | GGACTTGTTT | GTGGCACAGA | AGTAGAAGAT | 150 |

|    |            |             |            |            |             |     |
|----|------------|-------------|------------|------------|-------------|-----|
|    | ACTGGTAAAC | CAATCTCTGT  | ACCAGTTGGT | GATGTAACAC | TTGGTCGCGT  | 200 |
|    | ATTTAACGTA | TTAGGTGATG  | CAATTGACTT | AGATGGTGAG | GTTCCCTGCAG | 250 |
|    | ATGTACATCG | TGATCCAATT  | CACCGTCAAG | CACCTGCATT | CGAAGAATTA  | 300 |
|    | TCTACTAAAG | TAGAAATTCT  | TGAAACTGGT | ATTAAAGTAG | TAGACTTACT  | 350 |
| 5  | TGCTCCTTAC | ATTAAGGGTG  | GTAAGATCGG | CCTATTCGGT | GGTGCCGGCG  | 400 |
|    | TAGGTAAAC  | AGTATTAATT  | CAGGAATTAA | TTAACAACAT | CGCACAAGAG  | 450 |
|    | CACGGTGGTA | TCTCTGTATT  | CGCTGGTGTA | GGTGAGCGTA | CTCGTGAGGG  | 500 |
|    | TAATGACTTA | TACCACGAAA  | TGAGCGATTC | TGGCGTAATC | AAGAAAAC TG | 550 |
|    | CGATGGTATT | CGGACAAATG  | AACGAGCCAC | CTGGAGCACG | TCAACGTGTT  | 600 |
| 10 | GCATTAACAG | GTTTAAACAAT | GGCTGAGCAT | TTCCGTGATG | AGCAAGGACA  | 650 |
|    | AGACGTACTT | CTGTTTCATCG | ATAACATCTT | CCGTTTCACG | CAAGCGGGTT  | 700 |
|    | CTGAAGTATC | TGCCCTTCTT  | GGTCGTATGC | CATCTGCGGT | AGGTTACCAA  | 750 |
|    | CCAACACTTG | CAACAGAAAT  | GGGTC      |            |             | 775 |

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## 2) INFORMATION FOR SEQ ID NO: 1250

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 832 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*  
 (B) STRAIN: WSBC 10204

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250

|    |             |            |             |             |            |     |
|----|-------------|------------|-------------|-------------|------------|-----|
|    | CCAGCAATCT  | ACAACGCCCT | TACGGTAAAA  | CAAAGCAACG  | AAAACGGAGC | 50  |
|    | GAGCATCAAC  | TTAACATTTG | AAGTTGCACT  | TCATTTAGGT  | GATGACACAG | 100 |
| 35 | TTCGTACAGT  | TGCGATGTCT | TCCACAGATG  | GACTTGTTTCG | TGGCACAGAA | 150 |
|    | GTAAGAAGATA | CTGGTAAAGC | AATCTCTGTA  | CCAGTTGGTG  | ATGTAACACT | 200 |
|    | TGGTCGCGTA  | TTCAACGTAT | TAGGTGATGC  | AATTGACTTA  | GATGGTGATG | 250 |
|    | TTCCTGCGGA  | TGTACGTCGT | GATCCAATTC  | ACCGTCAAGC  | ACCTGCATTC | 300 |
|    | GAAGAACTAT  | CTACAAGAAT | AGAAATTCTT  | GAAACTGGTA  | TTAAAGTAGT | 350 |
| 40 | AGATTTACTT  | GCTCCTTACA | TTAAGGGTGG  | TAAGATCGGT  | CTATTCGGTG | 400 |
|    | GTGCCGGTGT  | AGGTAAAACG | GTATTAATTC  | AGGAATTAAT  | TAACAACATC | 450 |
|    | GCACAAGAGC  | ACGGTGGTAT | CTCTGTATTC  | GCTGGTGTAG  | GTGAGCGTAC | 500 |
|    | TCGTGAGGGT  | AATGACTTAT | ACCACGAAAT  | GAGCGATTCT  | GGCGTAATTA | 550 |
|    | AGAAAAC TGC | GATGGTATTT | GGACAAATGA  | ACGAGCCACC  | TGGAGCACGT | 600 |
| 45 | CAACGTGTTG  | CATTAACAGG | TTTAAACAATG | GCTGAACATT  | TCCGTGATGA | 650 |
|    | GCAAGGACAA  | GACGTACTAT | TGTTTCATCGA | TAACATCTTC  | CGTTTCACGC | 700 |
|    | AAGCAGGTTT  | TGAAGTATCT | GCCCTTCTTG  | GTCGTATGCC  | ATCTGCGGTA | 750 |
|    | GGTTACCAAC  | CAACACTTGC | AACAGAAATG  | GGTCAATTAC  | AAGAGCGTAT | 800 |
|    | TACATCTACA  | AATAAAGGGT | CTATCACGTC  | TA          |            | 832 |

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## 2) INFORMATION FOR SEQ ID NO: 1251

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*  
(B) STRAIN: HER 1418

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251

```
15 AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT      50
   AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC      100
   AGTTGCGATG TCTTCCACAG ATGGACTTGT TCGTGGCACA GAAGTAGAAG      150
   ATACTGGTAA ACCAATCTCT GTACCAGTTG GTGATGTAAC ACTTGGTCGC      200
20 GTATTTAACG TATTAGGTGA TGCAATTGAC TTAGATGGTG AGGTTCCCTGC      250
   AGATGTACAT CGTGATCCAA TTCACCGTCA AGCACCTGCA TTCGAAGAAT      300
   TATCTACTAA AGTAGAAATT CTTGAAACTG GTATTAAAGT AGTAGACTTA      350
   CTTGCTCCTT ACATTAAGGG TGGTAAGATC GGCCTATTTC GTGGTGCCGG      400
   CGTAGGTAAA ACAGTATTAA TTCAGGAATT AATTAACAAC ATCGCACAAAG      450
25 AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG TACTCGTGAG      500
   GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA TCAAGAAAAC      550
   TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA CGTCAACGTG      600
   TTGCATTAAC AGGTTTAAAC ATGGCTGAGC ATTTCCGTGA TGAGCAAGGA      650
   CAAGACGTAC TTCTGTTTCA CGATAACATC TTCCGTTTCA CGCAAGCGGG      700
30 TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG GTAGGTTACC      750
   AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG TATTACATCT      800
   AC                                                                802
```

## 2) INFORMATION FOR SEQ ID NO: 1252

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*  
(B) STRAIN: HER 1410

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252

```
AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT      50
AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC      100
```



|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | AGTTGCAATG | TCTTCCACAG | ATGGACTTGT | TCGTGGCACA | GAAGTAGAAG  | 150 |
|    | ATACTGGTAA | ACCAATCTCT | GTACCAGTTG | GTGATGTAAC | ACTTGGTCGC  | 200 |
|    | GTATTTAACG | TATTAGGTGA | TGCAATTGAC | TTAGATGGTG | AGGTTCTCTG  | 250 |
|    | AGATGTACAT | CGTGATCCAA | TTCACCGTCA | AGCACCTGCA | TTCGAAGAAT  | 300 |
| 5  | TATCTACTAA | AGTAGAAATT | CTTGAAACTG | GTATTAAAGT | AGTAGACTTA  | 350 |
|    | CTTGCTCCTT | ACATTAAGGG | TGGTAAGATC | GGCCTATTCG | GTGGTGCCGG  | 400 |
|    | CGTAGGTAAA | ACAGTATTAA | TTCAGGAATT | AATTAACAAC | ATCGCACAAAG | 450 |
|    | AGCACGGTGG | TATCTCTGTA | TTCGCTGGTG | TAGGTGAGCG | TACTCGTGAG  | 500 |
|    | GGTAATGACT | TATACCACGA | AATGAGCGAT | TCTGGCGTAA | TCAAGAAAAC  | 550 |
| 10 | TGCGATGGTA | TTCCGACAAA | TGAACGAGCC | ACCTGGAGCA | CGTCAACGTG  | 600 |
|    | TTGCATTAAC | AGGCTTAACA | ATGGCTGAGC | ATTTCCGTGA | TGAGCAAGGA  | 650 |
|    | CAAGACGTAC | TTCTGTTCAT | CGATAACATC | TTCCGTTTCA | CGCAAGCGGG  | 700 |
|    | TTCTGAAGTA | TCTGCCCTTC | TTGGTCGTAT | GCCATCTGCG | GTAGGTTACC  | 750 |
|    | AACCAACACT | TGCAACAGAA | ATGGGTCAAT | TACAAGAGCG | TATTACATCT  | 800 |
| 15 | ACAAATAAAG | GGTCTATCAC | GTC        |            |             | 823 |

## 2) INFORMATION FOR SEQ ID NO: 1253

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

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## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*  
 (B) STRAIN: ATCC 13472

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253

|    |             |             |             |             |             |     |
|----|-------------|-------------|-------------|-------------|-------------|-----|
| 35 | CCAGAAATCT  | ACAATGCCCT  | TACGGTAAAA  | CAAAGCAACG  | AAAACGGAAG  | 50  |
|    | CATGAACCTTA | ACATTTGAAG  | TTGCACTTCA  | TTTAGGTGAT  | GATACAGTTC  | 100 |
|    | GTACAGTTGC  | GATGTCTTCC  | ACAGATGGAC  | TTGTTTCGTGG | CACAGAAGTA  | 150 |
|    | GAAGATACTG  | GTAAAGCAAT  | CTCTGTACCA  | GTTGGTGATG  | CAACACTTGG  | 200 |
|    | ACGTGTATTTC | AACGTATTAG  | GTGATGCAAT  | TGACTTAGAT  | GGTGAACCTTC | 250 |
| 40 | CTGCGGATGT  | ACACCGTGAT  | CCAATTCACC  | GTCAAGCACC  | TGCATTCGAA  | 300 |
|    | GAATTATCTA  | CTAAAGTAGA  | AATTCTTGAA  | ACTGGTATTA  | AAGTAGTAGA  | 350 |
|    | CTTACTTGCT  | CCTTACATTA  | AGGGTGGTAA  | GATCGGCCTA  | TTCGGTGGTG  | 400 |
|    | CCGGCGTAGG  | TAAAACAGTA  | TTAATTCAGG  | AATTAATCAA  | TAACATCGCA  | 450 |
|    | CAAGAGCATG  | GTGGTATCTC  | TGTATTTCGCT | GGTGTAGGTG  | AGCGTACTCG  | 500 |
| 45 | TGAGGGGTAAT | GACTTATACC  | ACGAAATGAG  | CGATTCTGGC  | GTAATCAAGA  | 550 |
|    | AAACTGCGAT  | GGTATTTCGGA | CAAATGAACG  | AGCCACCTGG  | AGCACGTCAA  | 600 |
|    | CGTGTTGCAT  | TAACAGGTTT  | AACAATGGCT  | GAGCATTTCC  | GTGATGAGCA  | 650 |
|    | AGGACAAGAC  | GTACTTCTGT  | TCATCGATAA  | CATCTTCCGT  | TTCACGCAAG  | 700 |
|    | CGGGTTCTGA  | AGTATCTGCC  | CTTCTTGGTC  | GTATGCCATC  | TGCGGTAGGT  | 750 |
| 50 | TACCAACCGA  | CACTTGCAAC  | AGAAATGGGT  | CAATTACAAG  | AGCGTATT    | 798 |

## 2) INFORMATION FOR SEQ ID NO: 1254

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*  
 (B) STRAIN: ATCC 7064

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254

|            |            |             |            |            |     |
|------------|------------|-------------|------------|------------|-----|
| CATTTGAAGT | TGCACTTCAT | TTAGGTGATG  | ACACAGTTCG | TACAGTTGCA | 50  |
| ATGTCTTCCA | CAGATGGACT | TGTTTCGTGGC | ACAGAAGTAG | AAGATACTGG | 100 |
| TAAAGCAATC | TCTGTACCAG | TTGGTGATGC  | AACACTTGGT | CGTGTATTTA | 150 |
| ACGTATTAGG | TGATGCAATT | GACTTAGATG  | GTGAGGTTCC | TGCGGATGTA | 200 |
| CGTCGTGATC | CAATTCACCG | TCAAGCACCT  | GCATTCGAAG | AATTATCTAC | 250 |
| TAAAGTAGAA | ATTCTTGAAA | CTGGTATTAA  | AGTAGTAGAC | TTACTTGCTC | 300 |
| CTTACATTAA | GGGTGGTAAG | ATCGGTCTAT  | TCGGTGGTGC | CGGTGTAGGT | 350 |
| AAAACGGTAT | TAATTCAGGA | ATTAATCAAT  | AACATCGCAC | AAGAACACGG | 400 |
| TGGTATCTCT | GATTCGCTG  | GTGTAGGTGA  | GCGTACTCGT | GAGGGTAATG | 450 |
| ACTTATACCA | CGAAATGAGC | GATTCTGGCG  | TAATTAAGAA | AACTGCGATG | 500 |
| GTATTCGGAC | AAATGAACGA | GCCACCTGGA  | GCACGTCAAC | GTGTTGCGTT | 550 |
| AACAGGTTTA | ACAATGGCTG | AGCATTTCGG  | TGATGAGCAA | GGACAAGACG | 600 |
| TACTTCTGTT | CATCGATAAT | ATCTTCCGTT  | TCACGCAAGC | AGGTTCTGAA | 650 |
| GTATCTGCCC | TTCTTGGCCG | TATGCCATCT  | GCGGTAGGTT | ACCAACCAAC | 700 |
| ACTTGCAACA | GAAATGGGTC | AATTACAAGA  | GCGTATTACA | TCTACAAATA | 750 |
| AAGGGTCTAT | CACGTCT    |             |            |            | 767 |

## 2) INFORMATION FOR SEQ ID NO: 1255

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*  
 (B) STRAIN: C-14

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255

|            |             |            |            |            |     |
|------------|-------------|------------|------------|------------|-----|
| GAAATGCGTG | AATCATTTTT  | AGATTATGCG | ATGAGTGTTA | TCGTTGCTCG | 50  |
| TGCATTGCCA | GATGTTTCGTG | ACGGTTTAAA | ACCAGTACAT | CGTCGTATAC | 100 |

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | TATATGGATT | AAATGAACAA | GGTATGACAC | CGGATAAATC | ATATAAAAAA | 150  |
|    | TCAGCACGTA | TCGTTGGTGA | CGTAATGGGT | AAATATCACC | CTCATGGTGA | 200  |
|    | CTTATCTATT | TATGAAGCAA | TGGTACGTAT | GGCTCAAGAT | TTCAGTTATC | 250  |
|    | GTTATCCGCT | TGTTGATGGC | CAAGGTAACT | TTGGTTCAAT | GGATGGAGAT | 300  |
| 5  | GGCGCAGCAG | CAATGCGTTA | TACTGAAGCG | CGTATGACTA | AAATCACACT | 350  |
|    | TGAACTGTTA | CGTGATATTA | ATAAAGATAC | AATAGATTTT | ATCGATAACT | 400  |
|    | ATGATGGTAA | TGAAAGAGAG | CCGTCAGTCT | TACCTGCTCG | ATTCCCTAAC | 450  |
|    | TTATTAGCCA | ATGGTGCATC | AGGTATCGCG | GTAGGTATGG | CAACGAATAT | 500  |
|    | TCCACCACAT | AACTTAACAG | AATTAATCAA | TGGTGTACTT | AGCTTAAGTA | 550  |
| 10 | AGAACCCTGA | TATTTCAATT | GCTGAGTTAA | TGGAGGATAT | TGAAGGTCCT | 600  |
|    | GATTTCCCAA | CTGCTGGACT | TATTTTAGGT | AAGAGTGGTA | TTAGACGTGC | 650  |
|    | ATATGAAACA | GGTCGTGGTT | CAATTCAAAT | GCGTTCTCGT | GCAGTTATTG | 700  |
|    | AAGAACGTGG | AGNCGGACGT | CAACGTATTG | TTGTCACTGA | AATTCCTTTC | 750  |
|    | CAAGTGAATA | AGGCTCGTAT | GATTGAAAAA | ATTGCAGAGC | TCGTTCTGTA | 800  |
| 15 | CAAGAAAATT | GACGGTATCA | CTGATTTACG | TGATGAAACA | AGTTTACGTA | 850  |
|    | CTGGTGTGCG | TGTCGTTATT | GATGTGCGTA | AGGATGCAAA | TGCTAGTGTC | 900  |
|    | ATTTTAAATA | ACTTATACAA | ACAAACACCT | CTTCAAACAT | CATTTGGTGT | 950  |
|    | GAATATGATT | GCACTTGTA  | ATGGTAGACC | GAAGCTTATT | AATTTAAAG  | 1000 |
|    | AAGCGTTGGT | ACATTATTTA | GAGCATCAAA | AGACAGTTGT | TAGAAGACGT | 1050 |
| 20 | ACGCAATACA | ACTTACGTAA | AGCTAAAGAT | CGTGCCACA  | TTTGTAGAAG | 1100 |
|    | ATTACGTATC | GCACTTGACC | ATATCGATGA | AATTATTTC  | ACGATTCGTG | 1150 |
|    | AGTCAGATAC | AGATAAAGTT | GCAA       |            |            | 1174 |

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## 2) INFORMATION FOR SEQ ID NO: 1256

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

35

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*  
 (B) STRAIN: WSBC 10209

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATCTACAACG | CCCTTACGGT | AAAACAAAGC | AACGAAAACG | GAGCAAGCAT | 50  |
|    | TAACTTAACA | TTTGAAGTTG | CACTTCATTT | AGGTGATGAC | ACAGTTCGTA | 100 |
|    | CAGTTGCAAT | GTCTTCCACA | GATGGACTTG | TTCGTGGCAC | AGAAGTAGAA | 150 |
| 45 | GATACTGGTA | AAGCAATCTC | TGTACCAGTT | GGTGATGTAA | CACTTGGTGC | 200 |
|    | TGTATTTAAC | GTATTAGGTG | ATGCAATTGA | CTTAGATGGA | GATGTTCTTG | 250 |
|    | CGGATGTACG | TCGTGATCCA | ATTCACCGTC | AAGCGCCTGC | ATTCGAAGAG | 300 |
|    | TTATCTACTA | AAGTAGAAAT | TCTTGAAACT | GGTATTAAAG | TAGTAGACTT | 350 |
|    | ACTTGCTCCT | TACATTAAGG | GTGGTAAGAT | CGGTCTATTC | GGTGGTGCCG | 400 |
| 50 | GTGTAGGTAA | AACAGTATTA | ATTCAGGAAT | TAATTAACAA | CATCGCACAA | 450 |
|    | GAGCACGGTG | GTATCTCTGT | ATTCGCTGGT | GTAGGTGAGC | GTAATCGTGA | 500 |
|    | AGGTAACGAC | TTATACCACG | AAATGAGCGA | TTCTGGCGTA | ATTAAGAAAA | 550 |
|    | CTGCGATGGT | ATTCGGACAA | ATGAACGAGC | CACCTGGAGC | ACGTCAACGT | 600 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GTTGCATTAA | CAGGTTTAAC | AATGGCTGAA | CATTTCCTGT | ATGAGCAAGG | 650 |
| GCAAGACGTA | CTATTGTTCA | TCGATAACAT | CTTCCGTTTC | ACGCAAGCGG | 700 |
| GTTCTGAAGT | ATCTGCCCTT | CTTGGTCGTA | TGCCATCTGC | GGTAGGTTAC | 750 |
| CAGCCAACAC | TTGCAACAGA | AATGGGTCAA |            |            | 780 |

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## 2) INFORMATION FOR SEQ ID NO: 1257

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 7700

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| CTACCAGAAA    | TCTACAACGC | CCTTACGGTA | AAACAGAGCA | ACGAAAACGG | 50  |
| 25 AACAAGCATT | AACTTAACAT | TTGAAGTTGC | ACTTCATTTA | GGTGATGACA | 100 |
| CAGTTCGTAC    | AGTTGCAATG | TCTTCCACAG | ATGGACTTGT | TCGTGGCACA | 150 |
| GAAGTAGAAG    | ATACTGGTAA | AGCAATCTCT | GTACCAGTTG | GTGATGCAAC | 200 |
| ACTTGGTCGT    | GTATTTAACG | TATTAGGTGA | TGCAATTGAC | TTAGATGGTG | 250 |
| AGGTTTCCTGC   | GGATGTACGT | CGTGATCCAA | TTCACCGTCA | AGCACCTGCA | 300 |
| 30 TTCGAAGAAT | TATCTACTAA | AGTAGAAATT | CTTGAAACTG | GTATTAAAGT | 350 |
| AGTAGACTTA    | CTTGCTCCTT | ACATTAAGGG | TGGTAAGATC | GGTCTATTCT | 400 |
| GTGGTGCCGG    | TGTAGGTAAA | ACGGTATTAA | TTCAGGAATT | AATCAATAAC | 450 |
| ATCGCACAAAG   | AACACGGTGG | TATCTCTGTA | TTCGCTGGTG | TAGGTGAGCG | 500 |
| TACTCGTGAG    | GGTAATGACT | TATACCACGA | AATGAGCGAT | TCTGGCGTAA | 550 |
| 35 TTAAGAAAAC | TGCGATGGTA | TTCGGACAAA | TGAACGAGCC | ACCTGGAGCA | 600 |
| CGTCAACGTG    | TTGCGTTAAC | AGGTTTAACA | ATGGCTGAGC | ATTTCCGTGA | 650 |
| TGAGCAAGGA    | CAAGATGTAC | TTCTGTTCAT | CGATAATATC | TTCCGTTTCA | 700 |
| CGCAAGCAGG    | TTCTGAAGTA | TCTGCCCTTC | TTGGCCGTAT | GCCATCTGCG | 750 |
| GTAGGTTACC    | AACCAACACT | TGCAACAGAA | ATGGGTCAAT | TACAAGAGCG | 800 |
| 40 TATTACATCT | ACAAATA    |            |            |            | 817 |

## 2) INFORMATION FOR SEQ ID NO: 1258

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1404

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | CCAGAAATCT | ACAACGCCCT | TACGGTAAAA | CAAAGCAACG | AAAACGGAAG  | 50  |
|    | TATTAACTTA | ACATTTGAAG | TTGCACTTCA | TTTAGGTGAT | GATACAGTTC  | 100 |
|    | GTACAGTTGC | GATGTCTTCC | ACAGATGGAC | TTGTTCTGTG | CACAGAAGTA  | 150 |
| 10 | GAAGATACTG | GTAAACCAAT | CTCTGTACCA | GTTGGTGATG | TAACACTTGG  | 200 |
|    | TCGCGTATTT | AACGTATTAG | GTGATGCAAT | TGACTTAGAT | GGTGAGGTTC  | 250 |
|    | CTGCAGATGT | ACATCGTGAT | CCAATTCACC | GTCAAGCACC | TGCATTGCGAA | 300 |
|    | GAATTATCTA | CTAAAGTAGA | AATTCTTGAA | ACTGGTATTA | AAGTAGTAGA  | 350 |
|    | CTTACTTGCT | CCTTACATTA | AGGGTGGTAA | GATCGGCCTA | TTCGGTGGTG  | 400 |
| 15 | CCGGCGTAGG | TAAACAGTA  | TTAATTCAGG | AATTAATTAA | CAACATCGCA  | 450 |
|    | CAAGAGCACG | GTGGTATCTC | TGTATTCGCT | GGTGTAGGTG | AGCGTACTCG  | 500 |
|    | TGAGGGTAAT | GACTTATACC | ACGAAATGAG | CGATTCTGGC | GTAATCAAGA  | 550 |
|    | AAACTGCGAT | GGTATTCGGA | CAAATGAACG | AGCCACCTGG | AGCACGTCAA  | 600 |
|    | CGTGTTGCAT | TAACAGGTTT | AACAATGGCT | GAGCATTTCC | GTGATGAGCA  | 650 |
| 20 | AGGACAAGAC | GTACTTCTGT | TCATCGATAA | CATCTTCCGT | TTCACGCAAG  | 700 |
|    | CGGGTTCTGA | AGTATCTGCC | CTTCTTGGTC | GTATGCCATC | TGCGGTAGGT  | 750 |
|    | TACCAACCAA | CACTTGCAAC | AGAAATGGGT | CAATTACAAG | AGCGTATTAC  | 800 |
|    | ATCTACAAAT | AAAGGGTCTA | TCACGTCTA  |            |             | 829 |

25

## 2) INFORMATION FOR SEQ ID NO: 1259

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 844 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 35 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 15816

40 (C) ACCESSION NUMBER:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259

|    |            |             |            |            |             |     |
|----|------------|-------------|------------|------------|-------------|-----|
|    | TGGCGGAAAG | CTACCAGAAA  | TCTACAACGC | CCTTACGGTA | AAACAGAGCA  | 50  |
| 45 | ACGAAAACGG | TGAACCTAAC  | TTAACATTTG | AAGTTGCACT | TCATTTAGGT  | 100 |
|    | GATGATACAG | TTCGTACAGT  | TGCGATGTCT | TCCACAGATG | GACTTGTTTCG | 150 |
|    | TGGCACAGAA | GTAAGAAGATA | CTGGTAAAGC | AATCTCTGTA | CCAGTTGGTG  | 200 |
|    | ATGCAACACT | TGGTCGCGTA  | TTTAACGTAT | TAGGTGATGC | TATTGACTTA  | 250 |
|    | GATGGTGAGG | TTCCTGCGGA  | TGTACGTCGT | GATCCAATTC | ACCGTCAAGC  | 300 |
| 50 | ACCTGCATTC | GAAGAATTAT  | CTACTAAAGT | AGAAATTCTT | GAAACTGGTA  | 350 |
|    | TTAAAGTAGT | AGACTTACTT  | GCTCCTTACA | TTAAGGGTGG | TAAGATCGGC  | 400 |
|    | CTATTCGGTG | GTGCCGGTGT  | AGGTAAAACA | GTATTAATTC | AGGAGTTAAT  | 450 |
|    | CAACAACATC | GCACAAGAGC  | ACGGTGGTAT | CTCTGTATTC | GCTGGTGTAG  | 500 |

|   |            |            |            |             |            |     |
|---|------------|------------|------------|-------------|------------|-----|
|   | GTGAGCGTAC | TCGTGAGGGT | AATGACTTAT | ACCACGAAAT  | GAGCGATTCT | 550 |
|   | GGCGTAATTA | AGAAAAGTGC | GATGGTATTC | GGACAAATGA  | ACGAGCCACC | 600 |
|   | TGGAGCACGT | CAACGTGTTG | CATTAACAGG | CTTAACAATG  | GCTGAATATT | 650 |
|   | TCCGTGATGA | GCAAGGACAA | GACGTACTTC | TGTTTCATCGA | TAATATCTTC | 700 |
| 5 | CGTTTCACGC | AAGCAGGTTC | TGAAGTATCT | GCCCTTCTTG  | GCCGTATGCC | 750 |
|   | ATCTGCGGTA | GGTTACCAAC | CAACACTTGC | AACAGAAATG  | GGTCAATTAC | 800 |
|   | AAGAGCGTAT | TACATCTACA | AATAAAGGGT | CTATCACGTC  | TATC       | 844 |

10

## 2) INFORMATION FOR SEQ ID NO: 1260

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 840 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 49064

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
|    | AAGCTACCAG  | AAATCTACAA | CGCCCTTACG | GTAAAACAGA | GCAACGAAAA | 50  |
|    | CGGAACAAGC  | ATTAAGTTAA | CATTTGAAGT | TGCACTTCAT | TTAGGTGATG | 100 |
|    | ACACAGTTCG  | TACAGTTGCA | ATGTCTTCCA | CAGATGGACT | TGTTCTGTCG | 150 |
| 30 | ACAGAAAGTAG | AAGATACTGG | TAAAGCAATC | TCTGTACCAG | TTGGTGATGC | 200 |
|    | AACACTTGGT  | CGTGTATTTA | ACGTATTAGG | TGATGCAATT | GACTTAGATG | 250 |
|    | GTGAGGTTCC  | TGCGGATGTA | CGCCGTGATC | CAATTCACCG | TCAAGCACCT | 300 |
|    | GCAATCGAAG  | AATTATCTAC | TAAAGTAGAA | ATTCTTGAAA | CTGGTATTAA | 350 |
|    | AGTAGTAGAC  | TTACTTGCTC | CTTACATTAA | GGGTGGTAAG | ATCGGTCTAT | 400 |
| 35 | TCGGTGGTGC  | CGGTGTAGGT | AAAACAGTAT | TAATTCAGGA | ATTAATCAAC | 450 |
|    | AACATCGCAC  | AAGAACACGG | TGGTATCTCT | GTATTCGCTG | GTGTAGGTGA | 500 |
|    | GCGTACTCGT  | GAGGGTAATG | ACTTATACCA | CGAAATGAGC | GATTCAGGCG | 550 |
|    | TAATTAAGAA  | AACTGCGATG | GTATTCGGAC | AAATGAACGA | GCCACCTGGA | 600 |
|    | GCGCGTCAAC  | GTGTTGCGTT | AACAGGTTTA | ACAATGGCTG | AGCATTTCGG | 650 |
| 40 | TGATGAGCAA  | GGACAAGACG | TTCTTCTGTT | CATCGATAAT | ATCTTCCGTT | 700 |
|    | TCACGCAAGC  | AGGTTCTGAA | GTATCTGCCC | TTCTTGGTCG | TATGCCATCT | 750 |
|    | GCGGTAGGTT  | ACCAACCAAC | ACTTGCAACA | GAAATGGGTC | AATTACAAGA | 800 |
|    | GCGTATTACA  | TCTACAAATA | AAGGGTCTAT | CACGTCTATC |            | 840 |

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## 2) INFORMATION FOR SEQ ID NO: 1261

## (i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 839 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus thuringiensis*  
(B) STRAIN: BGSC 4AZ1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261

|    |             |            |            |            |             |     |
|----|-------------|------------|------------|------------|-------------|-----|
| 10 | GCGGAAAGCT  | ACCAGAAATC | TACAATGCCC | TTACGGTAAA | ACAAAGCAAC  | 50  |
|    | GAAAACGGAA  | GCATGAACCT | AACATTTGAA | GTTGCACTTC | ATTTAGGTGA  | 100 |
|    | TGATACAGTT  | CGTACAGTTG | CGATGTCTTC | CACAGATGGA | CTTGTTTCGTG | 150 |
|    | GCACAGAAGT  | AGAAGATACT | GGTAAAGCAA | TCTCTGTACC | AGTTGGTGAT  | 200 |
|    | GCAACACTTG  | GACGTGTATT | CAACGTATTA | GGTGATGCAA | TTGACTTAGA  | 250 |
| 15 | TGGTGAACTT  | CCTGCGGATG | TACACCGTGA | TCCAATTCAC | CGTCAAGCAC  | 300 |
|    | CTGCATTTCGA | AGAATTATCT | ACTAAAGTAG | AAATTCTTGA | AACTGGTATT  | 350 |
|    | AAAGTAGTAG  | ACTTACTTGC | TCCTTACATT | AAGGGTGGTA | AGATCGGCCT  | 400 |
|    | ATTCGGTGGT  | GCCGGCGTAG | GTAAAACAGT | ATTAATTCAG | GAGTTAATCA  | 450 |
|    | ATAACATCGC  | ACAAGAGCAC | GGTGGTATCT | CTGTATTCGC | TGGTGTAGGT  | 500 |
| 20 | GAGCGTACTC  | GTGAGGGTAA | TGACTTATAC | CACGAAATGA | GCGATTCTGG  | 550 |
|    | CGTAATCAAG  | AAAACCTGCG | TGGTATTCGG | ACAAATGAAC | GAGCCACCTG  | 600 |
|    | GAGCACGTCA  | ACGTGTTGCA | TTAACAGGTT | TAACAATGGC | TGAGCATTTT  | 650 |
|    | CGTGATGAGC  | AAGGACAAGA | CGTACTTCTG | TTCATCGATA | ACATCTTCCG  | 700 |
|    | TTTCACGCAA  | GCGGGTCTG  | AAGTATCTGC | CCTTCTTGGT | CGTATGCCAT  | 750 |
| 25 | CTGCGGTAGG  | TTACCAACCA | ACACTTGCAA | CAGAAATGGG | TCAATTACAA  | 800 |
|    | GAGCGTATTA  | CATCTACAAA | TAAAGGGTCT | ATCACGTCT  |             | 839 |

30 2) INFORMATION FOR SEQ ID NO: 1262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases  
(B) TYPE: Nucleic acid  
35 (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*  
(B) STRAIN: BGSC 4H2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 45 | AAGCTACCAG | AAATCTACAA | TGCCCTTACG | GTAAAACAAA | GCAACGAAAA | 50  |
|    | CGGAAGCATG | AACTTAACAT | TTGAAGTTGC | ACTTCATTTA | GGTGATGATA | 100 |
|    | CAGTTCGTAC | AGTTGCGATG | TCTTCCACAG | ATGGACTTGT | TCGTGGCACA | 150 |
|    | GAAGTAGAAG | ATACTGGTAA | AGCAATCTCT | GTACCAGTTG | GTGATGCAAC | 200 |
| 50 | ACTTGGACGT | GTATTCAACG | TATTAGGTGA | TGCAATTGAC | TTAGATGGTG | 250 |
|    | AACTTCCTGC | GGATGTACAC | CGTGATCCAA | TTCACCGTCA | AGCACCTGCA | 300 |
|    | TTCGAAGAAT | TATCTACTAA | AGTAGAAATT | CTTGAAACTG | GTATTAAAGT | 350 |
|    | AGTAGACTTA | CTTGCTCCTT | ACATTAAGGG | TGGTAAGATC | GGCCTATTCG | 400 |

|   |             |            |            |            |            |     |
|---|-------------|------------|------------|------------|------------|-----|
|   | GTGGTGCCGG  | CGTAGGTAAA | ACAGTATTAA | TTCAGGAATT | AATCAATAAC | 450 |
|   | ATCGCACAAAG | AGCACGGTGG | TATCTCTGTA | TTCGCTGGTG | TAGGTGAGCG | 500 |
|   | TACTCGTGAG  | GGTAATGACT | TATACCACGA | AATGAGCGAT | TCTGGCGTAA | 550 |
|   | TCAAGAAAAC  | TGCGATGGTA | TTCGGACAAA | TGAACGAGCC | ACCTGGAGCA | 600 |
| 5 | CGTCAACGTG  | TTGCATTAAC | AGGTTTAACA | ATGGCTGAGC | ATTTCCGTGA | 650 |
|   | TGAGCAAGGA  | CAAGACGTAC | TTCTGTTCAT | CGATAACATC | TTCCGTTTCA | 700 |
|   | CGCAAGCGGG  | TTCTGAAGTA | TCTGCCCTTC | TTGGTCGTAT | GCCATCTGCG | 750 |
|   | GTAGGTTACC  | AACCAACACT | TGCAACAGAA | ATGGGTCAAT | TACAAGAGCG | 800 |
|   | TATTACATCT  | ACAAATAAAG | GGTCTATCAC | GTC        |            | 833 |

## 2) INFORMATION FOR SEQ ID NO: 1263

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 790 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Bacillus thuringiensis*  
 25 (B) STRAIN: BGSC 4Q1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | CGAAAACGGA | AGCATGAACT | TAACATTTGA | AGTTGCACTT  | CATTTAGGTG | 50  |
| 30 | ATGATACAGT | TCGTACAGTT | GCGATGTCTT | CCACAGATGG  | ACTTGTTCTG | 100 |
|    | GGCACAGAAG | TAGAAGATAC | TGGTAAAGCA | ATTTCTGTAC  | CAGTTGGTGA | 150 |
|    | TGTAACACTT | GGACGTGTAT | TCAACGTATT | AGGTGATGCA  | ATTGACTTAG | 200 |
|    | ATGGTGAAGT | TCCTGCGGAT | GTACACCGTG | ATCCAATTCA  | CCGTCAAGCA | 250 |
|    | CCTGCATTCT | AAGAATTATC | TACTAAAGTA | GAAATTCTTG  | AAACTGGTAT | 300 |
| 35 | TAAAGTAGTA | GACTTACTTG | CTCCTTACAT | TAAGGGTGGT  | AAGATCGGCC | 350 |
|    | TATTCGGTGG | TGCCGGTGTA | GGTAAACAG  | TATTAATTCA  | GGAATTAATT | 400 |
|    | AACAACATCG | CACAAGAGCA | CGGTGGTATC | TCTGTATTCT  | CTGGTGTAGG | 450 |
|    | TGAGCGTACT | CGTGAGGGTA | ATGACTTATA | CCACGAAATG  | AGCGATTCTG | 500 |
|    | GCGTAATCAA | GAAAACTGCG | ATGGTATTCT | GACAAATGAA  | CGAGCCACCT | 550 |
| 40 | GGAGCACGTC | AACGTGTTGC | ATTAACAGGT | TTAACAATGG  | CTGAGCATTT | 600 |
|    | CCGTGATGAG | CAAGGACAAG | ACGTACTTCT | GTTTCATCGAT | AACATCTTCC | 650 |
|    | GTTTCACGCA | AGCGGGTTCT | GAAGTATCTG | CCCTTCTTGG  | TCGTATGCCA | 700 |
|    | TCTGCGGTAG | GTTACCAACC | AACACTTGCA | ACAGAAATGG  | GTCAATTACA | 750 |
|    | AGAGCGTATT | ACATCTACAA | ATAAAGGGTC | TATCACGTCT  |            | 790 |

## 2) INFORMATION FOR SEQ ID NO: 1264

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 644 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double



(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264

```

10 AGTTGCACTT CATTAGGTG ATGATACAGT TCGTACAGTT GCGATGTCTT 50
   CCACAGATGG ACTTGTTTCG GGCACAGAAG TAGAAGATAC TGGTAAACCA 100
   ATCTCTGTAC CAGTTGGTGA TGTAACACTT GGTCGCGTAT TTAACGTATT 150
   AGGTGATGCA ATTGACTTAG ATGGTGAGGT TCCTGCAGAT GTACATCGTG 200
15 ATCCAATTCA CCGTCAAGCA CCTGCATTCG AAGAATTATC TACTAAAGTA 250
   GAAATTCTTG AAAGTGGTAT TAAAGTAGTA GACTTACTTG CTCCTTACAT 300
   TAAGGGTGGT AAGATCGGCC TATTCGGTGG TGCCGGCGTA GGTAAAACAG 350
   TATTAATTCA GGAATTAATT AACAACATCG CACAAGAGCA CGGTGGTATC 400
   TCTGTATTCG CTGGTGTAGG TGAGCGTACT CGTGAGGGTA ATGACTTATA 450
20 CCACGAAATG AGCGATTCTG GCGTAATCAA GAAAAGTGGT ATGGTATTCG 500
   GACAAATGAA CGAGCCACCT GGAGCACGTC AACGTGTTGC ATTAACAGGT 550
   TTAACAATGG CTGAGCATTT CCGTGATGAG CAAGGACAAG ACGTACTTCT 600
   GTTCATCGAT AACATCTTCC GTTTCACGCA AGCGGGTTCT GAAG 644

```

25

2) INFORMATION FOR SEQ ID NO: 1265

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 823 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265

```

   GGCGGAAAGC TACCAGAAAT CTACAACGCC CTTACGGTAA AACAGAGCAA 50
   CGAAAACGGA ACAAGCATTG ACTTAACATT TGAAGTTGCA CTTCAATTTAG 100
45 GTGATGACAC AGTTCGTACA GTTGCAATGT CTTCCACAGA TGGACTTGTT 150
   CGTGGCACAG AAGTAGAAGA TACTGGTAAA GCAATCTCTG TACCAGTTGG 200
   TGATGCAACA CTTGGTCGTG TATTTAACGT ATTAGGTGAT GCAATTGACT 250
   TAGATGGTGA GGTTCCCTGCG GATGTACGTC GTGATCCAAT TCACCGTCAA 300
   GCACCTGCAT TCGAAGAATT ATCTACTAAA GTAGAAATTC TTGAAACTGG 350
50 TATTAAAGTA GTAGACTTAC TTGCTCCTTA CATTAGGGT GGTAAGATCG 400
   GTCTATTCGG TGGTGCCGGT GTAGGTAAAA CGGTATTAAT TCAGGAATTA 450
   ATCAATAACA TCGACAAGA ACACGGTGGT ATCTCTGTAT TCGCTGGTGT 500
   AGGTGAGCGT ACTCGTGAGG GTAATGACTT ATACCACGAA ATGAGCGATT 550

```

|   |            |            |            |             |            |     |
|---|------------|------------|------------|-------------|------------|-----|
|   | CTGGCGTAAT | TAAGAAACT  | GCGATGGTAT | TCGGACAAAT  | GAACGAGCCA | 600 |
|   | CCTGGAGCAC | GTCAACGTGT | TGCGTTAACA | GGTTTAACAA  | TGGCTGAGCA | 650 |
|   | TTTCCGTGAT | GAGCAAGGAC | AAGATGTACT | TCTGTTTCATC | GATAATATCT | 700 |
|   | TCCGTTTCAC | GCAAGCAGGT | TCTGAAGTAT | CTGCCCTTCT  | TGGCCGTATG | 750 |
| 5 | CCATCTGCGG | TAGGTTACCA | ACCAACACTT | GCAACAGAAA  | TGGGTCAATT | 800 |
|   | ACAAGAGCGT | ATTACATCTA | CAA        |             |            | 823 |

## 10 2) INFORMATION FOR SEQ ID NO: 1266

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*  
 (B) STRAIN: ATCC 200443

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266

|    |             |             |            |            |            |     |
|----|-------------|-------------|------------|------------|------------|-----|
| 25 | TGGTCCGAGR  | CCCGATTCTMA | TGAAATTATC | AAGGAAACCT | CCAAYTTCAT | 50  |
|    | TAAGAAGGTC  | GGATATAACC  | CCAAGACTGT | TCCTTTCGTT | CCCATTTCTG | 100 |
|    | GTTTCCAGGG  | TGACAACATG  | ATCGATSCCT | CTGCCAACTG | CCCATGGTAC | 150 |
|    | AAGGGCTGGT  | ACMAKGAGAC  | TGCCGACAGG | CAAGYACTCT | GGCAAGACCC | 200 |
| 30 | TTCTTGAGGC  | CATTGACGSC  | ATTGAGCCCC | CCAMSCGTCC | TWCCGATAAA | 250 |
|    | CCTCTCCGTC  | TTCCTCTCCA  | GGATGTCTAC | AAGATCTCCG | GTATTGGMAC | 300 |
|    | TGTTCTGTGTC | GGACGTRTTG  | AGACTGGAGT | CATCAAGCCC | GGTATGGTCG | 350 |
|    | TGACCTTCGC  | TCCCGCCAAC  | GTCACCACTG | AAGTCAAGTC | CGTTGAAATG | 400 |
|    | CACCACCAGC  | AGCTTTCCGA  | CGGTAWCCCC | GGTGACAACG | TCGGCTTCAA | 450 |
| 35 | CGTCAAGAAT  | GTTTCCGTCA  | AAGAAGTCCG | CCGTGGTAAC | GTTGCCTGGT | 500 |
|    | GACTCTAAGA  | ATGATCCCGC  | MAWGGGCTGC | GATTCCTTCA | ATGCYCAGGT | 550 |
|    | CATCGTCCTC  | AACCACCCTG  | GTCAGGTTGG | CGCTGGTTAT | GCCCCAGTCC | 600 |
|    | TCGAYTGCCA  | TACTGCCCAC  | ATTGCYTGCA | ARTTCGCTGA | GMTCMAGKAG | 650 |
|    | AAGATTGAYC  | GCCGAACCGG  | MAAGTCTGTT | GAGAACGCCC | CCAAGTTCAT | 700 |
| 40 | CAAGTCCGGT  | GATGC       |            |            |            | 715 |

## 2) INFORMATION FOR SEQ ID NO: 1267

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 875 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 50 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 56220

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | GAGTCCTCTT | ATTTACTTTT | GTCATGACTA | CCTTACTAAT  | CTGTCATAGA | 50  |
|    | TCGTTACAAC | GAAATCGTCA | AGGAGACTTC | CAACTTCATC  | AAGAAGGTCG | 100 |
|    | GATACAACCC | CAAGAACGTT | CCTTTCGTTC | CTATCTCCGG  | TTTCAACGGC | 150 |
| 10 | GACAACATGC | TTGAGCCCTC | CCCCAACTGC | CCCTGGTACA  | AGGGTTGGGA | 200 |
|    | GAAGGAGACC | AAGGCCGGTA | AGGTCACTGG | TAAGACCCTC  | CTCGAGGCCA | 250 |
|    | TCGACGCCAT | TGAGCCCCCT | ACCCGTCCCG | CCAACAAGGT  | CAGTACTACC | 300 |
|    | TCAATTACTT | GAACCTCTCT | CATACGTTCC | GATTACTGAC  | TGCTTCACAG | 350 |
|    | CCCCTCCGTC | TTCCCCTCCA | GGACGTTTAC | AAGATCGGTG  | GTATTGGAAC | 400 |
| 15 | GGTGCCCGTC | GGTCGTGTTG | AGACCGGTAC | CATCTCCCCCT | GGTATGGTCG | 450 |
|    | TTACCTTGTA | TGTATCCTGA | CCATCCCCCT | TGGCAATCAT  | TACGTACTAA | 500 |
|    | CTCACTCTTC | AGCGCTCCCG | CCAACGTCAC | CACTGAAGTC  | AAGAGTGTTG | 550 |
|    | AAATGCACCA | CCAGCAGCTC | GCTGCCGGTC | AGCCCGGTGA  | CAACGTTGGT | 600 |
|    | TTCAACGTGA | AGAACGTCTC | CGTCAAGGAA | ATCCGTCGTG  | GTAACGTTGC | 650 |
| 20 | TGGTGATAGC | AAGAACGACC | CCCCTGCCGG | TGCTGCTTCC  | TTCAACGCCC | 700 |
|    | AGGTCATCGT | CCTCAACCAC | CCCGGTCAGG | TCGGTGCTGG  | TTACGCCCCA | 750 |
|    | GTCCTTGACT | GCCACACTGC | CCACATTGCT | TGCAAGTTCT  | CTGAACTCCT | 800 |
|    | TGAGAAGATT | GACCGTCGTA | CCGGAAAGTC | TGTTGAGGAC  | CACCCCAAGT | 850 |
|    | TCATCAAGTC | CGGTGACGCT | GCCAT      |             |            | 875 |

## 2) INFORMATION FOR SEQ ID NO: 1268

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*

40

(B) STRAIN: WSA-377

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | GTGAGCGTGG | TATCACCATC | GATATTGCCC | TCTGGAAATT  | CGAGACCCCG | 50  |
| 45 | AAGTACAGTG | TCAGTGTCAT | TGGTGAGTGC | TTTTTACCCC  | TCTTAAGCAG | 100 |
|    | ATTTCAACTT | CCAGAGTATC | TACTCTAACA | TATCCGCTTA  | GATGCTCCCG | 150 |
|    | GCCATCGTGA | CTTCATCAAG | AACATGATCA | CTGGTACCTC  | CCAGGCTGAC | 200 |
|    | TGCGCTATCC | TCATCATTCG | TGCCGGTACT | GGTGAGTTCG  | AGGCTGGTAT | 250 |
|    | CTCCAAGGAT | GGCCAGACTC | GTGAGCACGC | TCTGCTTGCT  | TTCACCCTTG | 300 |
| 50 | GTGTGAGGCA | ACTCATCGTT | GCCATCAACA | AGATGGACAC  | CACCAAGTGG | 350 |
|    | TCCGAGTCCC | GTTTCAACGA | AATCATCAAG | GAGGTTTCCA  | ACTTCATCAA | 400 |
|    | GAAGGTCGGA | TATAACCCCA | AGGCTGTTCC | CTTCGTGCCA  | ATCTCTGGTT | 450 |
|    | TCGAGGGTGA | CAACATGATT | GAACCCTCCC | CCAACCTGCAC | CTGGTACAAG | 500 |

|    |            |            |            |            |             |      |
|----|------------|------------|------------|------------|-------------|------|
|    | GGCTGGAACA | AGGAGACTGC | CTCTGGCAAG | TCTTCTGGTA | AAACCCCTTCT | 550  |
|    | CGATGCCATT | GACGCCATTG | AACCCCCAAC | CCGTCCTACC | GATAAGCCTC  | 600  |
|    | TCCGTCTTCC | CCTCCAGGAT | GTTTACAAAA | TCTCTGGTAT | TGGCACTGTT  | 650  |
|    | CCCGTCGGAC | GTGTTGAGAC | TGGTGTCATC | AAGCCCGGTA | TGGTCGTGAC  | 700  |
| 5  | TTTCGCTCCC | TCCAACGTCA | CCACTGAAGT | CAAGTCCGTC | GAGATGCACC  | 750  |
|    | ACCAACAAC  | CCAGGCTGGT | TACCTGGTG  | ACAACGTCGG | CTTCAACGTC  | 800  |
|    | AAGAACGTTT | CAGTCAAGGA | AGTCCGCCGT | GGCAACGTTG | CTGGCGACTC  | 850  |
|    | CAAAAATGAT | CCCCCAAGG  | GCTGCGAATC | CTTCAATGCC | CAGGTCATCG  | 900  |
|    | TCCTTAACCA | CCCCGGCCAG | GTTGGCGCTG | GTTATGCCCC | AGTCCTCGAC  | 950  |
| 10 | TGCCACACTG | CCCACATTGC | TTGCAAGTTC | TCTGAACTCA | TTGAGAAGAT  | 1000 |
|    | CGACCGCCGT | ACTGGAAAGT | CTGTTGAGAA | CAACCCCAAG | TTCATCAAGT  | 1050 |
|    | CTGGTGATGC | TGCTATCGTC | AAGATGGTTC | CCTCCAAGCC | CATGTGCGTG  | 1100 |
|    | GAGCCCTTCA | CTGACTATCC | CCCT       |            |             | 1124 |

15

## 2) INFORMATION FOR SEQ ID NO: 1269

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1043 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Trichophyton rubrum*
- (B) STRAIN: WSA-224

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | GTGAGCGTGG | TATCACCATC | GATATCGCCC | TCTGGAAGTT | CGAGACCCCC | 50   |
|    | AAGTACAATG | TCACCGTCAT | TGGTATGTTT | CTTTGCCTTG | TTCCCTCATG | 100  |
| 35 | TGGTTGTACC | ATATCTAACG | AGAGTAGACG | CCCCCGGTCA | CCGTGACTTC | 150  |
|    | ATCAAGAACA | TGATCACTGG | TACCTCCCAG | GCTGACTGCG | CTATTCTCAT | 200  |
|    | CATTGCTGCC | GGTACTGGTG | AGTTCGAGGC | TGGTATCTCC | AAGGATGGCC | 250  |
|    | AGACCCGTGA | GCACGCTCTG | CTCGCCTTCA | CCCTCGGTGT | CAAGCAGCTC | 300  |
|    | ATCGTTGCCA | TCAACAAGAT | GGACACCACC | GGCTGGTCCG | AGGATCGTTT | 350  |
| 40 | CAAGGAAATT | ATCAAGGAAG | TCACCAACTT | CATCAAGAAG | GTTGGCTACG | 400  |
|    | ACCCCAAGGG | TGTTCCATTC | GTTCCAATCT | CTGGTTTCAA | CGGTGACAAC | 450  |
|    | ATGATTGAGG | CCTCCACCAA | CTGCCCATGG | TACAAGGGAT | GGAACAAGGA | 500  |
|    | GACCAAGGCC | GGTGGTGCCA | AGTCCGGCAA | GACCCTCCTC | GAGGCCATCG | 550  |
|    | ATGCCATCGA | CATGCCAACC | CGTCCTACCG | ACAAGCCCCT | CCGTCTCCCA | 600  |
| 45 | CTCCAGGATG | TCTACAAGAT | CTCTGGTATC | GGAAGTGTGC | CAGTCGGTCG | 650  |
|    | TGTTGAGACC | GGTATCATCA | AGCCCGGTAT | GGTCGTCACC | TTNGCCCCCG | 700  |
|    | CCAACGTCAC | CACTGAAGTC | AAGTCCGTYK | AAATGCACCA | CCAGCAGCTT | 750  |
|    | CAGCAGGGTG | TCCCCGGTGA | CAACGTCGGC | TTCAATGTCA | AGAACGTTTC | 800  |
|    | CGTCAAGGAA | GTCCGCCGTG | GTAACGTTGC | CGGTGACTCC | AAGAACGACC | 850  |
| 50 | CACCATCCGG | CTGTGCCTCC | TTCAACGCC  | AGGTCATYGT | CCTCAACCAC | 900  |
|    | CCCGGCCAGA | TCGGTGCTGG | TTACGSTCCA | GTCCTCGACT | GCCACACTGS | 950  |
|    | TCACATTGCT | TGCAAGTTCG | CTGAGCTCCT | CGAGAAGATT | GACCGCCGTA | 1000 |
|    | CCGGTAAATC | CGTCGAAGCC | AACCCCAAGT | TCGTCAAGTC | TGG        | 1043 |

## 2) INFORMATION FOR SEQ ID NO: 1270

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium canis*  
 (B) STRAIN: WSA-217

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270

```

GCTGAGCGTG AGCGTGGTAT CACCATTGAT ATCGCCCTCT GGAAGTTCGA      50
GACCCCAAG TACATGGTCA CCGTCATCGG TATGCTTTAT CTGTTTCCCA      100
TTTATAGTTG CGACCAGTAA CTAACAAAAA GTAGATGCCC CCGGGCACCG      150
TGACTTCATC AAGAACATGA TTACTGGTAC CTCCAGGCC GACTGCGCTA      200
TTCTCATCAT TGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG      250
GATGGCCAGA CTCGTGAGCA CGCCCTGCTC GCTTTCACCC TCGGTGTCAA      300
GCAGCTCATC GTTGCCATCA ACAAGATGGA CACCACCAAC TGGTCTGAGT      350
CCCGTTTCGG TGAAATCATC AAGGAAGTCA CCAACTTCAT CAAGAAGGTC      400
GGCTACGACC CCAAGGGTGT CCCATTTCGT CCAATCTCTG GCTTCAACGG      450
TGACAACATG ATTGAGCCCT CCACCAACTG CCCATGGTAC AAGGGATGGA      500
ACAAGGAGAC CAAGGCCGGT GGCAAATCCT CTGGTAAGAC CCTCCTTGAG      550
GCCATCGATG CCATTGACAT GCCCACTCGT CCCACCGACA AGCCTCTCCG      600
TCTCCCCTC CAGGATGTCT ACAAGATCTC TGGTATCGGA ACAGTACCAG      650
TCGGTCGTGT TGAGACTGGT ATCATCAAGC CTGGTATGGT TGTCACCTTY      700
GCCCCCGCCA ACGTCACCAC TGAAGTCAAG TCCGTCGAAA TGCACCACCA      750
GCAGCTYGTC CAGGGTGTTT CCGGTGACAA CGTTGGCTTC AACGTCAAGA      800
ACGTYTCTGT CAAGGAAGTC CGCCGTGGTA ACGTTGCCGG TGATTCCAAG      850
AACGACCCAC CAGCTGGCTG CGCCTCTTTC AAGGCCCAGG TCATCGTCCT      900
CAACCACCCC GGCCAGATCG GTGCTGGTTA CGCCCAGTC CTTGACTGCC      950
ACACTGCCCA CATTGCTTGC AAGTTCTCTG AGCTTCTTGA GAAGATTGAC     1000
CGCCGTACTG GTAAATCCGT CGAAACCAGC CCTAAGTTCG TCAAGTCTGG     1050
TGATGCCGCT ATTGCCACCA TGGTTCCATC CAAGCCCATG TGC GTTGAGG     1100
CTTTC

```

## 2) INFORMATION FOR SEQ ID NO: 1271

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus versicolor*  
 (B) STRAIN: WSA-175

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271

```

5      GAGCGTGAGC GTGGTATCAC CATCGATATC GCTCTCTGGA AGTTCCAGAC      50
      CCCTAAGTAT GAGGTCACCG TCATTGGTAT GTTGTCTTTC TTGTGTTACC      100
      ATCGAAACAT ATCTAACCTA CAACTGCAGA CGCCCCCGGT CACCGTGA CT      150
      TCATCAAGAA CATGATCACT GGTACCTCCC AGGCCGACTG CGCTATTCTC      200
10     ATCATTGCTT CCGGTACTGG TGAATTCGAG GCTGGTATCT CCAAGGATGG      250
      CCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTCGGT GTCCGTCAGC      300
      TCATCGTTGC CCTCAACAAG ATGGACACTG CTGGCTGGGC TGAGGCTCGT      350
      TACAACGAAA TCGTCAAGGA AACTTCCGGT TTCATCAAGA AGGTCGGCTA      400
      CAACCCCAAG TCGGTTCCCT TCGTCCCCAT CTCCGGTTTC AACGGTGACA      450
15     ACATGCTTGA GCCCTCCTCC AACTGCCCTT GGTACAAGGG TTGGGAGAAG      500
      GAGACCAAGG CTGGTAAGGC CACTGGTAAG ACCCTCCTCG AGGCCATCGA      550
      CGCCATTGAG CCTCCCGTCC GTCCCTCCAA CAAGCCTCTC CGTCTTCCCC      600
      TCCAGGATGT CTACAAGATC TCTGGTATTG GAACTGTCCC CGTCGGCCGT      650
      GTCGAGACCG GTACCATCGT CCCCGGTATG GTCGTACCT TCGTCCCGC      700
20     CAACGTCACC ACTGAAGTCA AGTCCGTTGA GATGCACCAC CAGCAGCTCA      750
      AGGAGGGTGT TCCCGGTKAC AACGTTGGTT TCAACGTGAA GAACGTTTCC      800
      GTCAAGGAAG TCCGCCGTGG TAACGTCGCT GGTGACTCCA AGAACGACCC      850
      CCCTGCCGGT GCTGCCTCTT TCACCGCCCA GGTCATCGTC CTCAACCACC      900
      CCGGTCAGGT CGGCGCTGGT TACGCTCCCG TCCTCGACTG CCACACCGCT      950
25     CACATTGCCT GCAAGTTCGC TGAGCTCCAG GAGAAGATCG ACCGCCGTAC      1000
      CGGAAAGTCT GTCGAATYTG CCCCCAAGTT CATCAAGTCT GGTGACGCCG      1050
      CTATCGTCAA GATGATTCCC TCCAAGCCCA TGTGTGTCGA GTCTTTTACT      1100
      GACTACCCTC CTYTCGGCCG TTTCGCCGTC CGTGACGTAA GTTCTTTCCC      1150
      CAGCTTTTCG ATGCTACCCT TCTMTGAATC ACGTGTGTCG TCTTGGCACC      1200
30     CGCCCATCAC ATGACCACGC AACCTATAC CCCGCCACAC CCTT          1244
  
```

## 2) INFORMATION FOR SEQ ID NO: 1272

```

35     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1032 bases
          (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
40     (D) TOPOLOGY: Linear

          (ii) MOLECULE TYPE: Genomic DNA

          (vi) ORIGINAL SOURCE:
45     (A) ORGANISM: Exophiala moniliae
          (B) STRAIN: WSA-219
  
```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272

```

50     GCTGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT GGAAGTTCGA      50
      GACCCCAAG TACTATGTCA CCGTCATCGA CGCCCCCGGT CATCGTGA CT      100
      TCATCAAGAA CATGATCACT GGTACTTCCC AAGCTGACTG CGCCATTCTC      150
      ATCATTGCTG CCGGTACTGG TGAATTCGAA GCCGGTATCT CCAAGGATGG      200
  
```

|    |            |            |             |            |            |      |
|----|------------|------------|-------------|------------|------------|------|
|    | TCAGACCCGT | GAGCACGCTC | TGCTTGCCTA  | CACCCTGGGT | GTCAAGCAGC | 250  |
|    | TCATTGTCGC | CATCAACAAG | ATGGACACTA  | CCAAGTGGTC | TGAGGACCGT | 300  |
|    | TTCAACGAAA | TCATCAAGGA | GACTTCCAGC  | TTCATCAAGA | AGGTCGGCTA | 350  |
|    | CAACCCCAAG | TCCGTTCCCT | TCGTCCCCAT  | CTCCGGCTTC | AACGGTGACA | 400  |
| 5  | ACATGATCGA | CGTCTCCACC | AACTGCCCCCT | GGTACAAGGG | CTGGGAGAAG | 450  |
|    | GAGACCAAGG | CTGGCAAGGC | CTCTGGCAAG  | ACTCTCCTTG | AGGCCATCGA | 500  |
|    | CGCCATTGAC | CCCCCTCTC  | GTCCCACCGA  | CAAGCCTYTC | CGTCTCCCTC | 550  |
|    | TCCAGGATGT | GTACAAGATC | TCTGGTATCG  | GAACGGTGCC | CGTCGGTCGT | 600  |
|    | GTCGAGACTG | GTATCATCAA | GGCCGGTATG  | GTCGTTACCT | TCGCTCCTGC | 650  |
| 10 | CAACGTCACC | ACTGAAGTCA | AGTCCGTCGA  | AATGCACCAC | GAACAGCTCG | 700  |
|    | CCGAGGGTGT | TCCAGGTGAC | AACGTCGGTT  | TCAACGTCAA | GAACGYTCC  | 750  |
|    | GTCAAGGAGG | TTCGTCGTGG | AAACGTTTGC  | GGTGACTCCA | AGAACGACCC | 800  |
|    | ACCCAAGGGC | GCTGATTCTT | TCAACGCCCA  | GGTCATCGTC | TTGAACCACC | 850  |
|    | CTGGTCAAGT | TGGTGCTGGC | TACGCCCCAG  | TGTTGGATTG | CCACACTGCC | 900  |
| 15 | CACATTGCTT | GCAAGTTCTC | TGAGCTTCTC  | GAGAAGATCG | ATCGTCGKAC | 950  |
|    | CGGAAAGTCG | ATCGAAAACA | ACCCCAAGTT  | CATCAAGTCT | GGTGACGCTG | 1000 |
|    | CCATCGTCAA | GATGGTTCCC | AGCAAGCCCA  | TG         |            | 1032 |

20

## 2) INFORMATION FOR SEQ ID NO: 1273

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hortaea werneckii*  
 (B) STRAIN: ATCC 34944

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
|    | TAACAGCCCCG | TGCGACCGTC | TCGTCCAATA | ACTAATGATT | CGCAGGTACT | 50  |
|    | ATGTCGTGAG  | TATCCGGTCC | TTTTTTGTTA | ATTTACCAGA | AATGACGAAA | 100 |
|    | TTTTTGACTA  | ATTAACACAC | TCAGACCGTC | ATTGACGCCC | CGGGTCACCG | 150 |
| 40 | TGACTTCATC  | AAGAACATGA | TCACTGGTAC | CTCCCAGGCC | GACTGCGCTG | 200 |
|    | TCCTCATCAT  | TGCTGCCGGT | ACTGGTGAGT | TCGAGGCTGG | TATCTCCAAG | 250 |
|    | GATGGCCAGA  | CCCGTGAGCA | CGCCCTGCTC | GCCTACACCC | TCGGTGTCAA | 300 |
|    | GCAGCTCATC  | GTCGCCATCA | ATAAGATGGA | CACCACCAAG | TGGTCCGAGG | 350 |
|    | AGCGTTACGG  | CGAGATCATC | AAGGAGACCT | CTGCCTTCAT | CAAGAAGGTC | 400 |
| 45 | GGTTTCAACC  | CGAAGCACGT | CCCGTTTCGT | CCGATCTCCG | GTTTCAACGG | 450 |
|    | TGACAACATG  | ATCGAGGCCT | YACCAACTG  | CCCGTGGTAC | AAGGGCTGGG | 500 |
|    | AGAAGGAGAC  | CAAGGCCAAG | GTCACCGGCA | AGACCCTYCT | TGAGGCCATT | 550 |
|    | GACAACATCG  | ACCCGCCGAG | CCGTCCTTCC | GACAAGCCGC | TCCGTCTTCC | 600 |
|    | CCTCCAGGAT  | GTCTACAAGA | TCGGTGGTAT | TGGGACAGTC | CCAGTCGGCC | 650 |
| 50 | GTGTCGAGAC  | CGGTACCATC | AAGGCCGGCA | TGGTCGTTAC | CTTCGCTCCG | 700 |
|    | GCTGGTGTCA  | CCACTGAAGT | GAAGTCCGTT | GARATGCACC | ACGAGCAGCT | 750 |
|    | CGCTGAGGGT  | YTGCCGGGTG | ACAACGTCGG | CTTCAACGTC | AAGAACGTTT | 800 |
|    | CCGTCAAGGA  | GATCCGTCGT | GGCAACGTTG | CTGGTGACAG | CAAGGCTGAC | 850 |

|   |            |            |            |            |            |      |
|---|------------|------------|------------|------------|------------|------|
|   | CCGCCGAAGG | GCTGCGACAG | CTTCAACGCC | CAGGTCATCG | TCCTGAACCA | 900  |
|   | CCCTGGCCAG | GTCGGTGCTG | GTTACGCTCC | AGTCCTGGAC | TGCCACACTG | 950  |
|   | CCCACATTGC | CTGCAAGTTC | GGCGAGCTCC | TCGAGAAGAT | CGACCGTCGC | 1000 |
|   | TYTGGCAAGT | CCATTGAAGC | CTYGCCTAAG | TACATCAAGT | CTGGTGACGC | 1050 |
| 5 | TGCCATYGTC | AAGATGATTC | CGTCCAAGCC | GATGTGCGTT | GAGCCATTCA | 1100 |
|   | CTGAGT     |            |            |            |            | 1106 |

10 2) INFORMATION FOR SEQ ID NO: 1274

(i) SEQUENCE CHARACTERISTICS:

|    |                          |
|----|--------------------------|
|    | (A) LENGTH: 1119 bases   |
|    | (B) TYPE: Nucleic acid   |
| 15 | (C) STRANDEDNESS: Double |
|    | (D) TOPOLOGY: Linear     |

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

|  |                                      |
|--|--------------------------------------|
|  | (A) ORGANISM: <i>Fusarium solani</i> |
|  | (B) STRAIN: ATCC 32793               |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274

|    |             |            |             |             |            |      |
|----|-------------|------------|-------------|-------------|------------|------|
| 25 | CTCAAGGCCG  | AGCGTGAGCG | TGGTATCACC  | ATCGACATTG  | CCCTCTGGAA | 50   |
|    | GTTTCGAGACT | CCCCGCTACT | ATGTCACCGT  | CATTGGTATG  | TTGCTGTCAC | 100  |
|    | CTCTCTCACA  | CATGTCTCAC | CACTAACAAT  | CAACAGACGC  | CCCCGGCCAC | 150  |
|    | CGTGATTTCA  | TCAAGAACAT | GATCACTGGT  | ACTTCCCAGG  | CCGACTGCGC | 200  |
| 30 | CATTCTCATC  | ATTGCCGCCG | GTACTGGTGA  | GTTTCGAGGCT | GGTATCTCCA | 250  |
|    | AGGATGGCCA  | GACCCGTGAG | CACGCCCTGC  | TCGCCTACAC  | CCTCGGTGTC | 300  |
|    | AAGAACCTCA  | TTGTCGCCAT | CAACAAGATG  | GACACCACCA  | AGTGGTCCGA | 350  |
|    | GTCCCGTTAC  | CAGGAGATCA | TCAAGGAGAC  | CTCCAACCTC  | ATCAAGAAGG | 400  |
|    | TCGGCTACAA  | CCCCAAGGCT | GTCGCTTTTCG | TCCCCATCTC  | CGGTTTCAAC | 450  |
| 35 | GGCGACAACA  | TGCTTACTCC | CTCCACCAAC  | TGCCCCTGGT  | ACAAGGGCTG | 500  |
|    | GGAGCGTGAG  | ATCAAGTCCG | GCAAGCTCAC  | TGGCAAGACC  | CTCCTCGAGG | 550  |
|    | CCATTGACTC  | CATCGAGCCC | CCCAAGCGTC  | CCGTCGACAA  | GCCCCTYCGA | 600  |
|    | CTTCCCCTCC  | AGGATGTCTA | CAAGATCGGT  | GGTATTGGCA  | CGGTTCCCCT | 650  |
|    | CGGCCGTATC  | GAGACTGGTG | TCATCAAGCC  | CGGTATGGTC  | GTTACCTTMG | 700  |
| 40 | CCCCCTCCAA  | CGTCACCACT | GAAGTCAAGT  | CCGTCGARAT  | GCACCACGAG | 750  |
|    | CAGCTCTYTG  | AGGGTCTTCC | CGGTGACAAC  | GTCGGCTTCA  | ACGTGAAGAA | 800  |
|    | CGTYTCCGTC  | AAGGAGATCC | GACGTGGCAA  | CGTCGCTGGT  | GACTCCAAGA | 850  |
|    | ACGACCCCCC  | TYTGGGTGCC | GCCTCTTTCA  | CCGCCCAGGT  | CATTGTCTCT | 900  |
|    | AACCACCCTG  | GCCAGGTCGG | TGCCCGTTAC  | GCCCCCGTTY  | TGGACTGCCA | 950  |
| 45 | CACTGCCCCAC | ATTGCCTGCA | AGTTCGCCGA  | GATCCAGGAG  | AAGATCGACC | 1000 |
|    | GCCGAAGTGG  | TAAGGCTGTT | GAGTCCGCCC  | CCAAGTTCAT  | CAAGTCTGGT | 1050 |
|    | GACTCCGCCA  | TCGTCAAGAT | GGTTCCCTCC  | AAGCCCATGT  | GCGTTGAGGC | 1100 |
|    | TTTCACTGAC  | TACCCCCCT  |             |             |            | 1119 |

50

2) INFORMATION FOR SEQ ID NO: 1275



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*  
 (B) STRAIN: WSA-234

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275

```

15 CTGAAGTCTG AGCGTGAGCG TGGTATCACT ATCGATATCG CCCTCTGGAA      50
   GTTCGAGACC CCCAAGTACA TGGTCACCGT CATCGATGCC CCCGGTCACC      100
   GTGATTTTCAT CAAGAACATG ATCACTGGTA CCTCCCAGGC TGA CTGCGCC      150
   ATTCTCATCA TTGCTGCCGG TACTGGTGAG TTCGAGGCTG GTATCTCCAA      200
   GGATGGCCAG ACTCGTGAGC ACGCTCTCCT CGCCTACACC CTTGGTGTCA      250
20 AGCAGCTCAT CGTTGCCATC AACAAGATGG ACACCACCAA GTGGTCTGAG      300
   GCCCGTTACC AGGAGATCAT CAAGGAGACC TCCGGTTTCA TCAAGAAGGT      350
   CGGCTACAAC CCCAAGCACG TTCCCTTCGT CCCCATCTCC GGCTTCAACG      400
   GAGACAACAT GATCGAGGTC AGCTCCAAC T GCCCTTGGTA CAAGGGTTGG      450
   GAGAAGGAGA CCAAGGCCAA GGCCACTGGC AAGACCCTCC TCGAGGCCAT      500
25 TGACGCCATC GACCCTCCTT CCCGTCCTAC CGACAAGCCC CTCCGTCTTC      550
   CCCTCCAGGA TGTCTACAAG ATCGGTGGTA TTGGCACGGT GCCCGTCGGT      600
   CGTGTTGAGA CCGGTAAGAT CATGGGTGGT ATGGTTGTCA CCTTCGCCCC      650
   CGCTGGTGTC ACCACCGAGG TCAAGTCCGT CGAGATGCAC CACGAGCAGC      700
   TCACCGAGGG TCTTCCCGGT GACAACGTCG GCTTCAACGT CAAGAACGTY      750
30 TCCGTCAAGG AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA      800
   CCCCCCAAG GGTTGTGACT CCTTCAACGC CCAGGTCATC GTCCTGAACC      850
   ACCCTGGTCA GGTCGGTGCT GGTTACGCAC CCGTCCTCGA CTGCCACACT      900
   GCCACATTG CTTGCAAGTT YTCCGAGCTT GTTGAGAAGA TTGACCGCAG      950
   AACCGGCAAG TCCGTTGAGG CTGCCCCCAA GTTCATCAAG TCTGGTGACG      1000
35 CCGCCATCGT CAAGATGGTT CCCTCCAAGC CCATGTGTGT TGAGGCTTTC      1050
   ACCGACTACC CTCCTYTCGG TCGTTTCGCC GTCCGGTATG TTTTCTTCT      1100
   TCAATCATTC TTC                                     1113

```

## 2) INFORMATION FOR SEQ ID NO: 1276

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*  
 (B) STRAIN: ATCC 14112

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GGTCTGAGAC | CCGTTTCAAC | GAAATTATCA | AGGAAGTCAG | CAACTTCATC | 50  |
| 5  | AAGAAGGTCG | GATACAACCC | CAAGTCTGTT | CCCTTCGTGC | CAATCTCCGG | 100 |
|    | TTTCGAGGGT | GACAACATGA | TTGAGCCTTC | CCCCAACTGC | CCTTGGTACA | 150 |
|    | AGGGCTGGAA | CAAGGAGACT | GCTGCTGGCA | AGGCCGCCGG | TAAGACTCTT | 200 |
|    | CTCGATGCCA | TTGACGCCAT | CGACCCCCCC | GTCCGTCCTA | CCGAGAAGCC | 250 |
|    | TCTCCGTCTT | CCCCTCCAGG | ATGTGTACAA | GATCTCCGGT | ATTGGCACTG | 300 |
| 10 | TTCCCGTTGG | ACGTGTCGAG | ACTGGTGTCA | TCAAGCCTGG | TATGGTCGTG | 350 |
|    | ACCTTCGCCC | CTGCCAACGT | CACCACTGAA | GTCAAGTCCG | TTGAAATGCA | 400 |
|    | CCACCAGCAG | CTCCAGGCTG | GTTACCTCTG | TGACAACGTC | GGCTTCAACG | 450 |
|    | TCAAGAACGT | TTCCGTCAAG | GAAGTCCGCC | GTGGCAACGT | TGCCGGTGAC | 500 |
|    | TCCAAGAACG | ACCCCCCCAA | GGGCTGCGAG | TCCTTCAACG | CCCAGGTCAT | 550 |
| 15 | CGTCCTCAAC | CACCCCGGCC | AGGTTGGCGC | TGGTTATGCC | CCAGTCCTCG | 600 |
|    | ACTGCCACAC | TGCCACATT  | GCTTGCAAGT | TCTCTGAGCT | CATCGAGAAG | 650 |
|    | ATTGACCGCC | GTACCGGAAA | GTCTGTTGAG | GACAACCCCA | AGTTCATCAA | 700 |
|    | GTCCGGTGAT | GCTGCTATCG | TCAAGATGAT | T          |            | 731 |

20

## 2) INFORMATION FOR SEQ ID NO: 1277

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1046 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 30 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exophiala dermatitidis*  
 (B) STRAIN: ATCC 76088

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | CCGAGCGTGA | GCGTGGTATC | ACCATCGATA  | TCGCCCTCTG | GAAGTTCGAG | 50  |
|    | ACCCCCAAGT | ACTATGTCAC | CGTCATCGAC  | GCCCCGGGTC | ATCGTGACTT | 100 |
| 40 | TATCAAGAAC | ATGATCACTG | GTACCTCGCA  | GGCCGACTGC | GCCATCTTGA | 150 |
|    | TCATTGCCGC | CGGTACCGGT | GAATTCGAAG  | CCGGTATCTC | CAAGGATGGT | 200 |
|    | CAGACCCGTG | AGCACGCTCT | GCTCGCCTAC  | ACCTTGGGTG | TCAAGCAGCT | 250 |
|    | CATCGTCGCC | ATCAACAAGA | TGGACACCAC  | CAAGTGGTCC | GAGGAGCGTT | 300 |
|    | TCAACGAAAT | CATCAAGGAG | ACTTCCAAC   | TCATCAAGAA | GGTCGGCTAC | 350 |
| 45 | AACCCCAAGG | CCGTTCCTTT | CGTCCCCATC  | TCCGGCTTCA | ACGGTGACAA | 400 |
|    | CATGATTGAG | GTCTCCACCA | ACTGCCCCGTG | GTACAAGGGA | TGGGAGAAGG | 450 |
|    | AGTCCAAGGC | TGGCAAGGCC | ACCGGCAAGA  | CCCTCCTCGA | GGCCATTGAC | 500 |
|    | GCCATCGACC | CACCCACCCG | TCCCACCGAC  | AAGCCTCTCC | GTCTCCCTCT | 550 |
|    | CCAGGATGTC | TACAAGATCT | CTGGTATCGG  | AACGGTTCCT | GTCGGTCGTG | 600 |
| 50 | TCGAGACCGG | TACCATCAAG | GCCGGTATGG  | TCGTCACCTT | CGCTCCGGCC | 650 |
|    | AACGTCACCA | CTGAAGTCAA | GTCCGTCGAA  | ATGCACCACG | AGCAGCTCGC | 700 |
|    | CGAGGGTYTG | CCAGGTGACA | ACGTTGGCTT  | CAACGTCAAG | AACGTYTCCG | 750 |
|    | TCAAGGAGGT | TCGTCGTGGT | AACGTTGCCG  | GTGACTCCAA | GAACGACCCG | 800 |

|   |            |            |            |            |            |      |
|---|------------|------------|------------|------------|------------|------|
|   | CCCAAGGGTG | CCGAGTCCTT | CAACGCCCAG | GTCATTGTCC | TCAACCACCC | 850  |
|   | TGGTCAGATC | GGTGCCGGCT | ACGCTCCAGT | CTTGGATTGC | CACACTGCCC | 900  |
|   | ACATTGCTTG | CAAGTTCGCC | GAGTTGCTCG | AGAAGATCGA | CCGTCGTACC | 950  |
|   | GGAAAGTCCA | TCGAGAACAA | CCCCAAGTTC | ATCAAGTCTG | GTGATGCTGC | 1000 |
| 5 | CATCGTCAAG | ATGATTCCCA | GCAAGCCCAT | GTGTGTCGAG | GCTTTC     | 1046 |

## 2) INFORMATION FOR SEQ ID NO: 1278

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*  
 (B) STRAIN: WSA-213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278

|    |             |            |            |            |             |      |
|----|-------------|------------|------------|------------|-------------|------|
| 25 | CGTGAGCGTG  | GTATCACCAT | CGATATTGCT | CTCTGGAAGT | TCGAGACTCC  | 50   |
|    | TCGCTACTAT  | GTCACCGTCA | TTGGTATGTT | GTCGCTCATA | CCTCATCCTA  | 100  |
|    | CTTCCTCATA  | CTAACACATC | ATTCAGACGC | TCCCGGTCAC | CGTGATTTCA  | 150  |
|    | TCAAGAACAT  | GATCACTGGT | ACTTCCCAGG | CCGATTGCGC | CATTCTCATC  | 200  |
|    | ATTGCCGCCG  | GTACTGGTGA | GTTCGAGGCT | GGTATCTCCA | AGGATGGCCA  | 250  |
| 30 | GACCCGTGAG  | CACGCTCTTC | TTGCCTACAC | CCTTGGTGTC | AAGAACCTCA  | 300  |
|    | TCGTGCGCCAT | CAACAAGATG | GACACCACCA | AGTGGTCTGA | GGCCCGTTAC  | 350  |
|    | CAGGAGATCA  | TCAAGGAGAC | CTCCTCTTTC | ATCAAGAAGG | TCGGCTACAA  | 400  |
|    | CCCCAAGGCT  | GTCGCTTTTC | TCCCCATCTC | CGGTTTCAAC | GGTGACAACA  | 450  |
|    | TGCTTACCCC  | CTCCACCAAC | TGCCCCTGGT | ACAAGGGTTG | GGAGCGTGAG  | 500  |
| 35 | ATCAAGTCCG  | GCAAGCTCTC | CGGCAAGACC | CTCCTCGAGG | CCATTGACTC  | 550  |
|    | CATCGAGCCT  | CCCAAGCGTC | CCGTTGACAA | GCCCCTCCGT | CTTCCCCTCC  | 600  |
|    | AGGATGTCTA  | CAAGATCGGT | GGTATTGGAA | CGGTTCCCGT | CGGCCGTATT  | 650  |
|    | GAGACTGGTG  | TCATCAAGCC | CGGTATGGTC | GTTACCTTCG | CTCCCTCCAA  | 700  |
|    | CGTCACCACT  | GAAGTCAAGT | CCGTCGARAT | GCACCACGAG | CAGYTCAGTK  | 750  |
| 40 | AGGGCCAGCC  | CGGTGACAAC | GTTGGTTTCA | ACGTGAAGAA | CGTTTCCGTC  | 800  |
|    | AAGGACATCC  | GACGTGGTAA | CGTCGCTGGT | GACTCCAAGA | ACGACCCCCC  | 850  |
|    | CCAGGGTGCC  | GCTTCTTTCA | CCGCCCAGGT | CATCGTCCTC | AACCACCCCG  | 900  |
|    | GCCAGGTCGG  | TGCTGGTTAC | GCTCCTGTCC | TCGATTGCCA | CACTGCCCCAC | 950  |
|    | ATTGCCTGCA  | AGTTCGCCGA | GATCCAGGAG | AAGATCGACC | GCCGAACCGG  | 1000 |
| 45 | TAAGGCTACT  | GAGGCCGCTC | CCAAGTTCAT | CAAGTCTGGT | GACTCCGCCA  | 1050 |
|    | TCGTCAAGAT  | GGTTCCTCCT | AAGCCCATGT | GTGTCGAGGC | TTTCACTGAC  | 1100 |
|    | TACCTCTCT   |            |            |            |             | 1109 |

## 2) INFORMATION FOR SEQ ID NO: 1279

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus terreus*  
 (B) STRAIN: WSA-174

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
|    | CCTGCAAGTG  | GTCTGAGGAC | CGTTACAACG | AAATCGTGAA | GGAGACCTCC | 50  |
| 15 | AACTTCATCA  | AGAAGGTCGG | CTACAACCCC | AAGGCCGTTC | CCTTCGTCCC | 100 |
|    | CATCTCCGGT  | TTCAACGGTG | ACAACATGCT | TGAGCCTTCC | CCCAACTGCC | 150 |
|    | CCTGGTACAA  | GGGTGGGAG  | AAGGAGGGCA | AGTCCGGCAA | GGTCACCGGT | 200 |
|    | AAGACTCTCC  | TCGAGGCCAT | CGATGCCATC | GAGCCCCCG  | TCCGTCCTGC | 250 |
|    | CAACAAGCCT  | CTCCGTCTTC | CCCTCCAGGA | TGTGTACAAG | ATCTCTGGTA | 300 |
| 20 | TCGGAAGTGT  | CCCCGTCGGC | CGTGTCGAGA | CTGGTGTCAT | CACCCCCGGC | 350 |
|    | ATGGTTGTTA  | CCTTCGCTCC | TTCCAACGTC | ACCACTGAAG | TGAAGTCCGT | 400 |
|    | TGAGATGCAC  | CACCAGCAGC | TCAAGGAGGG | TCTCCCCGGT | GACAACGTTG | 450 |
|    | GTTTCAACGT  | CAAGAACGTC | TCCGTCAAGG | AGGTCCGTCG | TGGTAACGTC | 500 |
|    | GCTGGTGACT  | CCAAGAACGA | CCCCCCTGCT | GGCGCTGCCT | CCTTCACCGC | 550 |
| 25 | CCAGGTCATC  | GTTCTCAACC | ACCCCGGTCA | GGTCGGCGCT | GGCTACGCCC | 600 |
|    | CCGTCCTCGA  | CTGCCACACT | GCCCACATTG | CCTGCAAGTT | CGCTGAGCTC | 650 |
|    | CAGGAGAAGA  | TTGACCGCCG | TACCGGAAAG | TCTGTTGAGT | CTTCTCCCAA | 700 |
|    | GTTTCATCAAG | TCTGGTGATG | CTGCCATCGT | CAAGATGATC | CCTYCAAAGC | 750 |
| 30 | CCATGTGCGT  | CGAAG      |            |            |            | 765 |

## 2) INFORMATION FOR SEQ ID NO: 1280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*  
 (B) STRAIN: ATCC 64746

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GCGTGGTATC | ACCATCGACA | TTGCCCTCTG | GAAGTTCCAG | ACTCCCAAGT | 50  |
| 50 | ATGAGGTCAC | TGTCATCGGT | AAGCTCGACT | CGCCCCGATA | TGTTTTGGTG | 100 |
|    | CTGTAGCTAA | CACGATCTGA | AGATGCCCCC | GGTCACCGTG | ACTTCATCAA | 150 |
|    | GAACATGATC | ACTGGTACCT | CCCAGGCTGA | CTGCGCTATC | CTCATCATTG | 200 |
|    | CCTCCGGTAC | TGGTGAGTTC | GAGGCTGGTA | TCTCCAAGGA | TGGCCAGACC | 250 |

|    |            |             |             |            |            |      |
|----|------------|-------------|-------------|------------|------------|------|
|    | CGTGAGCACG | CTCTGCTGGC  | TTTCACCCTC  | GGTGTCAAGC | AGCTCATCGT | 300  |
|    | CGCCCTCAAC | AAGATGGACA  | CCTGCAAGTG  | GTCCGAGGAT | CGTTACAACG | 350  |
|    | AAATTGTCAA | GGAAACCTCC  | AACTTCATCA  | AGAAGGTCGG | CTACAACCCC | 400  |
|    | AAGGCCGTTT | CCTTCGTMCC  | CATCKCTGGC  | TTCAACGGTG | ACAACATGCT | 450  |
| 5  | TGAGCCCTCC | TCCAAC TGCC | CCTGGTACAA  | GGGATGGGAG | AAGGAGACCA | 500  |
|    | AGGCCGGCAA | GGTCACTGGT  | AAGACCCTCA  | TCGAGGCCAT | YGACGCCATT | 550  |
|    | GAGCCCCCTG | TCCGTCCCTC  | CAACAAGCCC  | CTYCGTCTTC | CCCTCCAGGA | 600  |
|    | TGTYTACAAG | ATCTCTGGTA  | TCGGAACGGT  | CCCTGTCGGC | CGTGTCGAGA | 650  |
|    | CCGGTATCAT | CAAGCCCGGC  | ATGGTCGTCA  | CCTTTGCCCC | CGCCAACGTC | 700  |
| 10 | ACCACTGAAG | TCAAGTCCGT  | CGAAATGCAC  | CACCAGCAGC | TCCAGGAGGG | 750  |
|    | TGTCCCCGGT | GACAACGTCG  | GTTTCAACGT  | CAAGAACGTT | TCCGTCAAGG | 800  |
|    | AAGTCCSCCG | TGGTAACGTT  | TGCGGTGACT  | CCAAGAACGA | TCCCCCTCAG | 850  |
|    | GGTGCTGCCT | CCTTCAACGC  | CCAGGTCATC  | GTCTCAACC  | ACCCCGGTCA | 900  |
|    | GGTCGGCGCT | GGTTACGCCC  | CCGTCCCTCGA | CTGCCACACT | GCCCACATTG | 950  |
| 15 | CTTGCAAGTT | CTYT GAGCTG | CTTGAGAAGA  | TTGACCGCCG | TACCGGCAAG | 1000 |
|    | TCTGTTGAGA | ACAACCCCAA  | GTTTCATCAAG | TCCGGTGAWG | CCGCCATCGT | 1050 |
|    | GAAGATGGTT | CCTTCCAAGC  | CCATGTGTGT  | CGAGTCCTTC | ACTGACTACC | 1100 |
|    | CCCCT      |             |             |            |            | 1105 |

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## 2) INFORMATION FOR SEQ ID NO: 1281

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 1343 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptococcus laurentii*  
(B) STRAIN: ATCC 44096
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281

|    |            |            |             |             |             |     |
|----|------------|------------|-------------|-------------|-------------|-----|
|    | GCCGAGCGAG | AGCGAGGTAT | CACCATCGAC  | ATTGCTCTCT  | GGAAGTTCGA  | 50  |
|    | GACCCCCAAG | TACAACGTCA | CCGTCAATTGA | CGCCCCCGGA  | CACCGAGACT  | 100 |
| 40 | TCATCAAGAA | CATGATCACC | GGTACCTCCC  | AGGCCGACTG  | CGCCATCCTT  | 150 |
|    | ATCATTGCCA | CCGGTATCGG | AGAGTTCGAG  | GCCGGTATCT  | CTAAGGACGG  | 200 |
|    | TCAGACCCGA | GAGCACGCTT | TGCTCGCCTT  | CACCCTCGGT  | GTCAGGCAGC  | 250 |
|    | TCATCGTTGC | TTGCAACAAG | ATGGACACCT  | GCAAGTGGTC  | CGAGGACCGA  | 300 |
|    | TTCAACGAGA | TCGTCAAGGA | GACCAACGGT  | TTCATCAAGA  | AGGTCCGGATA | 350 |
| 45 | CAACCCCAAG | GCTGTTCCCT | TCGTCCCCAT  | CTCTGGATGG  | CACGGAGACA  | 400 |
|    | AGTGAGTGCC | GTTCTTTGCG | TTGAGCCCTC  | TTTGTCGCTC  | CCCCTCCCTC  | 450 |
|    | TCAAGTGGCG | GCGGCGGTCT | CCACCCACAA  | ATCGGGTGGC  | GAATCCGCCA  | 500 |
|    | CACCCACCAC | TTCTCGCCAC | CGAGTGTGGC  | ACTTCTTCCA  | ACTCCTCTTT  | 550 |
|    | CCACTCCTCC | TCGTCTCGTC | TCTTTTTTTC  | TCCGTTGTCT  | TTGACAAGGG  | 600 |
| 50 | GAGTGTGCTG | ATAGTAAAGC | ATGCTTGAGG  | AGACCACCAA  | CATGCCGTGG  | 650 |
|    | TACAAGGGAT | GGACCAAGGA | GACCAAGTCC  | GGTGTCTGTTA | AGGGTAAGAC  | 700 |
|    | CCTCCTCGAC | GCCATCGACG | CCATCGAGCC  | TCCTCAACGA  | CCCACCGACA  | 750 |
|    | AGCCCCTCCG | ACTTCCCCTC | CAGGATGTCT  | ACAAGATCGG  | TGGTATCGGT  | 800 |

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | ACGGTGCCCG | TCGGCCGAGT | CGAGACCGGT | GTCATCAAGG | CCGGGTAAGT | 850  |
|    | CACGGGAGCC | TGACGGCTGT | TGTTGCCACA | CCCAACTTAT | ATCCAGTATG | 900  |
|    | GTCGTCACCT | TCGCTCCTAC | CAACGTCACC | ACTGAGGTTA | AGTCCGTTGA | 950  |
|    | GATGCACCAC | GAGCAGATCC | CTGAGGGTCT | TCCCGGAGAC | AACGTTGGTT | 1000 |
| 5  | TCAACGTGAA | GAACGTTTCC | ATCAAGGACA | TCCGACGAGG | AAACGTYTGC | 1050 |
|    | TCCGACTCCA | AGAACGACCC | CGCTAAGGAG | GCCGCTTCTT | TCAACGCCCA | 1100 |
|    | GGTCATTGTC | CTCAACCACC | CTGGACAGAT | TGGTGCCGGT | TACACCCCCG | 1150 |
|    | TCCTCGACTG | CCACACCGCC | CACATTGCCT | GCAAGTTCGC | CGAGCTCATC | 1200 |
|    | GAGAAGATCG | ACCGACGAAC | TGGTAAGACC | ATGGAGGCCG | CCCCAAGTT  | 1250 |
| 10 | CGTCAAGTCC | GGAGACGCCG | CCATTGTCAA | GCTCGTTGCC | CAGAAGCCCA | 1300 |
|    | TCTGTGTCGA | GTCTTACTCT | GACTACCCTC | CCCTTGACG  | ATT        | 1343 |

## 15 2) INFORMATION FOR SEQ ID NO: 1282

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 bases  
 (B) TYPE: Nucleic acid  
 20 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*  
 (B) STRAIN: ATCC 10784

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 30 | TGGTCCGAGG | CTCGTTTCAA | CGAAATCATC | AAGGAAGTCA | CCAACTTCAT | 50  |
|    | CAAGAAGGTC | GGATACAACC | CCAAGTCTGT | TCCCTTCGTG | CCAATCTCTG | 100 |
|    | GTTTCGAGGG | TGATAACATG | ATTGAGCCCT | CCACCAACTG | CCCCTGGTAC | 150 |
|    | AAGGGCTGGA | CCAAGGAGAC | CGCTGCCGGC | AAGTCAACCG | GTAAGACTCT | 200 |
| 35 | TCTTGACGCC | ATTGATGCCA | TCGATCAACC | CTCCCGTCCT | ACCGACAAGC | 250 |
|    | CCCTCCGTCT | TCCCCTCCAG | GATGTGTACA | AGATCTCCGG | TATTGGCACT | 300 |
|    | GTTCCCGTTG | GACGTGTTGA | GACTGGTATC | ATCAAGCCTG | GTATGGTCGT | 350 |
|    | GACCTTCGCT | CCCTCCAACG | TCACCACTGA | AGTCAAGTCC | GTCGAAATGC | 400 |
|    | ACCACCAACA | GCTCTTGGCT | GGTAACCCCG | GTGACAACGT | CGGTTTCAAC | 450 |
| 40 | GTCAAGAACG | TTTCCGTCAA | GGAAAGTCCG | CGTGGCAACG | TTGCTGGTGA | 500 |
|    | CTCAAAGAAC | GACCCCCCCA | AGGGCTGCGA | CTCCTTCAAC | GCCCAGGTCA | 550 |
|    | TCGTCTCAA  | TCACCCCGGT | CAAGTTGGCG | CTGGTTATGC | CCCAGTCCTC | 600 |
|    | GACTGCCACA | CTGCCACAT  | TGCTTGCAAG | TTCTCTGAGC | TCCTCGAGAA | 650 |
|    | GATTGACCGC | CGTACCGGAA | AGTCCACTGA | GAACAACCCC | AAGTTCATCA | 700 |
| 45 | AGTCTGGTGA | CGCCGCTATC | GTCAAGATGG | TTCC       |            | 734 |

## 2) INFORMATION FOR SEQ ID NO: 1283

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases  
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium solani*

(B) STRAIN: ATCC 62877

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | CGTGAGCGTG | GTATCACCAT | CGACATTGCC | CTCTGGAAGT | TCGAGACTCC | 50   |
|    | CCGCTACTAT | GTCACCGTCA | TTGGTATGTT | GCTGTCACCT | CTCTCACACA | 100  |
|    | TGTCTCACCA | CTAACAATCA | ACAGACGCCC | CCGGCCACCG | TGACTTCATC | 150  |
| 15 | AAGAACATGA | TCACTGGTAC | TTCCCAGGCC | GACTGCGCCA | TTCTCATCAT | 200  |
|    | TGCCGCTGGT | ACTGGTGAGT | TCGAGGCTGG | TATCTCCAAG | GATGGCCAGA | 250  |
|    | CCCGTGAGCA | CGCCCTGCTC | GCCTACACCC | TCGGTGTCAA | GAACCTCATT | 300  |
|    | GTCGCCATCA | ACAAGATGGA | CACCACCAAG | TGGTCCGAGT | CCCGTTACCA | 350  |
|    | GGAGATCATC | AAGGAGACCT | CCAACTTCAT | CAAGAAGGTC | GGCTACAACC | 400  |
| 20 | CCAAGGCTGT | CGCTTTCGTC | CCCATCTCCG | GTTTCAACGG | CGACAACATG | 450  |
|    | CTTACTCCCT | CCACCAACTG | CCCCTGGTAC | AAGGGCTGGG | AGCGTGAGAT | 500  |
|    | CAAGTCCGGC | AAGCTCACTG | GCAAGACCCT | CCTCGAGGCC | ATTGACTCCA | 550  |
|    | TCGAGCCCCC | CAAGCGTCCC | GTCGACAAGC | CCCTCCGACT | TCCCCTCCAG | 600  |
|    | GATGTCTACA | AGATCGGTGG | TATTGGCACG | GTTCCCGTCG | GCCGTATCGA | 650  |
| 25 | GACTGGTGTC | ATCAAGCCCG | GTATGGTCGT | TACCTTCGCC | CCCTCCAACG | 700  |
|    | TCACCACTGA | AGTCAAGTCC | GTCGAGATGC | ACCACGAGCA | GCTCTYTGAG | 750  |
|    | GGTCTTCCCG | GTGACAACGT | CGGCTTCAAC | GTKAAGAACG | TYTCCGTCAA | 800  |
|    | GGAGATCCGA | CGTGGAACG  | TCGCTGGTGA | CTCCAAGAAC | GACCCCCCTY | 850  |
|    | TGGGTGCCGC | CTCTTTCACC | GCCCAGGTCA | TTGTCCTCAA | CCACCCTGGC | 900  |
| 30 | CAGGTCGGTG | CCGGTTACGC | CCCCGTTYTG | GACTGCCACA | CTGCCCACAT | 950  |
|    | TGCCTGCAAG | TTCGCCGAGA | TCCAGGAGAA | GATCGACCGC | CGAACTGGTA | 1000 |
|    | AGGCTGTTGA | GTCCGCCCCC | AAGTTCATCA | AGTCTGGTGA | CTCCGCCATC | 1050 |
|    | GTCAAGATGG | TTCCCTCCAA | GCCCATGTGC | GTTGAGGCTT | TCACTGACTA | 1100 |
|    | CCCCCCT    |            |            |            |            | 1107 |

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## 2) INFORMATION FOR SEQ ID NO: 1284

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1045 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*

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(B) STRAIN: ATCC 14285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284

|    |            |            |              |             |             |      |
|----|------------|------------|--------------|-------------|-------------|------|
|    | GCTCAAGGCC | GAGCGTGAGC | GCGGTATCAC   | CATCGATATT  | GCTCTGTGGA  | 50   |
|    | AGTTCGAGAC | CCCCAAGTAC | TACGTCACCG   | TCATTGACGC  | CCCCGGTCAT  | 100  |
|    | CGCGATTTCA | TCAAGAACAT | GATCACTGGT   | ACCTCGCAGG  | CCGACTGCGC  | 150  |
|    | CATTCTCATC | ATTGCCGCTG | GTA CTGGTGA  | GTTTCGAGGCT | GGTATCTCCA  | 200  |
| 5  | AGGATGGCCA | GACTCGTGAG | CACGCTCTGC   | TCGCCTACAC  | CCTGGGTGTG  | 250  |
|    | CGGCAGCTGA | TCGTCGCCAT | CAACAAGATG   | GACACGGCCA  | AGTGGGCTGA  | 300  |
|    | GGCTCGTTAC | CAGGAGATCA | TCAAGGAGAC   | CTCCAAC TTC | ATCAAGAAGG  | 350  |
|    | TCGGCTACAA | CCCCAAGACT | GTTGCC TTTCG | TCCCCATCTC  | GGGCTTCCAC  | 400  |
|    | GGCGACAACA | TGCTTACTCC | CTCGACCAAC   | TGCCCCTGGT  | ACAAGGGCTG  | 450  |
| 10 | GGAGAAGGAG | GGCAAGAGCG | GCAAGGTTAC   | CGGTAAGACT  | CTGCTGGACG  | 500  |
|    | CCATTGACGC | CGTCGAGCCC | CCCAAGCGCC   | CCACGGACAA  | GCCCCTGCGT  | 550  |
|    | CTGCCCCTCC | AGGATGTCTA | CAAGATCGGC   | GGTATCGGCA  | CTGTCCCTGT  | 600  |
|    | CGGCCGTATC | GAGACTGGTG | TCCTGAAGCC   | CGGCATGGTC  | GTCACCTTTG  | 650  |
|    | CCCCGTCCAA | CGTCACCACT | GAAGTCAAGT   | CCGTCGAGAT  | GCACCACGAG  | 700  |
| 15 | CAGCTTGTTG | AGGGTGTTCC | CGGCGACAAC   | GTCGGCTTCA  | ACGTCAAGAA  | 750  |
|    | CGTYTCCGTC | AAGGAGATCC | GTG TG GCAA  | CGTTGCCGGT  | GA CTCCAAGA | 800  |
|    | ACGACCCCCC | CTCGGGCGCC | GCCACCTTCA   | ACGCCCAGGT  | CATTGTCC TG | 850  |
|    | AACCACCCCG | GCCAGGTCGG | CAACGGCTAC   | GCCCCGGTTY  | TGGACTGCCA  | 900  |
|    | CACCGCCAC  | ATTGCCTGCA | AGTTCACCGA   | GATCCTTGAG  | AAGATCGACC  | 950  |
| 20 | GCCGTACCGG | CAAGTCGGTT | GAGAACAACC   | CCAAGTTCAT  | CAAGTCGGGT  | 1000 |
|    | GACGCCGCCA | TTGTCAAGCT | GACGCCCTYG   | AAGCCCATGT  | GCGTT       | 1045 |

## 25 2) INFORMATION FOR SEQ ID NO: 1285

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 bases  
 (B) TYPE: Nucleic acid  
 30 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*  
 (B) STRAIN: WSA-176

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285

|    |             |            |            |             |             |     |
|----|-------------|------------|------------|-------------|-------------|-----|
| 40 | TTGCCAGTGG  | TCCGAGGCCC | GTTACAACGA | AATCGTCAAG  | GAGACTTCCG  | 50  |
|    | GTTTCATCAA  | GAAGGTCGGA | TACAACCCCA | AGTCCGTTGC  | CTTCGTCCCC  | 100 |
|    | ATCTCCGTTT  | TCAACGGTGA | CAACATGCTC | GAGGCCCTCTA | CCA ACTGCCC | 150 |
|    | CTGGTACAAG  | GGTTGGGAGA | AGGAGACCAA | GGCCGGTAAG  | GCCACTGGTA  | 200 |
| 45 | AGACCCTCCT  | TGAGGCCATC | GACGCCATTG | AGCCCCCAC   | CCGTCCCTCC  | 250 |
|    | AACAAGCCCC  | TCCGTCTTCC | CCTCCAGGAT | GTCTACAAGA  | TCTCCGGTAT  | 300 |
|    | TGGA ACTGTC | CCCGTCGGCC | GTGTCGAGAC | TGGTGTTATC  | ACCCCCG GCA | 350 |
|    | TGGTCGTCAC  | CTTCGCTCCT | GCCAACGTCA | CCACTGAAGT  | CAAGTCCGTT  | 400 |
|    | GAGATGCACC  | ACCAGCAGCT | CAAGGAGGGT | GTCCCCGGTG  | ACAACGTCGG  | 450 |
| 50 | TTTCAACGTC  | AAGAACGTTT | CCGTCAAGGA | AATCCGTCGT  | GGTAACGTTG  | 500 |
|    | CCTCCGACTC  | CAAGAACGAC | CCCGCCTCCG | GCGCTGCCTC  | TTTCAACGCC  | 550 |
|    | CAGGTCATCG  | TTCTCAACCA | CCCCGGTCAG | GTCGGTGCTG  | GTTACGCCCC  | 600 |
|    | CGTCCTCGAC  | TGCCACACCG | CCCACATTGC | TTGCAAGTTC  | TCTGAGCTTC  | 650 |



|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TTGAGAAGAT | TGACCGCCGT | ACCGGAAAGG | CTGTTGAAAC | CAGCCCCAAG | 700 |
| TTCATCAAGT | CCGGTGACGC | TGCCATCGTC | AAGATGATTC | CTTCCAAGCC | 750 |
| CATGTGCGKT | CCGA       |            |            |            | 764 |

5

## 2) INFORMATION FOR SEQ ID NO: 1286

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 971 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cladophialophora carrionii*  
 (B) STRAIN: ATCC 16264

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286

|               |            |             |            |            |     |
|---------------|------------|-------------|------------|------------|-----|
| ACCATCGATA    | TCGCGCTCTG | GAAGTTCGAG  | ACTCCCAAGT | ACTTCGTCAC | 50  |
| CGTCATCGAT    | CCCCCTGGTC | ATCGTGACTT  | CATCAAGAAC | ATGATCACTG | 100 |
| 25 GTACCTCCCA | GGCTGATTGT | GCTATTCTCA  | TCATTGCCGC | TGGTACTGGT | 150 |
| GAGTTCGAGG    | CCGGTATCTC | CAAGGATGGC  | CAGACCCGTG | AGCATGCTCT | 200 |
| GCTCGCCTAC    | ACCCTGGGCG | TGAAGCAGCT  | TATCGTCGCC | ATCAACAAGA | 250 |
| TGGACACCAC    | CAAATGGTCT | GAGGATCGTT  | TCAACGAAAT | CATCAAGGAG | 300 |
| ACTTCCAAC     | TCATCAAGAA | GGTCGGATAC  | AACCCCAAGT | CCGTTCCATT | 350 |
| 30 CGTGCCCATC | TCCGGCTTCA | ACGGTGACAA  | CATGATCGAC | GTCTCCACCA | 400 |
| ATGCCCCCTG    | GTACAAGGGC | TGGGAAAAGG  | AGTCCAAGGC | TGGCAAGGCC | 450 |
| ACCGGCAAGA    | CCCTCCTTGA | GGCTATCGAC  | TCCATCGACC | CTCCTGCTCG | 500 |
| TCCCACCGAC    | AAGCCTCTCC | GTCTCCCACT  | CCAGGATGTC | TACAAGATTT | 550 |
| CTGGTATCGG    | CACGGTGCCC | GTCGGTCGTG  | TTGAGACTGG | TACCATCAAG | 600 |
| 35 GCCGGTATGG | TCGTCACCTT | TGCCCCCGCC  | AACGTCACCA | CTGAAGTCAA | 650 |
| GTCCGTCGAA    | ATGCACCACG | AACAGCTYGC  | CGAGGGCGTT | CCGGGTGACA | 700 |
| ACGTCGGCTT    | CAACGTCAAG | AACGTYTCCG  | TGAAGGAGGT | TCGTCTGTGA | 750 |
| AACGTTGCTG    | GTGACTCCAA | GAACGACCCC  | CCCAAGGGTG | CCGACTCCTT | 800 |
| CAACGCCCAG    | GTCATCGTCC | TCAACCACCC  | TGGTCAGGTC | GGTGCTGGCT | 850 |
| 40 ACGCCCCGGT | CTTGATTGTC | CACACTGCCC  | ACATTGCCTG | CAAGTTCTYT | 900 |
| GAGCTCCTCG    | AGAAGATCGA | TCGTCTGKACC | GGCAAGTCCA | TGGAAAACAA | 950 |
| CCCCAAGTTC    | ATCAAGTCTG | G           |            |            | 971 |

45

## 2) INFORMATION FOR SEQ ID NO: 1287

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 732 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Exserohilum rostratum*

(B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 10 | GGTCTGAGGA | CCGTTACCAG | GAGATCATCA | AGGAGACCTC | CAACTTCATC | 50  |
|    | AAGAAGGTCG | GCTACAACCC | CAAGCACGTT | CCCTTCGTCC | CCATCTCCGG | 100 |
|    | TTTCAACGGA | GACAACATGA | TCGAGGCCTC | CAGCAACTGC | CCCTGGTACA | 150 |
|    | AGGGTTGGGA | GAAGGAGACC | AAGGCCAAGG | CCACTGGTAA | GACCCTCCTT | 200 |
|    | GAGGCCATTG | ACGCCATCGA | CCCTCCCAGC | CGTCCTACCG | ACAAGCCCCT | 250 |
|    | CCGTCTTCCC | CTCCAGGATG | TCTACAAGAT | TGGTGGTATT | GGCACGGTTC | 300 |
| 15 | CCGTCGGTCG | TGTCGAGACC | GGTATCATCA | AGGCCGGTAT | GGTCGTCACC | 350 |
|    | TTCGCCCCCG | CTGGTGTGAC | CACTGAAAGT | AAGTCCGTCG | AGATGCACCA | 400 |
|    | CGAGCAGCTT | ACCGAGGGTG | TCCCCGGTGA | CAACGTCGGC | TTCAACGTCA | 450 |
|    | AGAACGTCTC | CGTCAAGGAG | ATCCGTCGTG | GTAACGTTGC | CGGTGACTCC | 500 |
|    | AAGAACGACC | CCCCCAAGGG | CTGCGAGTCT | TTCAACGCTC | AGGTCATTGT | 550 |
| 20 | CCTCAACCAC | CCTGGTCAGG | TCGGTGCCGG | TTACGCGCCA | GTCCTCGACT | 600 |
|    | GCCACACCGC | CCACATTGCC | TGCAAGTTCT | CTGAGCTCCT | CGAGAAGATT | 650 |
|    | GACCGCCGTA | CCGGAAGTC  | TGTCGAAGCC | TCTCCCAAGT | TCATCAAGTC | 700 |
|    | TGGTGACGCG | GCCATCGTCA | AGATGGTTCC | CT         |            | 732 |

25

2) INFORMATION FOR SEQ ID NO: 1288

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 337 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1236

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288

|    |            |             |            |            |            |     |
|----|------------|-------------|------------|------------|------------|-----|
| 45 | AATGGATCCT | GTATACGCAC  | AAAAATTAGG | CGTTAACATA | GATGAATTTC | 50  |
|    | TATTATCACA | GCCTGATACA  | GGGGAGCAAG | GATTGGAAAT | CGCGGAAGCA | 100 |
|    | CTTGTACGAA | GTGGTGCGGT  | TGACATTATC | GTAATTGACT | CTGTAGCAGC | 150 |
|    | TCTTGTACCG | AAAGCAGAGA  | TTGAAGGCGA | TATGGGTGAC | TCACACGTAG | 200 |
|    | GTTTACAAGC | ACGTTTAATG  | TCACAAGCAC | TTMGTAAGCT | TTCAGGAGCA | 250 |
|    | ATCAACAAAT | CARRARCAAT  | WGCAATCTTT | ATTAACCAAA | TTCGWGAAAA | 300 |
| 50 | AGTTGGGGTT | ATGTTTCGGAA | ACCCAGAAAC | AACTCCA    |            | 337 |

2) INFORMATION FOR SEQ ID NO: 1289

700

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*  
(B) STRAIN: HER 1232

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289

```
AATGGATCCT GTATATGCAC AAAAATTAGG CGTTAACATA GATGAATTTC 50
TATTATCACA GCCTGATACA GGGGAGCAAG GATTGGAAAT CGCGGAAGCA 100
CTTGACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC 150
TCTTGACCG AAAGCAGAGA TTGAAGGCGA TATGGGTGAC TCACACGTAG 200
GTTTACAAGC ACGTTTAATG TCACAAGCAC TTMGTAAGCT TTCAGGAGCA 250
ATCAACAAAT CARAARCAAT TGCAATCTTT ATTAACCAAA TTCGTGAAAA 300
AGTTGGGGTT ATGTTTCGAA ACCCAGAAAC AACTCC 336
```

## 2) INFORMATION FOR SEQ ID NO: 1290

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290

GAYTAYGCIA TGISIGTIAT HGT

23

## 2) INFORMATION FOR SEQ ID NO: 1291

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291

GCIYTICIG AYGTIMGIGA YGG

23

## 5 2) INFORMATION FOR SEQ ID NO: 1292

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292

ARISCYTCIA RIATRTGIGC

20

20

## 2) INFORMATION FOR SEQ ID NO: 1293

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293

ATGGCTGAAT TACCTCAATC

20

35

## 2) INFORMATION FOR SEQ ID NO: 1294

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294

ATGATTGTTG TATATCTTCT TCAAC

25

50

## 2) INFORMATION FOR SEQ ID NO: 1295

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295

CAGAAAGTTT GAAGCGTTGT

20

## 2) INFORMATION FOR SEQ ID NO: 1296

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296

AACGATTCGT GAGTCAGATA

20

## 2) INFORMATION FOR SEQ ID NO: 1297

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297

CGGTCAACAT TGAGGAAGAG CT

22

## 2) INFORMATION FOR SEQ ID NO: 1298

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298

ACGAAATCGA CCGTCTCTTT TTC

23

10

2) INFORMATION FOR SEQ ID NO: 1299

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 2711 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*  
(B) STRAIN: 601055  
(C) ACCESSION NUMBER: X71437

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299

|    |            |             |            |            |             |      |
|----|------------|-------------|------------|------------|-------------|------|
|    | ATGGCTGAAT | TACCTCAATC  | AAGAATAAAT | GAACGAAATA | TTACCAGTGA  | 50   |
|    | AATGCGTGAA | TCATTTTTAG  | ATTATGCGAT | GAGTGTTATC | GTTGCTCGTG  | 100  |
| 30 | CATTGCCAGA | TGTTTCGTGAC | GGTTTAAAAC | CAGTACATCG | TCGTATACTA  | 150  |
|    | TATGGATTAA | ATGAACAAGG  | TATGACACCG | GATAAATCAT | ATAAAAAATC  | 200  |
|    | AGCACGTATC | GTTGGTGACG  | TAATGGGTAA | ATATCACCTT | CATGGTGACT  | 250  |
|    | CATCTATTTA | TGAAGCAATG  | GTACGTATGG | CTCAAGATTT | CAGTTATCGT  | 300  |
|    | TATCCGCTTG | TTGATGGCCA  | AGGTAACTTT | GGTTCAATGG | ATGGAGATGG  | 350  |
| 35 | CGCAGCAGCA | ATGCGTTATA  | CTGAAGCGCG | TATGACTAAA | ATCACACTTG  | 400  |
|    | AACTGTTACG | TGATATTAAT  | AAAGATACAA | TAGATTTTAT | CGATAACTAT  | 450  |
|    | GATGGTAATG | AAAGAGAGCC  | GTCAGTCTTA | CCTGCTCGAT | TCCCTAATTT  | 500  |
|    | ATTAGCCAAT | GGTGCATCAG  | GTATCGCGGT | AGGTATGGCA | ACGAATATTC  | 550  |
|    | CACCACATAA | CTTAACAGAA  | TTAATCAATG | GTGTACTTAG | CTTAAGTAAG  | 600  |
| 40 | AACCCTGATA | TTTCAATTGC  | TGAGTTAATG | GAAGATATTG | AAGGTCCTGA  | 650  |
|    | TTTCCCAACT | GCTGGACTTA  | TTTTAGGTAA | GAGTGGTATT | AGACGTGCAT  | 700  |
|    | ATGAAACAGG | TCGTGGTTCA  | ATTCAAATGC | GTTCTCGTGC | AGTTATTGAA  | 750  |
|    | GAACGTGGAG | GCGGACGTCA  | ACGTATTGTT | GTCACTGAAA | TTCCTTTCCA  | 800  |
|    | AGTGAATAAG | GCTCGTATGA  | TTGAAAAAAT | TGCAGAGCTC | GTTTCGTGACA | 850  |
| 45 | AGAAAATTGA | CGGTATCACT  | GATTTACGTG | ATGAAACAAG | TTTACGTACT  | 900  |
|    | GGTGTGCGTG | TCGTTATTGA  | TGTGCGTAAG | GATGCAAATG | CTAGTGTCAT  | 950  |
|    | TTTAAATAAC | TTATACAAAC  | AAACACCTCT | TCAAACATCA | TTTGGTGTGA  | 1000 |
|    | ATATGATTGC | ACTTGTAAT   | GGTAGACCGA | AGCTTATTAA | TTTAAAAGAA  | 1050 |
|    | GCGTTGGTAC | ATTATTTAGA  | GCATCAAAAG | ACAGTTGTTA | GAAGACGTAC  | 1100 |
| 50 | GCAATATAAC | TTACGTAAAG  | CTAAAGATCG | TGCCCATATT | TTAGAAGGGT  | 1150 |
|    | TACGTATCGC | ACTTGACCAT  | ATCGATGAAA | TTATTTCAAC | GATTCGTGAG  | 1200 |
|    | TCAGATACAG | ATAAAGTTGC  | AATGGAAAGC | TTGCAACAAC | GCTTCAAAC   | 1250 |
|    | TTCTGAAAAA | CAAGCTCAAG  | CTATTTTAGA | CATGCGTTTA | AGACGTCTAA  | 1300 |

|    |             |            |            |            |            |      |
|----|-------------|------------|------------|------------|------------|------|
|    | CAGGTTTAGA  | GAGAAACAAA | ATTGAAGCTG | AATATAATGA | GTTATTAAAT | 1350 |
|    | TATATTAGTG  | AATTAGAAGC | CATCTTAGCT | GATGAAGAAG | TGTTATTACA | 1400 |
|    | GTTAGTTAGA  | GATGAATTGA | CTGAAATTAG | AGATCGTTTC | GGTGATGAGC | 1450 |
|    | GTCGTACAGA  | AATTCAATTA | GGTGGATTTG | AAGACTTAGA | GGACGAAGAC | 1500 |
| 5  | TTAATTCCAG  | AAGAACAAAT | AGTAATTACT | TTGAGCCATA | ATAACTACAT | 1550 |
|    | TAAACGTTTG  | CCGGTATCTA | CATATCGTGC | TCAAAACCGT | GGTGGTCGTG | 1600 |
|    | GTGTTCAAGG  | TATGAATACA | TTGGAAGAAG | ATTTTGTCTG | TCAATTGGTA | 1650 |
|    | ACTTTAAGTA  | CACATGACCA | TGTATTGTTC | TTTACTAACA | AAGGTCGTGT | 1700 |
|    | ATACAAACTA  | AAAGGTTATG | AAGTGCCTGA | GTTATCAAGA | CAGTCTAAAG | 1750 |
| 10 | GTATTCCTGT  | AGTGAATGCT | ATTGAACTTG | GAAATGATGA | AGTCATTAGT | 1800 |
|    | ACAATGATTG  | CTGTTAAAGA | CCTTGAAAGT | GAAGACAACT | TCTTAGTGTT | 1850 |
|    | TGCAACTAAA  | CGTGGTGTTG | TTAAACGTTT | AGCATTAAGT | AACTTCTCAA | 1900 |
|    | GAATAAATAG  | AAATGGTAAG | ATTGCGATTT | CGTTCAGAGA | AGATGATGAG | 1950 |
|    | TTAATTGCAG  | TTCGTTTAAC | AAGTGGTCAA | GAAGATATCT | TGATTGGTAC | 2000 |
| 15 | ATCACATGCA  | TCATTAATTC | GATTCCCTGA | ATCAACATTA | CGTCCTTTAG | 2050 |
|    | GCCGTACAGC  | AACGGGTGTG | AAAGGTATTA | CACTTCGTGA | AGGTGACGAA | 2100 |
|    | GTTGTAGGGC  | TTGATGTAGC | TCATGCAAAC | AGTGTTGATG | AAGTATTAGT | 2150 |
|    | AGTTACTGAA  | AATGGTTATG | GTAAACGTAC | GCCAGTTAAT | GACTATCGTT | 2200 |
|    | TATCAAATCG  | TGGTGGTAAA | GGTATTAAAA | CAGCTACGAT | TACTGAGCGT | 2250 |
| 20 | AATGGTAATG  | TTGTATGTAT | CACTACAGTA | ACTGGTGAAG | AAGATTTAAT | 2300 |
|    | GATTGTTACT  | AATGCCGGTG | TCATTATTCG | ACTAGATGTT | GCAGATATTT | 2350 |
|    | CTCAAATGG   | TCGTGCAGCA | CAAGGTGTTC | GCTTAATTCG | CTTAGGCGAT | 2400 |
|    | GATCAATTTG  | TTTCAACGGT | TGCTAAAGTA | AAAGAGGATG | CAGATGAAGT | 2450 |
|    | AAATGAAGAT  | GAACAATCTA | CTGTATCTGA | AGATGGTACT | GAACAACAAC | 2500 |
| 25 | GTGAAGCGGT  | TGTAAATGAT | GAAACACCAG | GAAATGCAAT | TCATACTGAA | 2550 |
|    | GTGATTGATT  | CAGAAGAAAA | TGATGAAGAT | GGACGTATTG | AAGTAAGACA | 2600 |
|    | AGATTTTCATG | GATCGTGTTG | AAGAAGATAT | ACAACAATCA | TCAGATGAAG | 2650 |
|    | ATGAAGAATA  | A          |            |            |            | 2711 |

30

## 2) INFORMATION FOR SEQ ID NO: 1300

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 2628 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: K12

45 (C) ACCESSION NUMBER: X57174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGAGCGACC | TTGCGAGAGA | AATTACACCG | GTCAACATTG | AGGAAGAGCT | 50  |
| 50 | GAAGAGCTCC | TATCTGGATT | ATGCGATGTC | GGTCATTGTT | GGCCGTGCGC | 100 |
|    | TGCCAGATGT | CCGAGATGGC | CTGAAGCCGG | TACACCGTCG | CGTACTTTAC | 150 |
|    | GCCATGAACG | TACTAGGCAA | TGACTGGAAC | AAAGCCTATA | AAAAATCTGC | 200 |
|    | CCGTGTCGTT | GGTGACGTAA | TCGGTAAATA | CCATCCCCAT | GGTGACTCGG | 250 |

|    |             |              |             |             |             |      |
|----|-------------|--------------|-------------|-------------|-------------|------|
|    | CGGTCTATGA  | CACGATCGTC   | CGCATGGCGC  | AGCCATTCTC  | GCTGCGTTAT  | 300  |
|    | ATGCTGGTAG  | ACGGTCAGGG   | TAAC TTCGGT | TCTATCGACG  | GCGACTCTGC  | 350  |
|    | GGCGGCAATG  | CGTTATACGG   | AAATCCGTCT  | GGCGAAAATT  | GCCCATGAAC  | 400  |
|    | TGATGGCCGA  | TCTCGAAAAA   | GAGACGGTCG  | ATTTTCGTTGA | TAAC TATGAC | 450  |
| 5  | GGCACGGAAA  | AAATTCCGGA   | CGTCATGCCA  | ACCAAAATTC  | CTAACCTGCT  | 500  |
|    | GGTGAACGGT  | TCTTCCGGTA   | TCGCCGTAGG  | TATGGCAACC  | AACATCCCGC  | 550  |
|    | CGCACAAACCT | GACGGAAGTC   | ATCAACGGTT  | GTCTGGCGTA  | TATTGATGAT  | 600  |
|    | GAAGACATCA  | GCATTGAAGG   | GCTGATGGAA  | CACATCCCGG  | AGCCGGACTT  | 650  |
|    | CCCGACGGCG  | GCAATCATT A  | ACGGTCGTCG  | CGGTATTGAA  | GAAGCTTACC  | 700  |
| 10 | GTACCGGTTCG | CGGCAAGGTG   | TATATCCGCG  | CTCGCGCAGA  | AGTGGAAGTT  | 750  |
|    | GACGCCAAAA  | CCGGTCGTGA   | AACCATTATC  | GTCCACGAAA  | TTCCGTATCA  | 800  |
|    | GGTAAACAAA  | GCGCGCCTGA   | TCGAGAAGAT  | TGCGGAACTG  | GTAAAAGAAA  | 850  |
|    | AACGCGTGGA  | AGGCATCAGC   | GCGCTGCGTG  | ACGAGTCTGA  | CAAAGACGGT  | 900  |
|    | ATGCGCATCG  | TGATTGAAGT   | GAAACGCGAT  | GCGGTCGGTG  | AAGTTGTGCT  | 950  |
| 15 | CAACAACCTC  | TACTCCCAGA   | CCCAGTTGCA  | GGTTTCTTTC  | GGTATCAACA  | 1000 |
|    | TGGTGGCATT  | GCACCATGGT   | CAGCCGAAGA  | TCATGAACCT  | GAAAGACATC  | 1050 |
|    | ATCGCGGCGT  | TTGTTCGTCA   | CCGCCGTGAA  | GTGGTGACCC  | GTCGTACTAT  | 1100 |
|    | TTTCGAACTG  | CGTAAAGCTC   | GCGATCGTGC  | TCATATCCTT  | GAAGCATTAG  | 1150 |
|    | CCGTGGCGCT  | GGCGAACATC   | GACCCGATCA  | TCGAACTGAT  | CCGTCATGCG  | 1200 |
| 20 | CCGACGCCTG  | CAGAAGCGAA   | AACTGCGCTG  | GTTGCTAATC  | CGTGGCAGCT  | 1250 |
|    | GGGCAACGTT  | GCCGCGATGC   | TCGAACGTGC  | TGGCGACGAT  | GCTGCGCGTC  | 1300 |
|    | CGGAATGGCT  | GGAGCCAGAG   | TTGGCGGTGC  | GTGATGGTCT  | GTACTACCTG  | 1350 |
|    | ACCGAACAGC  | AAGCTCAGGC   | GATTCTGGAT  | CTGCGTTTGC  | AGAAACTGAC  | 1400 |
|    | CGGTCTTGAG  | CACGAAAAAC   | TGCTCGACGA  | ATACAAAGAG  | CTGCTGGATC  | 1450 |
| 25 | AGATCGCGGA  | ACTGTTGCGT   | ATTCTTG GTA | GCGCCGATCG  | TCTGATGGAA  | 1500 |
|    | GTGATCCGTG  | AAGAGCTGGA   | GCTGGTTCGT  | GAACAGTTCG  | GTGACAAACG  | 1550 |
|    | TCGTACTGAA  | ATCACCGCCA   | ACAGCGCAGA  | CATCAACCTG  | GAAGATCTGA  | 1600 |
|    | TCACCCAGGA  | AGATGTGGTC   | GTGACGCTCT  | CTCACCAGGG  | CTACGTTAAG  | 1650 |
|    | TATCAGCCGC  | TTTCTGAATA   | CGAAGCGCAG  | CGTCGTGGCG  | GGAAAGGTAA  | 1700 |
| 30 | ATCTGCCGCA  | CGTATTAAAG   | AAGAAGACTT  | TATCGACCGA  | CTGCTGGTGG  | 1750 |
|    | CGAACACTCA  | CGACCATATT   | CTGTGCTTCT  | CCAGCCGTGG  | TCGCGTCTAT  | 1800 |
|    | TCGATGAAAG  | TTTATCAGTT   | GCCGGAAGCC  | ACTCGTGGCG  | CGCGCGGTCTG | 1850 |
|    | TCCGATCGTC  | AACCTGCTGC   | CGCTGGAGCA  | GGACGAACGT  | ATCACTGCGA  | 1900 |
|    | TCCTGCCAGT  | GACCGAGTTT   | GAAGAAGGCG  | TGAAAGTCTT  | CATGGCGACC  | 1950 |
| 35 | GCTAACGGTA  | CCGTGAAGAA   | AACTGTCCTC  | ACCGAGTTCA  | ACCGTCTGCG  | 2000 |
|    | TACCGCCGGT  | AAAGTGCGGA   | TCAAAC TGGT | TGACGGCGAT  | GAGCTGATCG  | 2050 |
|    | GCGTTGACCT  | GACCAGCGGC   | GAAGACGAAG  | TAATGCTGTT  | CTCCGCTGAA  | 2100 |
|    | GGTAAAGTGG  | TGCGCTTTAA   | AGAGTCTTCT  | GTCCGTGCGA  | TGGGCTGCAA  | 2150 |
|    | CACCACCGGT  | GTTTCGCGGT A | TTCGCTTAGG  | TGAAGGCGAT  | AAAGTCGTCT  | 2200 |
| 40 | CTCTGATCGT  | GCCTCGTGGC   | GATGGCGCAA  | TCCTCACC GC | AACGCAAAAC  | 2250 |
|    | GGTTACGGTA  | AACGTACCGC   | AGTGGCGGAA  | TACCCAACCA  | AGTCGCGTGC  | 2300 |
|    | GACGAAAGGG  | GTTATCTCCA   | TCAAGGTTAC  | CGAACGTAAC  | GGTTTAGTTG  | 2350 |
|    | TTGGCGCGGT  | ACAGGTAGAT   | GACTGCGACC  | AGATCATGAT  | GATCACCGAT  | 2400 |
|    | GCCGGTACGC  | TGGTACGTAC   | TCGCGTTTCG  | GAAATCAGCA  | TCGTGGGCCG  | 2450 |
| 45 | TAACACCCAG  | GGCGTGATCC   | TCATCCGTAC  | TGCGGAAGAT  | GAAAACGTAG  | 2500 |
|    | TGGGTCTGCA  | ACGTGTTGCT   | GAACCGGTTG  | ACGAGGAAGA  | TCTGGATACC  | 2550 |
|    | ATCGACGGCA  | GTGCCGCGGA   | AGGGGACGAT  | GAAATCGCTC  | CGGAAGTGGA  | 2600 |
|    | CGTTGACGAC  | GAGCCAGAAG   | AAGAATAA    |             |             | 2628 |

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2) INFORMATION FOR SEQ ID NO: 1301



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301

GTIMGIAWIM GICCIGSIAT GTA

## 2) INFORMATION FOR SEQ ID NO: 1302

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302

TAIADIGGIG GIKKIGCIAT RTA

## 2) INFORMATION FOR SEQ ID NO: 1303

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303

GGIGAIGAID YIMGIGARGG

## 2) INFORMATION FOR SEQ ID NO: 1304

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1304

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CIARYTTIKY ITTIGTYTG

19

10 2) INFORMATION FOR SEQ ID NO: 1305

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305

ATGGTGACTG CATTGTCAGA TG

22

25

2) INFORMATION FOR SEQ ID NO: 1306

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306

GTCTACGGTT TTCTACAACG TC

22

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2) INFORMATION FOR SEQ ID NO: 1307

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1923 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: M86227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307

|    |             |            |             |            |            |      |
|----|-------------|------------|-------------|------------|------------|------|
| 5  | ATGGTGACTG  | CATTGTCAGA | TGTAAACAAC  | ACGGATAATT | ATGGTGCTGG | 50   |
|    | GCAAATACAA  | GTATTAGAAG | GTTTAGAAGC  | AGTACGTAAA | AGACCAGGTA | 100  |
|    | TGTATATAGG  | ATCGACTCAG | AGAGAGTTGC  | ACATTAGTGT | GGAAATTGTC | 150  |
|    | GATAATAGTA  | TCGATGAAGC | ATTAGCTGGT  | TATGCAAATA | AAATTGAAGT | 200  |
|    | TGTTATTGAA  | AAAGATAACT | GGATTAAAGT  | AACGGATAAC | GGACGTGGTA | 250  |
| 10 | TCCCAGTTGA  | TATTCAAGAA | AAAATGGGAC  | GTCCAGCTGT | CGAAGTTATT | 300  |
|    | TTAACTGTTT  | TACATGCTGG | TGGTAAATTC  | GGCGGTGGCG | GATACAAAGT | 350  |
|    | ATCTGGTGGT  | TTACATGGTG | TTGGTTCATC  | AGTTGTAAAC | GCATTGTCAC | 400  |
|    | AAGACTTAGA  | AGTATATGTA | CACAGAAATG  | AGACTATATA | TCATCAAGCA | 450  |
|    | TATAAAAAAG  | GTGTACCTCA | ATTTGACTTA  | AAAGAAGTTG | GCACAACTGA | 500  |
| 15 | TAAGACAGGT  | ACTGTCATTC | GTTTTAAAGC  | AGATGGAGAA | ATCTTCACAG | 550  |
|    | AGACAACGTG  | ATACAACAT  | GAAACATTAC  | AGCAGCGTAT | TAGAGAGCTT | 600  |
|    | GCTTTCTTAA  | ACAAAGGAAT | TCAAATCACA  | TTAAGAGATG | AACGTGATGA | 650  |
|    | AGAAAACGTT  | AGAGAAGACT | CCTATCACTA  | TGAGGGCGGT | ATTAAATCGT | 700  |
|    | ACGTTGAGTT  | ATTGAACGAA | AATAAAGAAC  | CTATTCATGA | TGAGCCAATT | 750  |
| 20 | TATATTCATC  | AATCTAAAGA | TGATATTGAA  | GTAGAAATTG | CGATTCAATA | 800  |
|    | TAACCTCAGGA | TATGCCACAA | ATCTTTTAAAC | TTACGCAAAT | AACATTCATA | 850  |
|    | CGTACGAAGG  | TGGTACGCAT | GAAGACGGAT  | TCAAACGTGC | ATTAACGCGT | 900  |
|    | GTCTTAAATA  | GTTATGGTTT | AAGTAGCAGA  | TATGAAGAAG | AAAAGATAGC | 950  |
|    | TTCTGGTGAA  | GATACACGAG | AAGGTATGAC  | AGCAATTATA | TCTATCAAAC | 1000 |
| 25 | ATGGTGATCC  | TCAATTCGAA | GGTCAAACGA  | AGACAAAATT | AGGTAATTCT | 1050 |
|    | GAAGTGCGTC  | AAGTTGTAGA | TAAATTATTC  | TCAGAGCACT | TTGAACGATT | 1100 |
|    | TTTATATGAA  | AATCCACAAG | TCGCACGTAC  | AGTGGTTGAA | AAAGGTATTA | 1150 |
|    | TGGCGGCACG  | TGCACGTGTT | GCTGCGAAAA  | AAGCGCGTGA | AGTAACACGT | 1200 |
|    | CGTAAATCAG  | CGTTAGATGT | AGCAAGTCTT  | CCAGGTAAAT | TAGCCGATTG | 1250 |
| 30 | CTCTAGTCAA  | AGTCCTGAAG | AATGTGAGAT  | TTTCTTAGTC | GAAGGGGACT | 1300 |
|    | CTGCCGGAGG  | GTCTACAAAA | TCTGGTCGTG  | ACTCTAGAAC | GCAGGCGATT | 1350 |
|    | TTACCATTAC  | GAGGTAAGAT | ATTAAATGTT  | GAAAAAGCAC | GATTAGATAG | 1400 |
|    | AATTTTGAAT  | AACAATGAAA | TTCGTCAAAT  | GATCACAGCA | TTTGGTACAG | 1450 |
|    | GAATCGGTGG  | CGACTTTGAT | CTAGCGAAAG  | CAAGATATCA | CAAAATCGTC | 1500 |
| 35 | ATTATGACTG  | ATGCCGATGT | GGATGGAGCG  | CATATTAGAA | CATTGTTATT | 1550 |
|    | AATATTCTTC  | TATCGATTTA | TGAGACCGTT  | AATTGAAGCA | GGCTATGTGT | 1600 |
|    | ATATTGCACA  | GCCACCGTTG | TATAAACTGA  | CACAAGGTAA | ACAAAAGTAT | 1650 |
|    | TATGTATACA  | ATGATAGGGA | ACTTGATAAA  | CTTAAATCTG | AATTGAATCC | 1700 |
|    | AACACCAAAA  | TGGTCTATTG | CGCTATACAA  | AGGTCTTGGA | GAAATGAATG | 1750 |
| 40 | CAGATCAATT  | ATGGGAAACA | ACAATGAACC  | CTGAGCACCG | CGCTCTTTTA | 1800 |
|    | CAAGTAAAAC  | TTGAAGATGC | GATTGAAGCG  | GACCAAACAT | TTGAAATGTT | 1850 |
|    | AATGGGTGAC  | GTTGTAGAAA | ACCGTAGACA  | ATTTATAGAA | GATAATGCAG | 1900 |
|    | TTTATGCAAA  | CTTAGACTTC | TAA         |            |            | 1923 |

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## 2) INFORMATION FOR SEQ ID NO: 1308

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 23 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308

5

ATGTAYGTIA TIATGGAYMG IGC

23

10 2) INFORMATION FOR SEQ ID NO: 1309

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309

ATIATYTTRT TICCYTTICC YTT

23

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2) INFORMATION FOR SEQ ID NO: 1310

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310

ATIATITSIA TIACYTCRTC

20

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2) INFORMATION FOR SEQ ID NO: 1311

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311

GARATGAARA TIMGIGGIGA RCA

23

## 5 2) INFORMATION FOR SEQ ID NO: 1312

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312

AARTAYATIA TICARGARMG IGC

23

20

## 2) INFORMATION FOR SEQ ID NO: 1313

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313

AMIA YICKRT GIGGITTITT YTT

23

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## 2) INFORMATION FOR SEQ ID NO: 1314

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314

TAIGAITYA CIGAISMICA RGC

23

50

## 2) INFORMATION FOR SEQ ID NO: 1315

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315

ACIATIGCIT CIGCYTGIKS YTC

23

## 2) INFORMATION FOR SEQ ID NO: 1316

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316

GTGAGTGAAA TAATTCAAGA TT

22

## 2) INFORMATION FOR SEQ ID NO: 1317

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317

CACCAAAATC ATCTGTATCT AC

22

## 2) INFORMATION FOR SEQ ID NO: 1318

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318

ACCTAYTCSA TGTACGTRAT CATGGA

26

10

2) INFORMATION FOR SEQ ID NO: 1319

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319

AGRTCCTCIA CCATCGGYAG YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1320

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 2259 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: K-12 MG1655

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(C) ACCESSION NUMBER: AE000384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
| 45 | ATGAGCGATA | TGGCAGAGCG | CCTTGCGCTA  | CATGAATTTA | CGGAAAACGC | 50  |
|    | CTACTTAAAC | TACTCCATGT | ACGTGATCAT  | GGACCGTGCG | TTGCCGTTTA | 100 |
|    | TTGGTGATGG | TCTGAAACCT | GTTTCAGCGCC | GCATTGTGTA | TGCGATGTCT | 150 |
|    | GAAGTGGGCC | TGAATGCCAG | CGCCAAATTT  | AAAAAATCGG | CCCGTACCGT | 200 |
|    | CGGTGACGTA | CTGGGTAAAT | ACCATCCGCA  | CGGCGATAGC | GCCTGTTATG | 250 |
|    | AAGCGATGGT | CCTGATGGCG | CAACCGTTCT  | CTTACCGTTA | TCCGCTGGTT | 300 |
| 50 | GATGGTCAGG | GGAAGTGGGG | CGCGCCGGAC  | GATCCGAAAT | CGTTCGCGGC | 350 |
|    | AATGCGTTAC | ACCGAATCCC | GGTTGTCGAA  | ATATTCCGAG | CTGCTATTGA | 400 |
|    | GCGAGCTGGG | GCAGGGGACG | GCTGACTGGG  | TGCCAAACTT | CGACGGCACT | 450 |
|    | TTGCAGGAGC | CGAAAATGCT | ACCTGCCCGT  | CTGCCAAACA | TTTTGCTTAA | 500 |

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | CGGCACCACC | GGTATTGCCG | TCGGCATGGC | GACCGATATT | CCACCGCATA | 550  |
|    | ACCTGCGTGA | AGTGGCTCAG | GCGGCAATCG | CATTAATCGA | CCAGCCGAAA | 600  |
|    | ACCACGCTCG | ATCAGCTGCT | GGATATCGTG | CAGGGGCCGG | ATTATCCGAC | 650  |
|    | TGAAGCGGAA | ATTATCACTT | CGCGCGCCGA | GATCCGTAAA | ATCTACGAGA | 700  |
| 5  | ACGGACGTGG | TTCAGTGCCT | ATGCGCGCGG | TGTGGAAGAA | AGAAGATGGC | 750  |
|    | GCGGTGGTTA | TCAGCGCATT | GCCGCATCAG | GTTTCAGGTG | CGCGCGTACT | 800  |
|    | GGAGCAAATT | GCTGCGCAAA | TGCGCAACAA | AAAGCTGCCG | ATGGTTGACG | 850  |
|    | ATCTGCGCGA | TGAATCTGAC | CACGAGAACC | CGACCCGCCT | GGTGATTGTG | 900  |
|    | CCGCGTTCCA | ACCGCGTGGA | TATGGATCAG | GTGATGAACC | ACCTCTTCGC | 950  |
| 10 | TACCACCGAT | CTGGAAAAGA | GCTATCGTAT | TAACCTTAAT | ATGATCGGTC | 1000 |
|    | TGGATGGTCG | TCCGGCGGTG | AAAAACCTGC | TGGAAATCCT | CTCCGAATGG | 1050 |
|    | CTGGTGTTCC | GCCGCGATAC | CGTGCGCCGC | CGACTGAACT | ATCGTCTGGA | 1100 |
|    | GAAAGTCCTC | AAGCGCCTGC | ATATCCTCGA | AGGTTTGCTG | GTGGCGTTTC | 1150 |
|    | TCAATATCGA | CGAAGTGATT | GAGATCATTC | GTAATGAAGA | TGAACCGAAA | 1200 |
| 15 | CCGGCGCTGA | TGTCGCGGTT | TGGCCTTACG | GAAACCCAGG | CGGAAGCGAT | 1250 |
|    | CCTCGAACTG | AAACTGCGTC | ATCTTGCCAA | ACTGGAAGAG | ATGAAGATTC | 1300 |
|    | GCGGTGAGCA | GAGTGAAGTG | GAAAAAGAGC | GCGACCAGTT | GCAGGGCATT | 1350 |
|    | TTGGCTTCCG | AGCGTAAAAT | GAATAACCTG | CTGAAGAAAG | AACTGCAGGC | 1400 |
|    | AGACGCGCAA | GCCTACGGTG | ACGATCGTCG | TTCGCCGTTG | CAGGAACGCG | 1450 |
| 20 | AAGAAGCGAA | AGCGATGAGC | GAGCACGACA | TGCTGCCGTC | TGAACCTGTC | 1500 |
|    | ACCATTGTGC | TGTCGCAGAT | GGGCTGGGTA | CGCAGCGCTA | AAGGCCATGA | 1550 |
|    | TATCGACGCG | CCGGGCCTGA | ATTATAAAGC | GGGTGATAGC | TTCAAAGCGG | 1600 |
|    | CGGTGAAAGG | TAAGAGCAAC | CAACCGGTAG | TGTTTGTTGA | TTCCACCGGT | 1650 |
|    | CGTAGCTATG | CCATTGACCC | GATTACGCTG | CCGTCGGCGC | GTGGTCAGGG | 1700 |
| 25 | CGAGCCGCTC | ACCGGCAAAT | TAACGTTGCC | GCCTGGGGCG | ACCGTTGACC | 1750 |
|    | ATATGCTGAT | GGAAAGCGAC | GATCAGAAAC | TGCTGATGGC | TTCCGATGCG | 1800 |
|    | GGTTACGGTT | TCGTCTGCAC | CTTTAACGAT | CTGGTGCGCG | GTAACCGTGC | 1850 |
|    | AGGTAAGGCT | TTGATCACCT | TACCGGAAAA | TGCCCATGTT | ATGCCGCCGG | 1900 |
|    | TGGTGATTGA | AGATGCTTCC | GATATGCTGC | TGGCAATCAC | TCAGGCAGGC | 1950 |
| 30 | CGTATGTTGA | TGTTCCCGGT | AAGTGATCTG | CCGCAGCTGT | CGAAGGGCAA | 2000 |
|    | AGGCAACAAG | ATTATCAACA | TTCCATCGGC | AGAAGCCGCG | CGTGGAGAAG | 2050 |
|    | ATGGTCTGGC | GCAATTGTAC | GTTCTGCCGC | CGCAAAGCAC | GCTGACCATT | 2100 |
|    | CATGTTGGGA | AACGCAAAAT | TAAACTGCGC | CCGGAAGAGT | TACAGAAAGT | 2150 |
|    | CACTGGCGAA | CGTGGACGCC | GCGGTACGTT | GATGCGCGGT | TTGCAGCGTA | 2200 |
| 35 | TCGATCGTGT | TGAGATCGAC | TCTCCTCGCC | GTGCCAGCAG | CGGTGATAGC | 2250 |
|    | GAAGAGTAA  |            |            |            |            | 2259 |

40 2) INFORMATION FOR SEQ ID NO: 1321

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 2403 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*  
 (B) STRAIN: KMP9  
 (C) ACCESSION NUMBER: D67074



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321

|    |            |            |             |            |            |      |
|----|------------|------------|-------------|------------|------------|------|
|    | GTGAGTGAAA | TAATTCAAGA | TTTATCACTT  | GAAGATGTTT | TAGGTGATCG | 50   |
| 5  | CTTTGGAAGA | TATAGTAAAT | ATATTATTCA  | AGAGCGTGCA | TTGCCAGATG | 100  |
|    | TTCGTGATGG | TTTAAAACCA | GTACAACGTC  | GTATTTTATA | TGCAATGTAT | 150  |
|    | TCAAGTGGTA | ATACACACGA | TAAAAATTTT  | CGTAAAAGTG | CGAAAACAGT | 200  |
|    | CGGTGATGTT | ATTGGTCAAT | ATCATCCACA  | TGGAGACTTC | TCAGTGTACA | 250  |
|    | AAGCAATGGT | CCGTTTAAGT | CAAGACTGGA  | AGTTACGACA | TGTCTTAATA | 300  |
| 10 | GAAATGCATG | GTAATAATGG | TAGTATCGAT  | AATGATCCGC | CAGCGGCAAT | 350  |
|    | GCGTTACACT | GAAGCTAAGT | TAAGCTTACT  | AGCTGAAGAG | TTATTACGTG | 400  |
|    | ATATTAATAA | AGAGACAGTT | TCTTTCATTC  | CAAACATATG | TGATACGACA | 450  |
|    | CTCGAACCAA | TGGTATTGCC | ATCAAGATTT  | CCTAACTTAC | TAGTGAATGG | 500  |
|    | TTCTACAGGT | ATATCTGCAG | GTTACGCGAC  | AGATATACCA | CCACATAATT | 550  |
| 15 | TAGCTGAAGT | GATTCAAGCA | ACACTTAAAT  | ATATTGATAA | TCCGGATATT | 600  |
|    | ACAGTCAATC | AATTAATGAA | ATATATTTAA  | GGTCCTGATT | TTCCAACCTG | 650  |
|    | TGGTATTATT | CAAGGTATTG | ATGGTATTAA  | AAAAGCTTAT | GAATCAGGTA | 700  |
|    | AAGGTAGAAT | TATAGTTCGT | TCTAAAGTTG  | AAGAAGAAAC | TTTACGCAAT | 750  |
|    | GGACGTAAAC | AGTTAATTAT | TACTGAAATT  | CCATATGAAG | TGAACAAAAG | 800  |
| 20 | TAGCTTAGTA | AAACGTATCG | ATGAATTACG  | TGCTGACAAA | AAAGTCGATG | 850  |
|    | GTATCGTTGA | AGTACGTGAT | GAAACTGATA  | GAAGTGGTTT | ACGAATAGCA | 900  |
|    | ATTGAATTGA | AAAAAGATGT | GAACAGTGAA  | TCAATCAAAA | ATTATCTTTA | 950  |
|    | TAAAACTCT  | GATTTACAGA | TTTCATATAA  | TTTCAACATG | GTCGCTATTA | 1000 |
|    | GTGATGGTCG | TCCAAAATTG | ATGGGTATTC  | GTCAAATTAT | AGATAGTTAT | 1050 |
| 25 | TTGAATCATC | AAATTGAGGT | TGTTGCAAAT  | AGAACGAAGT | TTGAATTAGA | 1100 |
|    | TAATGCTGAA | AAACGTATGC | ATATCGTTGA  | AGGTTTGATT | AAAGCGTTGT | 1150 |
|    | CAATTTTAGA | TAAAGTAATT | GAATTGATTC  | GTAGCTCTAA | AAACAAGCGT | 1200 |
|    | GACGCTAAAG | AAAACCTTAT | CGAAGTATTC  | GAGTTCACAG | AAGAACAGGC | 1250 |
|    | TGAAGCAATT | GTAATGTTAC | AGTTATATCG  | TTTAACAAAC | ACTGACATAG | 1300 |
| 30 | TTGCGCTTGA | AGGTGAACAT | AAAGAACTTG  | AAGCATTAAT | CAAACAATTA | 1350 |
|    | CGTCATATTC | TTGATAACCA | TGATGCATTA  | TTGAATGTCA | TAAAAGAAGA | 1400 |
|    | ATTGAATGAA | ATTAATAAGA | AATTCAAATC  | TGAACGACTG | TCTTTAATTG | 1450 |
|    | AAGCAGAAAT | TGAAGAAATT | AAAATTGACA  | AAGAAGTTAT | GGTGCCTAGT | 1500 |
|    | GAAGAAGTTA | TTTTAAGTAT | GACACGTCAT  | GGATATATTA | AACGTACTTC | 1550 |
| 35 | TATTCGTAGC | TTTAATGCTA | GCGGTGTTGA  | GGATATTGGT | TTAAAAGATG | 1600 |
|    | GTGACAGTTT | ACTTAAACAT | CAAGAAGTAA  | ATACGCAAGA | TACCGTACTA | 1650 |
|    | GTATTTACAA | ATAAAGGTCG | TTATCTATTT  | ATACCGGTTT | ATAAATTAGC | 1700 |
|    | AGATATTTCG | TGGAAAGAAT | TGGGGCAACA  | TGTATCACAA | ATAGTTCCTA | 1750 |
|    | TCGAAGAAGA | TGAAGTGGTT | ATTAATGTCT  | TTAATGAAAA | GGACTTTAAT | 1800 |
| 40 | ACAGATGCAT | TTTATGTTTT | TGCGACTCAA  | AATGGCATGA | TTAAGAAAAG | 1850 |
|    | TACAGTGCCT | CTATTTAAAA | CAACGCGTTT  | TAATAAACCT | TTAATTGCTA | 1900 |
|    | CTAAAGTTAA | AGAAAATGAT | GATTTGATTA  | GTGTTATGCG | CTTTGAAAAA | 1950 |
|    | GATCAATTAA | TTACCGTCAT | TACTAATAAA  | GGTATGTCAT | TAACGTATAA | 2000 |
|    | TACAAGTGAA | CTATCAGATA | CCGGATTAAAG | GGCAGCTGGT | GTTAAATCAA | 2050 |
| 45 | TAAATCTTAA | AGCTGAAGAT | TTCGTTGTTA  | TGACAGAAGG | TGTTTCTGAA | 2100 |
|    | AATGATACTA | TATTGATGGC | CACACAACGC  | GGCTCGTTAA | AACGTATTAG | 2150 |
|    | TTTTAAATC  | TTACAAGTTG | CTAAAAGAGC  | ACAACGTGGA | ATAACTTTAT | 2200 |
|    | TAAAAGAATT | AAAGAAAAAT | CCACATCGTA  | TTGTAGCTGC | ACATGTAGTG | 2250 |
|    | ACAGGTGAAC | ATAGTCAATA | TACATTATAT  | TCAAAATCAA | ATGAAGAACA | 2300 |
| 50 | TGGTTTAATT | AATGATATTC | ATAAATCTGA  | ACAATATACA | AATGGCTCAT | 2350 |
|    | TCATTGTAGA | TACAGATGAT | TTTGGTGAAG  | TAATAGACAT | GTATATTAGC | 2400 |
|    | TAA        |            |             |            |            | 2403 |

## 2) INFORMATION FOR SEQ ID NO: 1322

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322

RTIGAIAAYI SIGTIGAYGA RG

22

## 2) INFORMATION FOR SEQ ID NO: 1323

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323

ACIAWRSAIG GIGGIACICA YG

22

## 2) INFORMATION FOR SEQ ID NO: 1324

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324

CCICCGICIS WRTCICCYTC

20

## 2) INFORMATION FOR SEQ ID NO: 1325

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325

RTTCATYTCI CCIARICCYT T

21

10

2) INFORMATION FOR SEQ ID NO: 1326

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326

TGATTCAATA CAGGTTTTAG AG

22

25

2) INFORMATION FOR SEQ ID NO: 1327

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327

40

CTAGATTTC TCCTCATCAA AT

22

2) INFORMATION FOR SEQ ID NO: 1328

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1992 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: RN4220

(C) ACCESSION NUMBER: D67075

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328

|    |            |             |             |            |             |      |
|----|------------|-------------|-------------|------------|-------------|------|
|    | ATGAATAAAC | AAAATAATTA  | TTCAGATGAT  | TCAATACAGG | TTTTAGAGGG  | 50   |
|    | GTTAGAAGCA | GTTTCGTAAA  | GACCTGGTAT  | GTATATTGGA | TCAACTGATA  | 100  |
| 10 | AACGGGGATT | ACATCATCTA  | GTATATGAAA  | TTGTCGATAA | CTCCGTCGAT  | 150  |
|    | GAAGTATTGA | ATGGTTACGG  | TAACGAAATA  | GATGTAACAA | TTAATAAAGA  | 200  |
|    | TGGTAGTATT | TCTATAGAAG  | ATAATGGACG  | TGGTATGCCA | ACAGGTATAC  | 250  |
|    | ATAAATCAGG | TAAACCGACA  | GTCGAAGTTA  | TCTTTACTGT | TTTACATGCA  | 300  |
|    | GGAGGTAAAT | TTGGACAAGG  | CGGCTATAAA  | ACTTCAGGTG | GTCTTCACGG  | 350  |
| 15 | TGTTGGTGCT | TCAGTTGTAA  | ATGCATTGAG  | TGAATGGCTT | GAAGTTGAAA  | 400  |
|    | TCCATCGAGA | TGGTAATATA  | TATCATCAAA  | GTTTTAAAAA | CGGTGGTTTCG | 450  |
|    | CCATCTTCTG | GTTTAGTGAA  | AAAAGGTAAG  | ACTAAGAAAA | CAGGTACCAA  | 500  |
|    | AGTAACATTT | AAACCTGATG  | ACACAATTTT  | TAAAGCATCT | ACATCATTTA  | 550  |
|    | ATTTTGATGT | TTTAAGTGAA  | CGACTACAAG  | AGTCTGCGTT | CTTATTGAAA  | 600  |
| 20 | AATTTAAAAA | TAACGCTTAA  | TGATTTACGC  | AGTGGTAAAG | AGCGTCAAGA  | 650  |
|    | GCATTACCAT | TATGAAGAAG  | GAATCAAAGA  | GTTTGTTAGT | TATGTCAATG  | 700  |
|    | AAGGAAAAGA | AGTTTTGTCAT | GACGTGGCTA  | CATTTTCAGG | TGAAGCAAAT  | 750  |
|    | GGTATAGAGG | TAGACGTAGC  | TTTCCAATAT  | AATGATCAAT | ATTCAGAAAG  | 800  |
|    | TATTTTAAGT | TTTGTAATA   | ATGTACGTAC  | TAAAGATGGT | GGTACACATG  | 850  |
| 25 | AAGTTGGTTT | TAAAACAGCA  | ATGACACGTG  | TATTTAATGA | TTATGCACGT  | 900  |
|    | CGTATTAATG | AACTTAAAAC  | AAAAGATAAA  | AACTTAGATG | GTAATGATAT  | 950  |
|    | TCGTGAAGGT | TTAACAGCTG  | TTGTGTCTGT  | TCGTATTCCA | GAAGAATTAT  | 1000 |
|    | TGCAATTTGA | AGGACAAACG  | AAATCTAAAT  | TGGGTACTTC | TGAAGCTAGA  | 1050 |
|    | AGTGCTGTTG | ATTCAGTTGT  | TGCAGACAAA  | TTGCCATTCT | ATTTAGAAGA  | 1100 |
| 30 | AAAAGGACAA | TTGTCTAAAT  | CACTTGTTGAA | AAAAGCGATT | AAAGCACAAAC | 1150 |
|    | AAGCAAGGGA | AGCTGCACGT  | AAAGCTCGTG  | AAGATGCTCG | TTCAGGTAAG  | 1200 |
|    | AAAAACAAGC | GTAAAGACAC  | TTTGCTATCT  | GGTAAATTAA | CACCTGCACA  | 1250 |
|    | AAGTAAAAAC | ACTGAAAAAA  | ATGAATTGTA  | TTTAGTCGAA | GGTGATTCTG  | 1300 |
|    | CGGGAGGTTT | AGCAAAACTT  | GGACGAGACC  | GCAAATTCCA | AGCGATATTA  | 1350 |
| 35 | CCATTACGTG | GTAAGGTAAT  | TAATACAGAG  | AAAGCACGTC | TAGAAGATAT  | 1400 |
|    | TTTTAAAAAT | GAAGAAATTA  | ATACAATTAT  | CCACACAATC | GGGGCAGGCG  | 1450 |
|    | TTGGTACTGA | CTTTAAAATT  | GAAGATAGTA  | ATTATAATCG | TGTAATTATT  | 1500 |
|    | ATGACTGATG | CTGATACTGA  | TGGTGCGCAT  | ATTCAAGTGC | TATTGTTAAC  | 1550 |
|    | ATTCTTCTTC | AAATATATGA  | AACCGCTTGT  | TCAAGCAGGT | CGTGTATTTA  | 1600 |
| 40 | TTGCTTTACC | TCCACTTTAT  | AAATTGGAAA  | AAGGTAAAGG | CAAAACAAAG  | 1650 |
|    | CGAGTTGAAT | ACGCTTGGAC  | AGACGAAGAG  | CTTAATAAAT | TGCAAAAAGA  | 1700 |
|    | ACTTGGTAAA | GGCTTCACGT  | TACAACGTTA  | CAAAGGTTTG | GGTGAAATGA  | 1750 |
|    | ACCCTGAGCA | ATTATGGGAA  | ACGACGATGA  | ACCCAGAAAC | ACGAACTTTA  | 1800 |
|    | ATTCGTGTAC | AAGTTGAAGA  | TGAAGTGCGT  | TCATCTAAAC | GTGTAACAAC  | 1850 |
| 45 | ATTAATGGGT | GACAAAGTAC  | AACCTAGACG  | TGAATGGATT | GAAAAGCATG  | 1900 |
|    | TTGAGTTTGG | TATGCAAGAG  | GACCAGAGTA  | TTTTAGATAA | TTCTGAAGTA  | 1950 |
|    | CAAGTGCTTG | AAAATGATCA  | ATTTGATGAG  | GAGGAAATCT | AG          | 1992 |

50

## 2) INFORMATION FOR SEQ ID NO: 1329

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329

10 TGTAGAGCGC GGTATCATCA AAGTA

25

## 2) INFORMATION FOR SEQ ID NO: 1330

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330

25

AGATTCGAAC TTGGTGTGCG GG

22

## 30 2) INFORMATION FOR SEQ ID NO: 1331

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331

GCCCTTGAGG TACAGAATGG TAATGAAGTT

30

45

## 2) INFORMATION FOR SEQ ID NO: 1332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332

5 GACCGCGGCG CAGACCATCA

20

2) INFORMATION FOR SEQ ID NO: 1333

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333

20

TCATGGTGAC TTATCTATTT ATG

23

2) INFORMATION FOR SEQ ID NO: 1334

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334

35

CATCTATTTA TAAAGCAATG GTA

23

2) INFORMATION FOR SEQ ID NO: 1335

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335

50

CTATTTATGG AGCAATGGT

19

## 2) INFORMATION FOR SEQ ID NO: 1336

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336

TGGAGACTAC TCAGTGT

17

## 2) INFORMATION FOR SEQ ID NO: 1337

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337

TGGAGACTTC TCAGTGT

17

## 2) INFORMATION FOR SEQ ID NO: 1338

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338

GTGTACGGAG CAATG

15

## 2) INFORMATION FOR SEQ ID NO: 1339

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339

CCAGCGGAAA TGCCT

15

10

2) INFORMATION FOR SEQ ID NO: 1340

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340

GAACAAGGTA TGACACCGGA TAAAT

25

25

2) INFORMATION FOR SEQ ID NO: 1341

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341

40

GATAACTGAA ATCCTGAGCC ATACG

25

2) INFORMATION FOR SEQ ID NO: 1342

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342

GATGTTATTG GTCAATATCA TCCA

24

5

2) INFORMATION FOR SEQ ID NO: 1343

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 29 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343

AAGAAACTGT CTCTTTATTA ATATCACGT

29

20

2) INFORMATION FOR SEQ ID NO: 1344

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344

35 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1345

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345

50

CCCGCCGAGC ATTTCAACTA TTG

23

## 2) INFORMATION FOR SEQ ID NO: 1346

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346

GATGTTACGC AGCAGGGCAG TC

22

## 2) INFORMATION FOR SEQ ID NO: 1347

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347

ACCAAGCAGG TTCGCAGTCA AGTA

24

## 2) INFORMATION FOR SEQ ID NO: 1348

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Unidentified bacterium  
 (C) ACCESSION NUMBER: X04555

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGCGCTCAC | GCAACTGGTC | CAGAACCTTG | ACCGAACGCA | GCGGTGGTAA | 50  |
| CGGCGCAGTG | GCGGTTTTCA | TGGCTTGTTA | TGACTGTTTT | TTTGTACAGT | 100 |
| CTATGCCTCG | GGCATCCAAG | CAGCAAGCGC | GTTACGCCGT | GGGTCGATGT | 150 |
| TTGATGTTAT | GGAGCAGCAA | CGATGTTACG | CAGCAGGGCA | GTCGCCCTAA | 200 |
| AACAAAGTTA | GGCCGCATGG | ACACAACGCA | GGTCACATTG | ATACACAAAA | 250 |

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | TTCTAGCTGC | GGCAGATGAG | CGAAATCTGC | CGCTCTGGAT | CGGTGGGGGC | 300 |
|    | TGGGCGATCG | ATGCACGGCT | AGGGCGTGTA | ACACGCAAGC | ACGATGATAT | 350 |
|    | TGATCTGACG | TTTCCCGGCG | AGAGGCGCGG | CGAGCTCGAG | GCAATAGTTG | 400 |
|    | AAATGCTCGG | CGGGCGCGTC | ATGGAGGAGT | TGGACTATGG | ATTCTTAGCG | 450 |
| 5  | GAGATCGGGG | ATGAGTTACT | TGACTGCGAA | CCTGCTTGGT | GGGCAGACGA | 500 |
|    | AGCGTATGAA | ATCGCGGAGG | CTCCGCAGGG | CTCGTGCCCA | GAGGCGGCTG | 550 |
|    | AGGGCGTCAT | CGCCGGGCGG | CCAGTCCGTT | GTAACAGCTG | GGAGGCGATC | 600 |
|    | ATCTGGGATT | ACTTTTACTA | TGCCGATGAA | GTACCACCAG | TGGACTGGCC | 650 |
|    | TACAAAGCAC | ATAGAGTCCT | ACAGGCTCGC | ATGCACCTCA | CTCGGGGCGG | 700 |
| 10 | AAAAGGTTGA | GGTCTTGCGT | GCCGCTTTCA | GGTCGCGATA | TGCGGCCTAA | 750 |

## 2) INFORMATION FOR SEQ ID NO: 1349

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349

25

CAGCCGACCA ATGAGTATCT TGCC

24

## 30 2) INFORMATION FOR SEQ ID NO: 1350

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350

40

TAATCAGGGC AGTTGCGACT CCTA

24

45

## 2) INFORMATION FOR SEQ ID NO: 1351

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Pseudomonas aeruginosa*  
(B) STRAIN: Stone 130  
(C) ACCESSION NUMBER: L06157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351

```
10 ATGTTATGGA GCAGCAACGA TGTTACGCAG CAGGGCAGTC GCCCTAAAC      50
   AAAGTTAGGT GGCTCAATGA GCATCATTGC AACCGTCAAG ATCGGCCCTG      100
   ACGAAATTTT AGCCATGAGG GCTGTGCTCG ATCTCTTCGG CAAAGAGTTT      150
   GAGGACATTC CAACCTACTC TGATCGCCAG CCGACCAATG AGTATCTTGC      200
   CAATCTTCTG CACAGCGAGA CGTTCATCGC GCTCGCTGCT TTTGACCGCG      250
15 GAACAGCAAT AGGTGGGCTC GCCGCCTACG TTCTACCCAA GTTCGAGCAA      300
   GCGCGAAGCG AGATCTACAT TTATGACTTG GCAGTCGCTT CCAGCCATCG      350
   AAGGCTAGGA GTCGCAACTG CCCTGATTAG CCACCTGAAG CGTGTGGCGG      400
   TTGAACTTGG CGCGTATGTA ATCTATGTGC AAGCAGACTA CGGTGACGAT      450
   CCGGCAGTCG CTCTCTACAC AAAGCTTGGA GTTCGGAAG ACGTCATGCA      500
20 CTTCGACATT GATCCAAGAA CCGCCACCTA A              531
```

2) INFORMATION FOR SEQ ID NO: 1352

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352

35

CCACGCTGAC AGAGCCGCAC CG

22

40 2) INFORMATION FOR SEQ ID NO: 1353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
45 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353

GGCCAGCTCC CATCGGACCC TG

22

## 2) INFORMATION FOR SEQ ID NO: 1354

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354

CACGCTGACA GAGCCGCACC G

21

15

## 2) INFORMATION FOR SEQ ID NO: 1355

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355

ATGCCGTTGC TGTCGAAATC CTCG

24

30

## 2) INFORMATION FOR SEQ ID NO: 1356

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 810 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*  
 45 (C) ACCESSION NUMBER: M97172

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356

50 ATGAACACGA TCGAATCGAT CACGGCGGAC CTGCACGGAC TGGGCGTCCG 50  
 GCCCGGCGAC CTGATCATGG TCCATGCATC GCTGAAAGCC GTCGGCCCCG 100  
 TCGAGGGAGG TGCGGCCTCG GTGGTGTCTCG CCCTTCGCGC CGCGGTCTGG 150  
 TCCGCAGGGA CCCTGATGGG TTATGCCTCA TGGGACCGCT CGCCCTATGA 200  
 GGAGACGCTG AACGGCGCGC GGATGGACGA AGAACTGCGC CGCCGGTGGC 250

|    |            |             |            |            |            |     |
|----|------------|-------------|------------|------------|------------|-----|
|    | CACCCTTCGA | TCTGGCCACA  | TCCGGTACCT | ATCCCGGCTT | CGGCCTGCTC | 300 |
|    | AACCGGTTTC | TGCTTGAGGC  | GCCCGACGCA | CGGCGCAGCG | CGCATCCCGA | 350 |
|    | CGCCTCCATG | GTCGCGGTCTG | GCCCCCTTGC | CGCCACGCTG | ACAGAGCCGC | 400 |
|    | ACCGGCTTGG | GCAGGCGCTG  | GGCGAAGGCT | CGCCGCTGGA | GCGCTTCGTC | 450 |
| 5  | GGGCATGGCG | GAAAGGTCCT  | GCTTCTGGGA | GCGCCGCTCG | ACTCCGTCAC | 500 |
|    | CGTGCTGCAT | TACGCCGAGG  | CCATCGCCCC | CATCCCGAAC | AAACGCCGCG | 550 |
|    | TGACCTATGA | AATGCCGATG  | CTCGGCCCGG | ATGGCAGGGT | CCGATGGGAG | 600 |
|    | CTGGCCGAGG | ATTTGACAG   | CAACGGCATT | CTCGATTGCT | TCGCGGTCGA | 650 |
|    | TGGGAAGCCG | GATGCCGTCTG | AGACGATCGC | CAAGGCTTAT | GTCGAACTGG | 700 |
| 10 | GCCGGCATCG | GGAAGGCATC  | GTCGGTCTCG | CACCCTCCTA | TCTGTTTGAA | 750 |
|    | GCGCAGGATA | TCGTCTCGTT  | CGGCGTCACC | TATCTCGAAC | AGCATTTCGG | 800 |
|    | CGCGCCCTGA |             |            |            |            | 810 |

15

## 2) INFORMATION FOR SEQ ID NO: 1357

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357

GCCCATCCAT TTGCCTTTGC

20

30

## 2) INFORMATION FOR SEQ ID NO: 1358

## (i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358

GCGTACCAAC TTGCCATCCT GAAG

24

45

## 2) INFORMATION FOR SEQ ID NO: 1359

## (i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359

TGCCCCCTGCC ACCTCACTC

19

10

2) INFORMATION FOR SEQ ID NO: 1360

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360

CGTACCAACT TGCCATCCTG AAGA

24

25

2) INFORMATION FOR SEQ ID NO: 1361

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 786 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: X01385

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361

45

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| GTGCAATACG    | AATGGCGAAA | AGCCGAGCTC | ATCGGTCAGC | TTCTCAACCT | 50  |
| TGGGGTTACC    | CCCGGCGGTG | TGCTGCTGGT | CCACAGCTCC | TTCCGTAGCG | 100 |
| TCCGGCCCCCT   | CGAAGATGGG | CCACTTGGAC | TGATCGAGGC | CCTGCGTGCT | 150 |
| GCGCTGGGTC    | CGGGAGGGAC | GCTCGTCATG | CCCTCGTGGT | CAGGTCTGGA | 200 |
| CGACGAGCCG    | TTGATCCTG  | CCACGTCGCC | CGTTACACCG | GACCTTGGAG | 250 |
| TTGTCTCTGA    | CACATTCTGG | CGCCTGCCAA | ATGTAAAGCG | CAGCGCCCAT | 300 |
| CCATTTGCCT    | TTGCGGCAGC | GGGGCCACAG | GCAGAGCAGA | TCATCTCTGA | 350 |
| 50 TCCATTGCCC | CTGCCACCTC | ACTCGCCTGC | AAGCCCGGTC | GCCCGTGTCC | 400 |
| ATGAACTCGA    | TGGGCAGGTA | CTTCTCCTCG | GCGTGCGACA | CGATGCCAAC | 450 |
| ACGACGCTGC    | ATCTTGCCGA | GTTGATGGCA | AAGGTTCCCT | ATGGGGTGCC | 500 |
| GAGACACTGC    | ACCATTCTTC | AGGATGGCAA | GTTGGTACGC | GTCGATTATC | 550 |

TCGAGAATGA CCACTGCTGT GAGCGCTTTG CTTGGCGGA CAGGTGGCTC 600  
AAGGAGAAGA GCCTTCAGAA GGAAGGTCCA GTCGGTCATG CCTTTGCTCG 650  
GTTGATCCGC TCCCGCGACA TTGTGGCGAC AGCCCTGGGT CAACTGGGCC 700  
GAGATCCGTT GATCTTCCTG CATCCGCCAG AGGGCGGGAT GCGAAGAATG 750  
5 CGATGCCGCT CGCCAGTCGA TTGGCTGAGC TCATGA 786

## 2) INFORMATION FOR SEQ ID NO: 1362

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362

CGCCGCCATC GCCCAAAGCT GG

22

## 2) INFORMATION FOR SEQ ID NO: 1363

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363

CGGCATAATG GAGCGCGGTG ACTG

24

## 2) INFORMATION FOR SEQ ID NO: 1364

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364

TTTCTCGCCC ACGCAGGAAA AATC

24



## 2) INFORMATION FOR SEQ ID NO: 1365

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365

CATCCTCGAC GAATATGCCG CG

22

## 2) INFORMATION FOR SEQ ID NO: 1366

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*  
 (C) ACCESSION NUMBER: M88012

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | ATGACTGATC | CCCGCAAAAA | CGGCGATTTG | CACGAACCCG | CGACGGCACC  | 50  |
|    | CGCGACGCCC | TGGTCCAAAA | GCGAGCTGGT | CCGGCAATTG | CGCGACCTCG  | 100 |
| 35 | GCGTGCGCTC | AGGCGATATG | GTGATGCCGC | ATGTGTCGTT | GCGCGCCGTC  | 150 |
|    | GGGCCGCTGG | CGGACGGACC | GCAGACACTT | GTCGATGCGC | TGATCGAGGC  | 200 |
|    | CGTCGGCCCC | ACCGGGAATA | TTCTCGCCTT | CGTCTCGTGG | CGCGATTTCGC | 250 |
|    | CCTATGAACA | GACGCTGGGT | CATGATGCGC | CGCCCGCCGC | CATCGCCCCA  | 300 |
|    | AGCTGGCCTG | CGTTCGACCC | CGACCATGCG | CCCGCCTACC | CCGGCTTTGG  | 350 |
| 40 | CGCGATCAAC | GAATTTATCC | GAACCTATCC | GGGGTGTCGG | CGCACGGCCC  | 400 |
|    | ATCCCGACGC | ATCGATGGCG | GCGATCGGGC | CCGATGCGGC | GTGGCTGGTG  | 450 |
|    | GCGCCGCACG | AGATGGGCGC | CGCTTATGGC | CCCCGCTCGC | CGATCGCGCG  | 500 |
|    | TTTTCTCGCC | CACGCAGGAA | AAATCCTGTC | GATCGGCGCC | GGGCCCAGATG | 550 |
|    | CAGTCACCGC | GCTCCATTAT | GCCGAAGCGG | TGGCGCGGAT | CGAGGGCAAG  | 600 |
| 45 | CGCCGCGTCA | CTTATTCGAT | GCCCTTACTG | CGCGAAGGCA | AGCGCGTCTG  | 650 |
|    | GGTCACCACG | TCCGACTGGG | ATTCGAACGG | CATCCTCGAC | GAATATGCCG  | 700 |
|    | CGCCCGACGG | CCCCGACGCG | GTCGAACGGA | TCGCCCCGCA | CTATCTCGCC  | 750 |
|    | CGCACCAGGG | TTGCGCAAGG | CCCGGTCGGC | GGCGCGCAAT | CCCGGCTGAT  | 800 |
|    | CGACGCGGCC | GATATCGTTT | CCTTCGGCAT | CGAATGGCTC | GAGGCGCGCC  | 850 |
| 50 | ACGCCGCGCC | AGCGGCGGCA | GCGCTGAAGC | CGAAACAACG | CCGCGACTGA  | 900 |

## 2) INFORMATION FOR SEQ ID NO: 1367

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367

CAAATATACT AACAGAAGCG TTCA

24

## 2) INFORMATION FOR SEQ ID NO: 1368

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368

AGGATCTTGC CAATACCTTT AT

22

## 2) INFORMATION FOR SEQ ID NO: 1369

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369

AAACCTTTGT TTCGGTCTGC TAAT

24

## 2) INFORMATION FOR SEQ ID NO: 1370

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370

AAGCGATTCC AATAATACCT TGCT

24

10

2) INFORMATION FOR SEQ ID NO: 1371

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 558 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter diversus*  
(C) ACCESSION NUMBER: M18967

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGAATTATC | AAATTGTGAA | TATTGCGGAA | TGCAGCAATT | ATCAGTTAGA | 50  |
|    | AGCAGCAAAT | ATACTAACAG | AAGCGTTCAA | TGATCTTGGT | AACAATTCAT | 100 |
| 30 | GGCCAGATAT | GACGAGTGCA | ACAAAAGAAG | TAAAAGAATG | TATTGAGAGT | 150 |
|    | CCAAACCTTT | GTTTCGGTCT | GCTAATAAAT | AACCTCTTAG | TTGGCTGGAT | 200 |
|    | AGGCTTAAGG | CCAATGTACA | AGGAAACCTG | GGAATTGCAT | CCATTGGTTG | 250 |
|    | TCAGACCAGA | TTATCAAAAT | AAAGGTATTG | GCAAGATCCT | GCTTAAGGAA | 300 |
|    | TTAGAAAACA | GAGCTAGAGA | GCAAGGTATT | ATTGGAATCG | CTTTAGGAAC | 350 |
| 35 | AGATGATGAA | TACTATAGAA | CAAGTCTCTC | TTTAATAACT | ATAACAGAAG | 400 |
|    | ATAATATATT | TGATTCAATA | AAAAATATTA | AAAATATTAA | TAAACATCCA | 450 |
|    | TATGAGTTTT | ATCAGAAGAA | TGGTTATTAT | ATTGTTGGAA | TAATTCCAAA | 500 |
|    | TGCCAATGGT | AAAAACAAAC | CAGATATTTG | GATGTGGAAA | AGTTTAATCA | 550 |
|    | AAGAGTAA   |            |            |            |            | 558 |

40

2) INFORMATION FOR SEQ ID NO: 1372

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372

GCTTTCGTTG CCTTTGCCGA GGTC

24

5

2) INFORMATION FOR SEQ ID NO: 1373

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373

CACCCCTGTT GCTTCGCCCA CTC

23

20

2) INFORMATION FOR SEQ ID NO: 1374

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374

AGATATTGGC TTCGCCGCAC CACA

24

35

2) INFORMATION FOR SEQ ID NO: 1375

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375

50 CCCTGTTGCT TCGCCCACTC CTG

23

## 2) INFORMATION FOR SEQ ID NO: 1376

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*  
(C) ACCESSION NUMBER: M94066

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376

|            |            |            |            |             |     |
|------------|------------|------------|------------|-------------|-----|
| ATGATCGTCA | TCTGCGACCA | CGACAACCTC | GACGCCTGGC | TGGCGCTGCG  | 50  |
| CACCGCGCTG | TGGCCCTCCG | GCTCGCCTGA | AGATCACCGC | GCGGAAATGC  | 100 |
| GCGAGATATT | GGCTTCGCCG | CACCACACCG | CGTTTATGGC | GCGGGGGCTG  | 150 |
| GACGGCGCTT | TCGTTGCCTT | TGCCGAGGTC | GCGCTGCGCT | ACGATTACGT  | 200 |
| CAACGGCTGC | GAATCGTCGC | CGGTGGCGTT | TTTGAAGGA  | ATTTATACCG  | 250 |
| CCGAACGCGC | CCGCCGCCAG | GGCTGGGCCG | CGCGCCTGAT | CGCGCAGGTG  | 300 |
| CAGGAGTGGG | CGAAGCAACA | GGGGTGCAGC | GAGCTGGCGT | CGGATAACCGA | 350 |
| TATCGCCAAT | CTGGACTCCC | AGCGCCTGCA | TGCGGCGCTG | GGCTTTGCCG  | 400 |
| AAACGGAGCG | AGTAGTGTTT | TACCGCAAAA | CGCTGGGCTG | A           | 441 |

## 2) INFORMATION FOR SEQ ID NO: 1377

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377

GCCGTGGGTC GATGTTTGAT GTTA

24

## 2) INFORMATION FOR SEQ ID NO: 1378

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378

GCTCGATGAC GCCAACTACC TCTG

24

2) INFORMATION FOR SEQ ID NO: 1379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379

AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380

CGCTCGATGA CGCCAACTAC CTCT

24

2) INFORMATION FOR SEQ ID NO: 1381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: X02340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | GTGGTAACGG | CGCAGTGGCG | GTTTTTCATGG | CTTCTTGTTA | TGACATGTTT | 50  |
|    | TTTTGGGGTA | CAGTCTATGC | CTCGGGCATC  | CAAGCAGCAA | GCGCGTTACG | 100 |
| 5  | CCGTGGGTCG | ATGTTTGATG | TTATGGAGCA  | GCAACGATGT | TACGCAGCAG | 150 |
|    | GGCAGTCGCC | CTAAAACAAA | GTTAAACATC  | ATGAGGGAAG | CGGTGATCGC | 200 |
|    | CGAAGTATCG | ACTCAACTAT | CAGAGGTAGT  | TGGCGTCATC | GAGCGCCATC | 250 |
|    | TCGAACCGAC | GTTGCTGGCC | GTACATTTGT  | ACGGCTCCGC | AGTGGATGGC | 300 |
|    | GGCCTGAAGC | CACACAGTGA | TATTGATTTG  | CTGGTTACGG | TGACCGTAAG | 350 |
| 10 | GCTTGATGAA | ACAACGCGGC | GAGCTTTGAT  | CAACGACCTT | TTGGAAACTT | 400 |
|    | CGGCTTCCCC | TGGAGAGAGC | GAGATTCTCC  | GCGCTGTAGA | AGTCACCATT | 450 |
|    | GTTGTGCACG | ACGACATCAT | TCCGTGGCGT  | TATCCAGCTA | AGCGCGAACT | 500 |
|    | GCAATTTGGA | GAATGGCAGC | GCAATGACAT  | TCTTGCAAGT | ATCTTCGAGC | 550 |
|    | CAGCCACGAT | CGACATTGAT | CTGGCTATCT  | TGCTGACAAA | AGCAAGAGAA | 600 |
| 15 | CATAGCGTTG | CCTTGGTAGG | TCCAGCGGCG  | GAGGAACTCT | TTGATCCGGT | 650 |
|    | TCCTGAACAG | GATCTATTTG | AGGCGCTAAA  | TGAAACCTTA | ACGCTATGGA | 700 |
|    | ACTCGCCGCC | CGACTGGGCT | GGCGATGAGC  | GAAATGTAGT | GCTTACGTTG | 750 |
|    | TCCCGCATTT | GGTACAGCGC | AGTAACCGGC  | AAAATCGCGC | CGAAGGATGT | 800 |
|    | CGCTGCCGAC | TGGGCAATGG | AGCGCCTGCC  | GGCCCAGTAT | CAGCCCGTCA | 850 |
| 20 | TACTTGAAGC | TAGACAGGCT | TATCTTGGAC  | AAGAAGAAGA | TCGCTTGGCC | 900 |
|    | TCGCGCGCAG | ATCAGTTGGA | AGAATTTGTC  | CACTACGTGA | AAGGCGAGAT | 950 |
|    | CACCAAGGTA | GTCGGCAAAT | AA          |            |            | 972 |

25

2) INFORMATION FOR SEQ ID NO: 1382

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382

TAGATATGAT AGGCGGTAAA AAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1383

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383

CCCAAATTCG AGTAAGAGGT ATT

23

## 5 2) INFORMATION FOR SEQ ID NO: 1384

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384

GATATGATAG GCGGTAAAAA GC

22

20

## 2) INFORMATION FOR SEQ ID NO: 1385

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385

TCCCAAATTC GAGTAAGAGG TA

22

35

## 2) INFORMATION FOR SEQ ID NO: 1386

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 477 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 45 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01282

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386

ATGAAAGAAA GATATGGAAC AGTATATAAA GGCTCTCAGA GGCTCATAGA

50



|   |            |            |             |            |            |     |
|---|------------|------------|-------------|------------|------------|-----|
|   | CGAGGAAAGT | GGAGAAGTAA | TAGAGGTAGA  | TAAGCTATAC | CGTAAACAAA | 100 |
|   | CGTCTGGTAA | CTTTGTAAAA | GCGTATATCG  | TCCAATTAAT | AAGTATGTTA | 150 |
|   | GATATGATAG | GCGGTAAAAA | GCTCAAGATT  | GTTAATTATA | TATTAGATAA | 200 |
|   | TGTACATCTA | AGTAATAACA | CAATGATAGC  | AACTGTTAGA | GAAATAGCAG | 250 |
| 5 | AAGGAACAAA | TACAAGCACG | AAAACCGTAA  | ATACAACGCT | TAAAATCTTA | 300 |
|   | GAAGAAGGAA | ATATCATTAA | AAGAAGAACT  | GGAGCATTAA | TGCTAAACCC | 350 |
|   | AGAGCTACTC | ATGAGAGGCG | ATGACC AAAA | ACAAAAATAC | CTCTTACTCG | 400 |
|   | AATTTGGGAA | CTTTGAGCAA | GAGGACGACC  | AAAAGCAAGA | AAATGCTTTA | 450 |
|   | TCAGAATATT | ATTCTTTCAA | GGAGTAG     |            |            | 477 |

10

## 2) INFORMATION FOR SEQ ID NO: 1387

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387

25 TTATGCCTCT TCCGACCATC AAGC

24

## 2) INFORMATION FOR SEQ ID NO: 1388

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388

40

TACGCTCGTC ATCAAAATCA CTCG

24

## 45 2) INFORMATION FOR SEQ ID NO: 1389

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389

GAATAACGGT TTGGTTGATG CGAG

24

2) INFORMATION FOR SEQ ID NO: 1390

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390

ATGGCAAGAT CCTGGTATCG GTCT

24

2) INFORMATION FOR SEQ ID NO: 1391

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: J01839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391

|    |   |     |
|----|---|-----|
| 40 | ATGAGCCATA TTCAACGGGA AACGTCTTGC TCGAGGCCGC GATTAAATTC  | 50  |
|    | CAACATGGAT GCTGATTTAT ATGGGTATAA ATGGGCTCGC GATAATGTCG  | 100 |
|    | GGCAATCAGG TGCGACAATC TATCGATTGT ATGGGAAGCC CGATGCGCCA  | 150 |
|    | GAGTTGTTTC TGAAACATGG CAAAGGTAGC GTTGCCAATG ATGTTACAGA  | 200 |
|    | TGAGATGGTC AGACTAAACT GGCTGACGGA ATTTATGCCT CTTCCGACCA  | 250 |
| 45 | TCAAGCATTT TATCCGTACT CCTGATGATG CATGGTTACT CACCACTGCG  | 300 |
|    | ATCCCCGGGA AAACAGCATT CCAGGTATTA GAAGAATATC CTGATTCAGG  | 350 |
|    | TGAAAATATT GTTGATGCGC TGGCAGTGTT CCTGCGCCGG TTGCATTCGA  | 400 |
|    | TTCCTGTTTG TAATTGTCCT TTTAACAGCG ATCGCGTATT TCGTCTCGCT  | 450 |
|    | CAGGCGCAAT CACGAATGAA TAACGGTTTG GTTGATGCGA GTGATTTTGA  | 500 |
| 50 | TGACGAGCGT AATGGCTGGC CTGTTGAACA AGTCTGGAAA GAAATGCATA  | 550 |
|    | AGCTTTTGCC ATTCTCACCG GATTTCAGTCG TCACTCATGG TGATTTCTCA | 600 |
|    | CTTGATAACC TTATTTTGA CGAGGGGAAA TTAATAGGTT GTATTGATGT   | 650 |
|    | TGGACGAGTC GGAATCGCAG ACCGATACCA GGATCTTGCC ATCCTATGGA  | 700 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ACTGCCTCGG | TGAGTTTTCT | CCTTCATTAC | AGAAACGGCT | TTTTCAAAAA | 750 |
| TATGGTATTG | ATAATCCTGA | TATGAATAAA | TTGCAGTTTC | ATTTGATGCT | 800 |
| CGATGAGTTT | TTCTAA     |            |            |            | 816 |

5

## 2) INFORMATION FOR SEQ ID NO: 1392

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392

TGGGTGGAGA GGCTATTCGG CTAT

24

20

## 2) INFORMATION FOR SEQ ID NO: 1393

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393

35 CAGTCCCTTC CCGCTTCAGT GAC

23

## 2) INFORMATION FOR SEQ ID NO: 1394

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394

50

GACGTTGTCA CTGAAGCGGG AAGG

24

## 2) INFORMATION FOR SEQ ID NO: 1395

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1395

CTTGGTGGTC GAATGGGCAG GTAG

24

## 2) INFORMATION FOR SEQ ID NO: 1396

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
(C) ACCESSION NUMBER: V00618

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396

|             |             |            |            |             |     |
|-------------|-------------|------------|------------|-------------|-----|
| ATGATTGAAC  | AAGATGGATT  | GCACGCAGGT | TCTCCGGCCG | CTTGGGTGGA  | 50  |
| GAGGCTATTC  | GGCTATGACT  | GGGCACAACA | GACAATCGGC | TGCTCTGATG  | 100 |
| CCGCCGTGTT  | CCGGCTGTCA  | GCGCAGGGGC | GCCCGGTTCT | TTTTGTCAAG  | 150 |
| ACCGACCTGT  | CCGGTGCCCT  | GAATGAACTG | CAGGACGAGG | CAGCGCGGCT  | 200 |
| ATCGTGCTG   | GCCACGACGG  | GCGTTCCTTG | CGCAGCTGTG | CTCGACGTTG  | 250 |
| TCACTGAAGC  | GGGAAGGGAC  | TGGCTGCTAT | TGGGCGAAGT | GCCGGGGCAG  | 300 |
| GATCTCCTGT  | CATCTCACCT  | TGCTCCTGCC | GAGAAAGTAT | CCATCATGGC  | 350 |
| TGATGCAATG  | CGGCGGCTGC  | ATACGCTTGA | TCCGGCTACC | TGCCCCATTCG | 400 |
| ACCACCAAGC  | GAAACATCGC  | ATCGAGCGAG | CACGTACTCG | GATGGAAGCC  | 450 |
| GGTCTTGTCG  | ATCAGGATGA  | TCTGGACGAA | GAGCATCAGG | GGCTCGCGCC  | 500 |
| AGCCGAACTG  | TTCGCCAGGC  | TCAAGGCGCG | CATGCCCGAC | GGCGAGGATC  | 550 |
| TCGTCTGTGAC | CCATGGCGAT  | GCCTGCTTGC | CGAATATCAT | GGTGGAAAAT  | 600 |
| GGCCGCTTTT  | CTGGATTTCAT | CGACTGTGGC | CGGCTGGGTG | TGGCGGACCG  | 650 |
| CTATCAGGAC  | ATAGCGTTGG  | CTACCCGTGA | TATTGCTGAA | GAGCTTGCGG  | 700 |
| GCGAATGGGC  | TGACCGCTTC  | CTCGTGCTTT | ACGGTATCGC | CGCTCCCGAT  | 750 |
| TCGCAGCGCA  | TCGCCTTCTA  | TCGCCTTCTT | GACGAGTTCT | TCTGA       | 795 |

## 2) INFORMATION FOR SEQ ID NO: 1397

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397

GTGGGAGAAA ATGAAACCT AT

22

## 2) INFORMATION FOR SEQ ID NO: 1398

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398

ATGGAGTGAA AGAGCCTGAT

20

## 2) INFORMATION FOR SEQ ID NO: 1399

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399

ACCTATGATG TGGAACGGGA AAAG

24

## 2) INFORMATION FOR SEQ ID NO: 1400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400

5

CGATGGAGTG AAAGAGCCTG ATG

23

10 2) INFORMATION FOR SEQ ID NO: 1401

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(C) ACCESSION NUMBER: V01547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401

25

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| ATGGCTAAAA    | TGAGAATATC | ACCGGAATTG | AAAAAACTGA | TCGAAAAATA | 50  |
| CCGCTGCGTA    | AAAGATACGG | AAGGAATGTC | TCCTGCTAAG | GTATATAAGC | 100 |
| TGGTGGGAGA    | AAATGAAAAC | CTATATTTAA | AAATGACGGA | CAGCCGGTAT | 150 |
| AAAGGGACCA    | CCTATGATGT | GGAACGGGAA | AAGGACATGA | TGCTATGGCT | 200 |
| 30 GGAAGGAAAG | CTGCCTGTTC | CAAAGGTCCT | GCACTTTGAA | CGGCATGATG | 250 |
| GCTGGAGCAA    | TCTGCTCATG | AGTGAGGCCG | ATGGCGTCCT | TTGCTCGGAA | 300 |
| GAGTATGAAG    | ATGAACAAAG | CCCTGAAAAG | ATTATCGAGC | TGTATGCGGA | 350 |
| GTGCATCAGG    | CTCTTTCACT | CCATCGACAT | ATCGGATTGT | CCCTATACGA | 400 |
| ATAGCTTAGA    | CAGCCGCTTA | GCCGAATTGG | ATTACTTACT | GAATAACGAT | 450 |
| 35 CTGGCCGATG | TGGATTGCGA | AAACTGGGAA | GAAGACACTC | CATTTAAAGA | 500 |
| TCCGCGCGAG    | CTGTATGATT | TTTTAAAGAC | GGAAAAGCCC | GAAGAGGAAC | 550 |
| TTGTCTTTTC    | CCACGGCGAC | CTGGGAGACA | GCAACATCTT | TGTGAAAGAT | 600 |
| GGCAAAGTAA    | GTGGCTTTAT | TGATCTTGGG | AGAAGCGGCA | GGGCGGACAA | 650 |
| GTGGTATGAC    | ATTGCCTTCT | GCGTCCGGTC | GATCAGGGAG | GATATCGGGG | 700 |
| 40 AAGAACAGTA | TGTCGAGCTA | TTTTTTGACT | TACTGGGGAT | CAAGCCTGAT | 750 |
| TGGGAGAAAA    | TAAATATTA  | TATTTTACTG | GATGAATTGT | TTTAG      | 795 |

45 2) INFORMATION FOR SEQ ID NO: 1402

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402

TATTCAACAA TTTATCGGAA ACAG

24

5

2) INFORMATION FOR SEQ ID NO: 1403

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403

TCAGAGAGCC AACTCAACAT TTT

23

20

2) INFORMATION FOR SEQ ID NO: 1404

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404

AAACAGCGTT TTAGAGCCAA ATAA

24

35

2) INFORMATION FOR SEQ ID NO: 1405

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405

TTCTCAGAGA GCCAACTCAA CATT

24

50

## 2) INFORMATION FOR SEQ ID NO: 1406

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*  
 (B) STRAIN: BM2580  
 (C) ACCESSION NUMBER: X07753

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406

|            |            |            |             |            |     |
|------------|------------|------------|-------------|------------|-----|
| ATGGAATTGC | CCAATATTAT | TCAACAATTT | ATCGGAAACA  | GCGTTTTAGA | 50  |
| GCCAAATAAA | ATTGGTCAGT | CGCCATCGGA | TGTTTATTCT  | TTTAATCGAA | 100 |
| ATAATGAAAC | TTTTTTTCTT | AAGCGATCTA | GCACTTTATA  | TACAGAGACC | 150 |
| ACATACAGTG | TCTCTCGTGA | AGCGAAAATG | TTGAGTTGGC  | TCTCTGAGAA | 200 |
| ATTAAAGGTG | CCTGAACTCA | TCATGACTTT | TCAGGATGAG  | CAGTTTGAAT | 250 |
| TCATGATCAC | TAAAGCGATC | AATGCAAAAC | CAATTTTCAGC | GCTTTTTTTA | 300 |
| ACAGACCAAG | AATTGCTTGC | TATCTATAAG | GAGGCACTCA  | ATCTGTTAAA | 350 |
| TTCAATTGCT | ATTATTGATT | GTCCATTTAT | TTCAAACATT  | GATCATCGGT | 400 |
| TAAAAGAGTC | AAAATTTTTT | ATTGATAACC | AACTCCTTGA  | CGATATAGAT | 450 |
| CAAGATGATT | TTGACACTGA | ATTATGGGGA | GACCATAAAA  | CTTACCTAAG | 500 |
| TCTATGGAAT | GAGTTAACCG | AGACTCGTGT | TGAAGAAAGA  | TTGGTTTTTT | 550 |
| CTCATGGCGA | TATCACGGAT | AGTAATATTT | TTATAGATAA  | ATTCAATGAA | 600 |
| ATTTATTTTT | TAGATCTTGG | TCGTGCTGGG | TTAGCAGATG  | AATTTGTAGA | 650 |
| TATATCCTTT | GTTGAACGTT | GCCTAAGAGA | GGATGCATCG  | GAGGAAACTG | 700 |
| CGAAAATATT | TTTAAAGCAT | TTAAAAAATG | ATAGACCTGA  | CAAAGGAAT  | 750 |
| TATTTTTTAA | AACTTGATGA | ATTGAATTGA |             |            | 780 |

## 2) INFORMATION FOR SEQ ID NO: 1407

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407

CCCTGTAATA GAAAAGCAAG TAGG

24

## 2) INFORMATION FOR SEQ ID NO: 1408



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408

TTGTCGTATC CCTCAAATCA CC

22

## 2) INFORMATION FOR SEQ ID NO: 1409

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409

TGGGATTACA ATGGCAATCA GCG

23

## 2) INFORMATION FOR SEQ ID NO: 1410

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410

GGGGAATAGG TCACAAGATC TGCTT

25

## 2) INFORMATION FOR SEQ ID NO: 1411

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(C) ACCESSION NUMBER: S46063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411

```

10  ATGCTTTTAT ATAAAATGTG TGACAATCAA AATTATGGGG TTACTTACAT      50
    GAAGTTTTTA TTGGCATTTT CGCTTTTAAT ACCATCCGTG GTTTTTGCAA      100
    GTAGTTCAAA GTTTCAGCAA GTTGAACAAG ACGTTAAGGC AATTGAAGTT      150
    TCTCTTCTG CTCGTATAGG TGTTTCCGTT CTTGATACTC AAAATGGAGA      200
15  ATATTGGGAT TACAATGGCA ATCAGCGCTT CCCGTTAACA AGTACTTTTA      250
    AAACAATAGC TTGCGCTAAA TTAATAATATG ATGCTGAGCA AGGAAAAGTT      300
    AATCCCAATA GTACAGTCGA GATTAAGAAA GCAGATCTTG TGACCTATTC      350
    CCCTGTAATA GAAAAGCAAG TAGGGCAGGC AATCACACTC GATGATGCGT      400
    GCTTCGCAAC TATGACTACA AGTGATAATA CTGCGGCAAA TATCATCCTA      450
20  AGTGCTGTAG GTGGCCCCAA AGGCGTACT GATTTTTTAA GACAAATTGG      500
    GGACAAAGAG ACTCGTCTAG ACCGTATTGA GCCTGATTTA AATGAAGGTA      550
    AGCTCGGTGA TTTGAGGGAT ACGACAATC CTAAGGCAAT AGCCAGTACT      600
    TTGAATAAAC TTTTATTTGG TTCCGCGCTA TCTGAAATGA ACCAGAAAAA      650
    ATTAGAGTCT TGGATGGTGA ACAATCAAGT CACTGGTAAT TTACTACGTT      700
25  CAGTATTGCC GCGGGGATGG AACATTGCGG ATCGCTCAGG TGCTGGCGGA      750
    TTTGGTGCTC GGAGTATTAC AGCAGTTGTG TGGAGTGAGC ATCAAGCCCC      800
    AATTATTGTG AGCATCTATC TAGCTCAAAC ACAGGCTTCA ATGGCAGAGC      850
    GAAATGATGC GATTGTAAA ATTGGTCATT CAATTTTGA CGTTTATACA      900
    TCACAGTCGC GC                                          912
30

```

2) INFORMATION FOR SEQ ID NO: 1412

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412

45 GAGAAAACGC TCCAGCAGGG C

21

2) INFORMATION FOR SEQ ID NO: 1413

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413

CATGAGGCTT TCACTGCGGG G

21

10

2) INFORMATION FOR SEQ ID NO: 1414

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414

TATCGTTAAT CGCACCATCA C

21

25

2) INFORMATION FOR SEQ ID NO: 1415

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415

40

ATGCAGTAAT GCGGCTTTAT C

21

2) INFORMATION FOR SEQ ID NO: 1416

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(B) STRAIN: HEL-1

(C) ACCESSION NUMBER: X91840

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | ATGATGAAAA | AATCGTTATG | CTGCGCTCTG | CTGCTGACAG | CCTCTTTCTC | 50   |
|    | CACATTTGCT | GCCGCAAAAA | CAGAACAACA | GATTGCCGAT | ATCGTTAATC | 100  |
| 10 | GCACCATCAC | CCCGTTGATG | CAGGAGCAGG | CTATTCCGGG | TATGGCCGTT | 150  |
|    | GCCGTTATCT | ACCAGGGAAA | ACCTATTAT  | TTCACCTGGG | GTAAAGCCGA | 200  |
|    | TATCGCCAAT | AACCACCCAG | TCACGCAGCA | AACGCTGTTT | GAGCTAGGAT | 250  |
|    | CGGTTAGTAA | GACGTTTAAC | GGCGTGTTGG | GCGGCGATGC | TATCGCCCCG | 300  |
|    | GGCGAAATTA | AGCTCAGCGA | TCCGGTCACG | AAATACTGGC | CAGAACTGAC | 350  |
| 15 | AGGCAAACAG | TGGCAGGGTA | TCCGCCTGCT | GCACTTAGCC | ACCTATACGG | 400  |
|    | CAGGCGGCCT | ACCGCTGCAG | ATCCCCGATG | ACGTTAGGGA | TAAAGCCGCA | 450  |
|    | TTACTGCATT | TTTATCAAAA | CTGGCAGCCG | CAATGGACTC | CGGGCGCTAA | 500  |
|    | GCGACTTTAC | GCTAACTCCA | GCATTGGTCT | GTTTGGCGCG | CTGGCGGTGA | 550  |
|    | AACCCTCAGG | AATGAGTTAC | GAAGAGGCAA | TGACCAGACG | CGTCCTGCAA | 600  |
| 20 | CCATTAAAAC | TGGCGCATA  | CTGGATTACG | GTTCCGCAGA | ACGAACAAAA | 650  |
|    | AGATTATGCC | TGGGGCTATC | GCGAAGGGAA | GCCCGTACAC | GTTTCTCCGG | 700  |
|    | GACAACTTGA | CGCCGAAGCC | TATGGCGTGA | AATCCAGCGT | TATTGATATG | 750  |
|    | GCCCGCTGGG | TTCAGGCCAA | CATGGATGCC | AGCCACGTTC | AGGAGAAAAC | 800  |
|    | GCTCCAGCAG | GGCATTGCGC | TTGCGCAGTC | TCGCTACTGG | CGTATTGGCG | 850  |
| 25 | ATATGTACCA | GGGATTAGGC | TGGGAGATGC | TGAACTGGCC | GCTGAAAGCT | 900  |
|    | GATTCGATCA | TCAACGGCAG | CGACAGCAAA | GTGGCATTGG | CAGCGCTTCC | 950  |
|    | CGCCGTTGAG | GTAAACCCGC | CCGCCCCCGC | AGTGAAAGCC | TCATGGGTGC | 1000 |
|    | ATAAAACGGG | CTCCACTGGT | GGATTTGGCA | GCTACGTAGC | CTTCGTTCCA | 1050 |
|    | GAAAAAAACC | TTGGCATCGT | GATGCTGGCA | AACAAAAGCT | ATCCTAACCC | 1100 |
| 30 | TGTCCGTGTC | GAGGCGGCCT | GGCGCATTCT | TGAAAAGCTG | CAATAA     | 1146 |

## 2) INFORMATION FOR SEQ ID NO: 1417

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417

45

TGGTTAACTA YAATCCSATT GCGGA

25

## 50 2) INFORMATION FOR SEQ ID NO: 1418

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418

10 ATGCTTTACC CAGCGTCAGA TT

22

2) INFORMATION FOR SEQ ID NO: 1419

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419

25 CGATGAATAA GCTGATTCT CACG

24

2) INFORMATION FOR SEQ ID NO: 1420

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420

40

TGCTTTACCC AGCGTCAGAT TACG

24

45 2) INFORMATION FOR SEQ ID NO: 1421

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421

AATTAGAGCG GCAGTCGGGA GGAA

24

2) INFORMATION FOR SEQ ID NO: 1422

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422

GAAATCAGCT TATTCATCGC CACG

24

2) INFORMATION FOR SEQ ID NO: 1423

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: GRI-1
- (C) ACCESSION NUMBER: X92506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 40 | ATGGTTAAAA | AATCACTGCG | TCAGTTCACG | CTGATGGCGA | CGGCAACCGT | 50  |
|    | CACGCTGTTG | TTAGGAAGTG | TGCCGCTGTA | TGCGCAAACG | GCGGACGTAC | 100 |
|    | AGCAAAAAC  | TGCCGAATTA | GAGCGGCAGT | CGGGAGGAAG | ACTGGGTGTG | 150 |
|    | GCATTGATTA | ACACAGCAGA | TAATTCGCAA | ATACTTTATC | GTGCTGATGA | 200 |
| 45 | GCGCTTTGCG | ATGTGCAGCA | CCAGTAAAGT | GATGGCCGTG | GCCGCGGTGC | 250 |
|    | TGAAGAAAAG | TGAAAGCGAA | CCGAATCTGT | TAAATCAGCG | AGTTGAGATC | 300 |
|    | AAAAAATCTG | ACTTGGTAA  | CTATAATCCG | ATTGCGGAAA | AGCACGTCGA | 350 |
|    | TGGGACGATG | TCACTGGCTG | AGCTTAGCGC | GGCCGCGCTA | CAGTACAGCG | 400 |
|    | ATAACGTGGC | GATGAATAAG | CTGATTTCTC | ACGTTGGCGG | CCCGGCTAGC | 450 |
| 50 | GTCACCGCGT | TCGCCCGACA | GCTGGGAGAC | GAAACGTTCC | GTCTCGACCG | 500 |
|    | TACCGAGCCG | ACGTAAACA  | CCGCCATTCC | GGGCGATCCG | CGTGATACCA | 550 |
|    | CTTCACCTCG | GGCAATGGCG | CAAACCTCTG | GTAATCTGAC | GCTGGGTAAA | 600 |
|    | GCATTGGGTG | ACAGCCAACG | GGCGCAGCTG | GTGACATGGA | TGAAAGGCAA | 650 |

TACCACCGGT GCAGCGAGCA TTCAGGCTGG ACTGCCTGCT TCCTGGGTTG 700  
 TGGGGGATAA AACCGGCAGC GGTGACTATG GCACCACCAA CGATATCGCG 750  
 GTGATCTGGC CAAAAGATCG TGCGCCGCTG ATTCTGGTCA CTTACTTCAC 800  
 CCAGCCTCAA CCTAAGGCAG AAAGCCGTCG CGATGTATTA GCGTCGGCGG 850  
 5 CTAAAATCGT CACCAACGGT TTGTAA 876

2) INFORMATION FOR SEQ ID NO: 1424

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424

20

GTTAACGGTG ATGGCGACGC TAC

23

2) INFORMATION FOR SEQ ID NO: 1425

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425

35

GAATTATCGG CGGTGTTAAT CAGC

24

2) INFORMATION FOR SEQ ID NO: 1426

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426

50

CACGCTCAAT ACCGCCATTC CA

22

## 2) INFORMATION FOR SEQ ID NO: 1427

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427

TTATCGCCCA CTACCCATGA TTTC

24

## 2) INFORMATION FOR SEQ ID NO: 1428

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*  
 (B) STRAIN: CAS-5  
 (C) ACCESSION NUMBER: X92507

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | ATGATGACTC | AGAGCATTCG | CCGCTCAATG  | TTAACGGTGA | TGGCGACGCT | 50  |
| 35 | ACCCCTGCTA | TTTAGCAGCG | CAACGCTGCA  | TGCGCAGGCG | AACAGCGTGC | 100 |
|    | AACAGCAGCT | GGAAGCCCTG | GAGAAAAGTT  | CGGGAGGTCG | GCTTGCGCTT | 150 |
|    | GCGCTGATTA | ACACCGCCGA | TAATTCGCAG  | ATTCTCTACC | GTGCCGATGA | 200 |
|    | ACGTTTTGCG | ATGTGCAGTA | CCAGTAAGGT  | GATGGCGGCC | GCGGCGGTGC | 250 |
|    | TTAAACAGAG | CGAGAGCGAT | AAGCACCTGC  | TAAATCAGCG | CGTTGAAATC | 300 |
| 40 | AAGAAGAGCG | ACCTGGTTAA | CTACAATCCC  | ATTGCGGAGA | AACACGTTAA | 350 |
|    | CGGCACGATG | ACGCTGGCTG | AGCTTGGCGC  | AGCGGCGCTG | CAGTATAGCG | 400 |
|    | ACAATACTGC | CATGAATAAG | CTGATTGCCC  | ATCTGGGTGG | TCCCGATAAA | 450 |
|    | GTGACGGCGT | TTGCTCGCTC | GTTGGGTGAT  | GAGACCTTCC | GTCTGGACAG | 500 |
|    | AACCGAGCCC | ACGCTCAATA | CCGCCATTCC  | AGGCGACCCG | CGTGATACCA | 550 |
| 45 | CCACGCCGCT | CGCGATGGCG | CAGACCCTGA  | AAAATCTGAC | GCTGGGTAAA | 600 |
|    | GCGCTGGCGG | AAACTCAGCG | GGCACAGTTG  | GTGACGTGGC | TTAAGGGCAA | 650 |
|    | TACTACCGGT | AGCGCGAGCA | TTCGGGCGGG  | TCTGCCGAAA | TCATGGGTAG | 700 |
|    | TGGGCGATAA | AACCGGCAGC | GGAGATTATG  | GCACCACCAA | CGATATCGCG | 750 |
|    | GTTATCTGGC | CGGAAAACCA | CGCACCCTG   | GTTCTGGTGA | CCTACTTTAC | 800 |
| 50 | CCAACCGGAG | CAGAAGGCGG | AAAGCCGTCTG | GGATATTCTG | GCTGCGGCGG | 850 |
|    | CGAAAATCGT | AACCCACGGT | TTCTGA      |            |            | 876 |



## 2) INFORMATION FOR SEQ ID NO: 1429

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429

TTTACGGCTA AAGATACTGA AAAGT

25

## 2) INFORMATION FOR SEQ ID NO: 1430

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430

GTTTAATAAA ACAACCACCG AATAAT

26

## 2) INFORMATION FOR SEQ ID NO: 1431

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431

TAATTGACAC TCCATTTACG GCTAA

25

## 2) INFORMATION FOR SEQ ID NO: 1432

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432

ACCGAATAAT ATTTTCCTTT CAGGCA

26

2) INFORMATION FOR SEQ ID NO: 1433

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*  
(C) ACCESSION NUMBER: AJ223604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGAGCAAGT | TATCTGTATT | CTTTATATTT | TTGTTTTGCA | GCATTGCTAC | 50  |
| CGCAGCAGAG | TCTTTGCCAG | ATTTAAAAAT | TGAAAAGCTT | GATGAAGGCG | 100 |
| TTTATGTTCA | TACTTCGTTT | GAAGAAGTTA | ACGGGTGGGG | CGTTGTTCTT | 150 |
| AAACATGGTT | TGGTGGTTCT | TGTAAATGCT | GAGGCTTACC | TAATTGACAC | 200 |
| TCCATTTACG | GCTAAAGATA | CTGAAAAGTT | AGTCACTTGG | TTTGTGGAGC | 250 |
| GTGGCTATAA | AATAAAAGGC | AGCATTTTCT | CTCATTTTCA | TAGCGACAGC | 300 |
| ACGGGCGGAA | TAGAGTGGCT | TAATTCTCGA | TCTATCCCCA | CGTATGCATC | 350 |
| TGAATTAACA | AATGAACTGC | TTAAAAAAGA | CGGTAAGGTT | CAAGCCACAA | 400 |
| ATTCATTTAG | CGGAGTTAAC | TATTGGCTAG | TTAAAAATAA | AATTGAAGTT | 450 |
| TTTTATCCAG | GCCCGGGACA | CACTCCAGAT | AACGTAGTGG | TTTGGTTGCC | 500 |
| TGAAAGGAAA | ATATTATTCG | GTGGTTGTTT | TATTAAACCG | TACGGTTTAG | 550 |
| GCAATTTGGG | TGACGCAAAT | ATAGAAGCTT | GGCCAAAGTC | CGCCAAATTA | 600 |
| TTAAAGTCCA | AATATGGTAA | GGCAAACCTG | GTTGTTCCAA | GTCACAGTGA | 650 |
| AGTTGGAGAC | GCATCACTCT | TGAAACTTAC | ATTAGAGCAG | GCGGTTAAAG | 700 |
| GGTTAAACGA | AAGTAAAAAA | CCATCAAAAC | CAAGCAACTA | A          | 741 |

2) INFORMATION FOR SEQ ID NO: 1434

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434

5 CACAATCAAG ACCAAGATTT GCGAT

25

2) INFORMATION FOR SEQ ID NO: 1435

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435

20

GAAAGGGCAG CTCGTTACGA TAGAG

25

25 2) INFORMATION FOR SEQ ID NO: 1436

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436

CAGCATCAAC ATTTAAGATC CCCA

24

40

2) INFORMATION FOR SEQ ID NO: 1437

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437

CTCCACTTGA TTAAGTGGG AAATTC

26

## 2) INFORMATION FOR SEQ ID NO: 1438

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
(C) ACCESSION NUMBER: X06046

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438

|            |             |            |            |            |     |
|------------|-------------|------------|------------|------------|-----|
| ATGGCAATCC | GAATCTTCGC  | GATACTTTTC | TCCATTTTTT | CTCTTGCCAC | 50  |
| TTTCGCGCAT | GCGCAAGAAG  | GCACGCTAGA | ACGTTCTGAC | TGGAGGAAGT | 100 |
| TTTTCAGCGA | ATTTCAAGCC  | AAAGGCACGA | TAGTTGTGGC | AGACGAACGC | 150 |
| CAAGCGGATC | GTGCCATGTT  | GGTTTTTGAT | CCTGTGCGAT | CGAAGAAACG | 200 |
| CTACTCGCCT | GCATCGACAT  | TCAAGATACC | TCATACACTT | TTTGCACTTG | 250 |
| ATGCAGGCGC | TGTTCTGTGAT | GAGTTCCAGA | TTTTTCGATG | GGACGGCGTT | 300 |
| AACAGGGGCT | TTGCAGGCCA  | CAATCAAGAC | CAAGATTTGC | GATCAGCAAT | 350 |
| GCGGAATTCT | ACTGTTTGGG  | TGTATGAGCT | ATTTGCAAAG | GAAATTGGTG | 400 |
| ATGACAAAGC | TCGGCGCTAT  | TTGAAGAAAA | TCGACTATGG | CAACGCCGAT | 450 |
| CCTTCGACAA | GTAATGGCGA  | TTACTGGATA | GAAGGCAGCC | TTGCAATCTC | 500 |
| GGCGCAGGAG | CAAATTGCAT  | TTCTCAGGAA | GCTCTATCGT | AACGAGCTGC | 550 |
| CCTTTCGGGT | AGAACATCAG  | CGCTTGGTCA | AGGATCTCAT | GATTGTGGAA | 600 |
| GCCGGTTCGA | ACTGGATACT  | GCGTGCAAAG | ACGGGCTGGG | AAGGCCGTAT | 650 |
| GGGTTGGTGG | GTAGGATGGG  | TTGAGTGGCC | GACTGGCTCC | GTATTCTTCG | 700 |
| CACTGAATAT | TGATACGCCA  | AACAGAATGG | ATGATCTTTT | CAAGAGGGAG | 750 |
| GCAATCGTGC | GGGCAATCCT  | TCGCTCTATT | GAAGCGTTAC | CGCCCAACCC | 800 |
| GGCAGTCAAC | TCGGACGCTG  | CGCGATAA   |            |            | 828 |

## 2) INFORMATION FOR SEQ ID NO: 1439

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*  
(C) ACCESSION NUMBER: J03427

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439

|            |            |            |            |            |    |
|------------|------------|------------|------------|------------|----|
| ATGAAAACAT | TTGCCGCATA | TGTAATTATC | GCGTGTCTTT | CGAGTACGGC | 50 |
|------------|------------|------------|------------|------------|----|

```

ATTAGCTGGT TCAATTACAG AAAATACGTC TTGGAACAAA GAGTTCTCTG      100
CCGAAGCCGT CAATGGTGTC TTCGTGCTTT GTAAAAGTAG CAGTAAATCC      150
TGCCTACCA ATGACTTAGC TCGTGCATCA AAGGAATATC TTCCAGCATC      200
AACATTTAAG ATCCCCAACG CAATTATCGG CCTAGAAACT GGTGTCATAA      250
5 AGAATGAGCA TCAGGTTTTTC AAATGGGACG GAAAGCCAAG AGCCATGAAG      300
CAATGGGAAA GAGACTTGAC CTTAAGAGGG GCAATACAAG TTTCAGCTGT      350
TCCCGTATTT CAACAAATCG CCAGAGAAGT TGGCGAAGTA AGAATGCAGA      400
AATACCTTAA AAAATTTTCC TATGGCAACC AGAATATCAG TGGTGGCATT      450
GACAAATTCT GGTGGAAGG CCAGCTTAGA ATTTCCGCAG TTAATCAAGT      500
10 GGAGTTTCTA GAGTCTCTAT ATTTAAATAA ATTGTCAGCA TCTAAAGAAA      550
ACCAGCTAAT AGTAAAAGAG GCTTTGGTAA CGGAGGCGGC ACCTGAATAT      600
CTAGTGCATT CAAAAACTGG TTTTCTGGT GTGGGAACTG AGTCAAATCC      650
TGGTGTGCGA TGGTGGGTTG GGTGGGTGA GAAGGAGACA GAGGTTTACT      700
TTTTCGCCTT TAACATGGAT ATAGACAACG AAAGTAAGTT GCCGCTAAGA      750
15 AAATCCATTC CCACCAAAT CATGGAAAGT GAGGGCATCA TTGGTGGCTA      800
A                                                                801

```

20 2) INFORMATION FOR SEQ ID NO: 1440

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440

AGACCGTTAT CGTAAACAGG GCTAAG

26

35 2) INFORMATION FOR SEQ ID NO: 1441

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases  
 40 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441

TTTTTTGCTC AAACTTTTTC AGGATC

26

50 2) INFORMATION FOR SEQ ID NO: 1442

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*  
 (B) STRAIN: RNL-1  
 (C) ACCESSION NUMBER: Z21957

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442

```

15  ATGAATGTCA TTATAAAAGC TGTAAGTTACT GCCTCGACGC TACTGATGGT      50
    ATCTTTTAGT TCATTCGAAA CCTCAGCGCA ATCCCCACTG TTAAAAGAGC      100
    AAATTGAATC CATAGTCATT GGAAAAAAG CCACTGTAGG CGTTGCAGTG      150
    TGGGGGGCCTG ACGATCTGGA ACCTTTACTG ATTAATCCTT TTGAAAAATT      200
20  CCAATGCAA AGTGTATTTA AATTGCATTT AGCTATGTTG GTACTGCATC      250
    AGGTTGATCA GGGAAAGTTG GATTTAAATC AGACCGTTAT CGTAAACAGG      300
    GCTAAGGTTT TACAGAATAC CTGGGCTCCG ATAATGAAAG CGTATCAGGG      350
    AGACGAGTTT AGTGTTCCAG TGCAGCAACT GCTGCAATAC TCGGTCTCGC      400
    ACAGCGATAA CGTGGCCTGT GATTTGTTAT TTGAACTGGT TGGTGGACCA      450
25  GCTGCTTTGC ATGACTATAT CCAGTCTATG GGTATAAAGG AGACCGCTGT      500
    GGTGCGAAAT GAAGCGCAGA TGCACGCCGA TGATCAGGTG CAGTATCAAA      550
    ACTGGACCTC GATGAAAGGT GCTGCAGAGA TCCTGAAAAA GTTTGAGCAA      600
    AAAACACAGC TGTCTGAAAC CTCGCAGGCT TTGTTATGGA AGTGGATGGT      650
    CGAAACCACC ACAGGACCAG AGCGGTTAAA AGGTTTGTTA CCAGCTGGTA      700
30  CTGTGGTCGC ACATAAAACT GGTACTTCGG GTATCAAAGC CGGAAAAACT      750
    GCGGCCACTA ATGATTTAGG TATCATTCTG TTGCCTGATG GACGGCCCTT      800
    GCTGGTTGCT GTTTTGTGA AAGACTCAGC CGAGTCAAGC CGAACCAATG      850
    AAGCTATCAT TGCGCAGGTT GCTCAGACTG CGTATCAATT TGAATTGAAA      900
    AAGCTTTCTG CCCTAAGCCC AAATTAA      927
35

```

## 2) INFORMATION FOR SEQ ID NO: 1443

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443

```

50  CTTCTGCTCT GCTGATGCTT GGC

```

23

## 2) INFORMATION FOR SEQ ID NO: 1444

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444

GGCGACCAGG TATTTTGTAA TACTGC

26

## 2) INFORMATION FOR SEQ ID NO: 1445

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*  
(B) STRAIN: JMC  
(C) ACCESSION NUMBER: X93314

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
| 35 | ATGAATGTCA | TCACAAAATG | TGTTTTTCACC | GCTTCTGCTC | TGCTGATGCT | 50  |
|    | TGGCTTAAGT | TCATTTGTAG | TATCAGCCCA  | ATCCCCTTTG | TTAAAAGAGC | 100 |
|    | AGATTGAAAC | CATAGTGACG | GGTAAAAAGG  | CCACTGTAGG | TGTAGCAGTG | 150 |
|    | TGGGGGCGTG | ACGATCTGGA | ACCTTTGTTG  | CTGAATCCAT | TTGAAAAGTT | 200 |
|    | TCCGATGCAA | AGTGTGTTTA | AACTGCATTT  | AGCTATGTTA | GTTCTGCATC | 250 |
|    | AGGTCGATCA | GGGGAAACTG | GATTTAAATC  | AGTCTGTTAC | TGTTAATCGT | 300 |
| 40 | GCTGCAGTAT | TACAAAATAC | CTGGTCGCCA  | ATGATGAAAG | ATCATCAGGG | 350 |
|    | CGATGAATTT | ACTGTTGCAG | TACAGCAGTT  | ACTGCAGTAT | TCGGTGTCAC | 400 |
|    | ACAGCGACAA | TGTGGCCTGC | GATTTGTTAT  | TTGAACTGGT | GGGCGGGCCG | 450 |
|    | CAAGCTTTGC | ATGCTTATAT | CCAGTCTTTA  | GGCGTTAAAG | AAGCTGCCGT | 500 |
|    | GGTAGCAAAT | GAAGCGCAAA | TGCATGCGGA  | TGATCAGGTG | CAATATCAAA | 550 |
| 45 | ACTGGACGTC | GATGAAAGCC | GCAGCACAAG  | TTCTGCAAAA | GTTTGAACAG | 600 |
|    | AAAAAGCAGT | TGTCTGAAAC | CTCTCAGGCC  | TTGTTATGGA | AATGGATGGT | 650 |
|    | TGAAACCACC | ACAGGACCAC | AGCGGTAAA   | AGGCTTGTTA | CCTGCTGGTA | 700 |
|    | CTATAGTGGC | GCATAAAACC | GGTACTTCGG  | GCGTCAGAGC | AGGAAAAACT | 750 |
|    | GCGGCGACTA | ATGATGCGGG | CGTCATTATG  | TTGCCTGATG | GACGGCCTTT | 800 |
| 50 | ATTGGTGCG  | GTATTTGTCA | AGGATTCGGC  | TGAATCAGAA | CGAACCAATG | 850 |
|    | AAGCTATTAT | TGCGCAGGTT | GCGCAAGCGG  | CTTATCAGTT | TGAGCTGAAA | 900 |
|    | AAACTCTCTG | CAGTGAGTCC | GGATTGA     |            |            | 927 |

## 2) INFORMATION FOR SEQ ID NO: 1446

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446

GGCCTGYGAT TTGTTATTTG AACTGGT

27

## 2) INFORMATION FOR SEQ ID NO: 1447

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447

CGCTSTGGTC CTGTGGTGGT TTC

23

## 2) INFORMATION FOR SEQ ID NO: 1448

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448

GATCAGGTGC ARTATCAAAA CTGGAC

26

## 2) INFORMATION FOR SEQ ID NO: 1449

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid



- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449

AGCWGGTAAC AAYCCTTTTA ACCGCT

26

2) INFORMATION FOR SEQ ID NO: 1450

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450

ACCACTGGGA ATACACTTGT AATGGC

26

2) INFORMATION FOR SEQ ID NO: 1451

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451

ATCTACCTGG TCAATCATTG CTCGT

26

2) INFORMATION FOR SEQ ID NO: 1452

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*  
(B) STRAIN: BM10393  
(C) ACCESSION NUMBER: AF045472

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | ATGACATTAT | CAATAATTGT | CGCTCACGAT | AAACAAAGAG  | TCATTGGGTA | 50  |
|    | CCAAAATCAA | TTACCTTGGC | ACTTACCAA  | TGATTTAAAG  | CATATTAAAC | 100 |
| 10 | AACTGACCAC | TGGGAATACA | CTTGTAATGG | CACGGAAAAC  | TTTTAATTCT | 150 |
|    | ATAGGGAAGC | CATTGCCAAA | TAGACGTAAC | GTCGTACTCA  | CTAACCAAGC | 200 |
|    | TTCATTTTAC | CATGAAGGGG | TAGATGTTAT | AAACTCTCTT  | GATGAAATTA | 250 |
|    | AAGAGTTATC | TGGTCATGTT | TTTATATTTG | GAGGACAAAC  | GTTATACGAA | 300 |
|    | GCAATGATTG | ACCAGGTAGA | TGATATGTAT | ATCACAGTAA  | TAGATGGAAA | 350 |
| 15 | GTTTCAAGGA | GACACATTCT | TTCCACCATA | CACATTTCGAA | AACTGGGAAG | 400 |
|    | TCGAATCTTC | AGTAGAAGGT | CAACTAGATG | AAAAAAATAC  | TATACCGCAT | 450 |
|    | ACATTCTTAC | ATTTAGTGCG | TAGAAAAGGG | AAATAG      |            | 486 |

20

## 2) INFORMATION FOR SEQ ID NO: 1453

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

25

## (ii) MOLECULE TYPE: DNA

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453

ATCGAAGAAT GGAGTTATCG GRAATG 26

35

## 2) INFORMATION FOR SEQ ID NO: 1454

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

40

## (ii) MOLECULE TYPE: DNA

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454

CCTAAAYTR CTGGGGATTT CWGGA 25

50

## 2) INFORMATION FOR SEQ ID NO: 1455

764

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455

CAGGTGGTGG GGAGATATAC AAAA

24

## 2) INFORMATION FOR SEQ ID NO: 1456

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456

TATGTTAGAS RCGAAGTCTT GGKTAA

26

## 2) INFORMATION FOR SEQ ID NO: 1457

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457

CAAAGGTGAA CAGCTCCTGT TT

22

## 2) INFORMATION FOR SEQ ID NO: 1458

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458

TCCGTTATTT TCTTTAGGTT GGTAAA

27

10

2) INFORMATION FOR SEQ ID NO: 1459

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1459

AAGGTGAACA GTCCTGTTT

20

25

2) INFORMATION FOR SEQ ID NO: 1460

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460

GATCACTACG TTCTCATTGT CA

22

40

2) INFORMATION FOR SEQ ID NO: 1461

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*  
(C) ACCESSION NUMBER: AJ238350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461

5 GTGAAACTAT CACTAATGGT AGCTATATCG AAGAATGGAG TTATCGGGAA 50  
TGGCCCTGAT ATTCCATGGA GTGCCAAAGG TGAACAGCTC CTGTTTAAAG 100  
CTATTACCTA TAACCAATGG CTGTTGGTTG GACGCAAGAC TTTTGAATCA 150  
ATGGGAGCAT TACCCAACCG AAAGTATGCG GTCGTAACAC GTCCAAGTTT 200  
10 TACATCTGAC AATGAGAACG TAGTGATCTT TCCATCAATT AAAGATGCTT 250  
TAACCAACCT AAAGAAAATA ACGGATCATG TCATTGTTTC AGGTGGTGGG 300  
GAGATATACA AAAGCCTGAT CGATCAAGTA GATACACTAC ATATATCTAC 350  
AATAGACATC GAGCCGGAAG GTGATGTTTA CTTTCCTGAA ATCCCCAGCA 400  
ATTTTAGGCC AGTTTTTACC CAAGACTTCG CCTCTAACAT AAATTATAGT 450  
15 TACCAAATCT GGCAAAGGG TTAA 474

2) INFORMATION FOR SEQ ID NO: 1462

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462

30

GCACTCCCYA ATAGGAAATA CGC

23

35 2) INFORMATION FOR SEQ ID NO: 1463

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
40 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463

AGTGTTGCTC AAAAACAAC TCG

23

50

2) INFORMATION FOR SEQ ID NO: 1464

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464

10 ACGTTYGAAT CTATGGGMGC ACT

23

## 2) INFORMATION FOR SEQ ID NO: 1465

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465

25

GTCGATAAGT GGAGCGTAGA GGC

23

## 30 2) INFORMATION FOR SEQ ID NO: 1466

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466

AAGCATTGAC CTACAATCAG TGT

23

45

## 2) INFORMATION FOR SEQ ID NO: 1467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467

5 AATACAAC TA CATTGTCATC ATTTGAT

27

2) INFORMATION FOR SEQ ID NO: 1468

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468

CGTTACCCGC TCAGGTTGGA CATCAA

26

2) INFORMATION FOR SEQ ID NO: 1469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1469

CATCCCCCTC TGGCTCGATG TCG

23

2) INFORMATION FOR SEQ ID NO: 1470

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: Z50804

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470

```

5  TTGAAAGTAT CATTGATAGC TGCGAAACGA AAAAACGGCG TGATTGGTTG      50
   CGGTCCAGAC ATACCGTGGT CCGCGAAAGG GGAGCAGCTA CTTTTTAAAG      100
   CATTGACCTA CAATCAGTGT CTTCTGGTGG GTCGCAAGAC GTTTGAATCT      150
   ATGGGCGCAC TCCCAATAG GAAATACGCG GTCGTTACCC GCTCAGGTTG      200
   GACATCAAAT GATGACAATG TAGTTGTATT TCAGTCAATC GAAGAGGCCA      250
   TGGACAGGCT AGCTGAATTC ACCGGTCACG TTATAGTGTC TGGTGGCGGA      300
10 GAAATTTACC GAGAAACATT ACCCATGGCC TCTACGCTCC ACTTATCGAC      350
   GATCGACATC GAGCCAGAGG GGGATGTTTT CTTCCCGAGT ATTCCAAATA      400
   CCTTCGAAGT TGTTTTTGAG CAACACTTTA CTTCAAACAT TAACTATTGC      450
   TATCAAATTT GGAAAAGGG TTAA                                     474

```

15

## 2) INFORMATION FOR SEQ ID NO: 1471

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471

```

30 GATAATGACA ACGTAATAGT ATTCCC                                     26

```

## 2) INFORMATION FOR SEQ ID NO: 1472

```

35 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

40

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472

```

45 GCTCAATATC AATCGTCGAT ATA                                     23

```

## 2) INFORMATION FOR SEQ ID NO: 1473

50

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 bases
    (B) TYPE: Nucleic acid

```



(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473

TTAAAGCCTT GACGTACAAC CAGTGG

26

10

2) INFORMATION FOR SEQ ID NO: 1474

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474

TGGGCAATGT TTCTCTGTAA ATCTCC

26

25

2) INFORMATION FOR SEQ ID NO: 1475

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 474 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Escherichia coli*  
(C) ACCESSION NUMBER: X12868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 45 | GTGAAAGTAT | CATTAATGGC | TGCAAAAGCG | AAAAACGGAG | TGATTGGTTG | 50  |
|    | CGGTCCACAC | ATACCCTGGT | CCGCGAAAGG | AGAGCAGCTA | CTCTTTAAAG | 100 |
|    | CCTTGACGTA | CAACCAGTGG | CTTTTGGTGG | GCCGCAAGAC | GTTCGAATCT | 150 |
|    | ATGGGAGCAC | TCCCTAATAG | GAAATACGCG | GTCGTTACTC | GCTCAGCCTG | 200 |
|    | GACGGCCGAT | AATGACAACG | TAATAGTATT | CCCGTCGATC | GAAGAGGCCA | 250 |
|    | TGTACGGGCT | GGCTGAACTC | ACCGATCACG | TTATAGTGTC | TGGTGGCGGG | 300 |
| 50 | GAGATTTACA | GAGAAACATT | GCCCATGGCC | TCTACGCTCC | ATATATCGAC | 350 |
|    | GATTGATATT | GAGCCGGAAG | GAGATGTTTT | CTTTCCGAAT | ATTCCCAATA | 400 |
|    | CCTTCGAAGT | TGTTTTTGAG | CAACACTTTA | GCTCAAACAT | TAATAATTGC | 450 |
|    | TATCAAATTT | GGCAAAAGGG | TTAA       |            |            | 474 |

## 2) INFORMATION FOR SEQ ID NO: 1476

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476

GGCGAGCAGC TCCTATTCAA AG

22

## 2) INFORMATION FOR SEQ ID NO: 1477

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477

TAGGTAAGCT AATGCCGATT CAACA

25

## 2) INFORMATION FOR SEQ ID NO: 1478

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478

GAGAATGGAG TAATTGGCTC TGGATT

26

## 2) INFORMATION FOR SEQ ID NO: 1479

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479

GCGAAATACA CAACATCAGG GTCAT

25

2) INFORMATION FOR SEQ ID NO: 1480

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*  
(B) STRAIN: J120  
(C) ACCESSION NUMBER: Z86002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480

|             |            |            |            |            |     |
|-------------|------------|------------|------------|------------|-----|
| ATGAAAATAT  | CTCTTATGGC | AGCTGTTTCC | GAGAATGGAG | TAATTGGCTC | 50  |
| TGGATTGGAT  | ATACCTTGGC | ATGTACAAGG | CGAGCAGCTC | CTATTCAAAG | 100 |
| CCATGACTTA  | CAATCAATGG | CTTCTAGTTG | GTCGTAAAAC | CTTCGACTCA | 150 |
| ATGGGTAAAC  | TTCCGAATAG | AAAATATGCA | GTGGTTACTC | GTTCTAAAAT | 200 |
| TATCTCGAAT  | GACCCTGATG | TTGTGTATTT | CGCAAGTGTT | GAATCGGCAT | 250 |
| TAGCTTACCT  | AAACAATGCG | ACAGCACATA | TCTTTGTTTC | TGGTGGTGGT | 300 |
| GAAATATATA  | AAGCTTTAAT | CGATCAAGCA | GATGTTATCC | ATCTTTCAGT | 350 |
| GATTCAACAAG | CATATCTCTG | GCGATGTGTT | TTTTCCTCCA | GTTCCACAGG | 400 |
| GCTTCAAGCA  | AACATTTGAG | CAAAGTTTCA | GTTCAAATAT | TGATTACACG | 450 |
| TACCAAATTT  | GGGCAAAGGG | CTAA       |            |            | 474 |

2) INFORMATION FOR SEQ ID NO: 1481

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481

RTTACAGATC ATKTATATGT CTCT

24

## 5 2) INFORMATION FOR SEQ ID NO: 1482

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482

TAATTTATAT TAGACAWAAA AAAC TG

26

20

## 2) INFORMATION FOR SEQ ID NO: 1483

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483

CARYGTCAGA AAATGGCGTA ATC

23

35

## 2) INFORMATION FOR SEQ ID NO: 1484

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1484

TKCAAAGCRW TTTCTATTGA AGGAAA

26

50

## 2) INFORMATION FOR SEQ ID NO: 1485

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485

AAAATGGCGT AATCGGTAAT GGC

23

## 2) INFORMATION FOR SEQ ID NO: 1486

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486

CATTTGAGCT TGAAATTCCT TTCCTC

26

## 2) INFORMATION FOR SEQ ID NO: 1487

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487

AATCGAAAAT ATGCAGTAGT GTCGAG

26

## 2) INFORMATION FOR SEQ ID NO: 1488

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488

AGACTATTGT AGATTTGACC GCCA

24

10

2) INFORMATION FOR SEQ ID NO: 1489

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: VA292

(C) ACCESSION NUMBER: U31119

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489

30

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| TTGAAAATTT    | CATTGATTTC | TGCAACGTCA | GAAAATGGCG | TAATCGGTAA | 50  |
| TGGCCCTGAT    | ATCCCATGGT | CAGCAAAAGG | TGAGCAGTTA | CTCTTTAAAG | 100 |
| CGCTCACATA    | TAATCAGTGG | CTCCTTGTTG | GAAGGAAAAC | ATTTGACTCT | 150 |
| ATGGGTGTTC    | TTCCAAATCG | AAAATATGCA | GTAGTGTCTG | GGAAAGGAAT | 200 |
| TTCAAGCTCA    | AATGAAAATG | TATTAGTCTT | TCCTTCAATA | GAAATCGCTT | 250 |
| TGCAAGAACT    | ATCGAAAATT | ACAGATCATT | TATATGTCTC | TGGTGGCGGT | 300 |
| CAAATCTACA    | ATAGTCTTAT | TGAAAAAGCA | GATATAATTC | ATTTGTCTAC | 350 |
| 35 TGTTCACGTT | GAGGTTGAAG | GTGATATCAA | TTTTCCTAAA | ATTCCAGAGA | 400 |
| ATTTCAATTT    | GGTTTTTGAG | CAGTTTTTTT | TGTCTAATAT | AAATTACACA | 450 |
| TATCAGATTT    | GGAAAAAAGG | CTAA       |            |            | 474 |

40

2) INFORMATION FOR SEQ ID NO: 1490

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490

GACCTATGAG AGCTTGCCCG TCAAA

25

## 2) INFORMATION FOR SEQ ID NO: 1491

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491

TCGCCTTCGT ACAGTCGCTT AACAAA

26

## 2) INFORMATION FOR SEQ ID NO: 1492

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492

CATTTTAGCT GCCACCGCCA ATGGTT

26

## 2) INFORMATION FOR SEQ ID NO: 1493

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493

GCGTCGCTGA CGTTGTTTAC GAAGA

25

## 2) INFORMATION FOR SEQ ID NO: 1494

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*  
(B) STRAIN: BL26A  
(C) ACCESSION NUMBER: U10186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| ATGATCGAGC    | TTCATGCCAT | TTTAGCTGCC | ACCGCCAATG | GTTGCATTGG | 50  |
| GAAGGACAAC    | GCACTTCCCT | GGCCACCACT | AAAAGGCGAT | CTGGCCAGAT | 100 |
| 15 TCAAAAAATT | GACCATGGGG | AAGGTGGTCA | TTATGGGGCG | CAAGACCTAT | 150 |
| GAGAGCTTGC    | CCGTCAAATT | AGAAGGTCGC | ACCTGCATCG | TTATGACGCG | 200 |
| CCAAGCGCTG    | GAGCTTCCGG | GTGTTCTGTA | CGCTAACGGC | GCTATCTTCG | 250 |
| TGAACAACGT    | CAGCGACGCC | ATGCGGTTCG | CTCAAGAAGA | GAGCGTGGGC | 300 |
| GATGTGGCCT    | ACGTCATTGG | TGGCGCTGAG | ATATTCAAGC | GACTTGCCTT | 350 |
| 20 GATGATCACG | CAGATTGAAT | TGACCTTTGT | TAAGCGACTG | TACGAAGGCG | 400 |
| ACACCTACGT    | TGATCTGGCC | GAAATGGTCA | AAGACTACGA | GCAGAATGGC | 450 |
| ATGGAAGAAC    | ATGACCTTCA | CACTTACTTC | ACTTACCGTA | AAAAGGAGCT | 500 |
| TACAGAATGA    |            |            |            |            | 510 |

2) INFORMATION FOR SEQ ID NO: 1495

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495

TCTCTAAACA TGATTGTCGC TGTC

24

2) INFORMATION FOR SEQ ID NO: 1496

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496



CAGTGAGGCA AAAGTTTTTC TACC

24

5

2) INFORMATION FOR SEQ ID NO: 1497

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1497

CGGACGACTT CATGTGGTAG TCAGT

25

20

2) INFORMATION FOR SEQ ID NO: 1498

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498

TTTGTTTTCA GTAATGGTCG GGACCT

26

35

2) INFORMATION FOR SEQ ID NO: 1499

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 534 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: X57730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGGCTTCTC | TAAACATGAT | TGTCGCTGTC | AATAAGACAG | GAGGTATCGG | 50  |
|    | ATTTGAAAAT | CAGATTCGGT | GGCATGAACC | AGAAGATTTA | AAACACTTCA | 100 |
|    | AAGCTGTTAC | AATGAACTCA | GTTTTGATTA | TGGGTAGAAA | AACTTTTGCC | 150 |
|    | TCACTGCCTA | AAGTGCTGCC | CGGACGACTT | CATGTGGTAG | TCAGTAAAC  | 200 |
| 5  | AGTACCACCC | ACCCAGAACA | CTGATCAAGT | TGTGTATGTA | AGTACATACC | 250 |
|    | AGATCGCAGT | AAGAACTGCA | AGCTTGTTGG | TTGACAAACC | AGAGTATTCT | 300 |
|    | CAAATTTTGT | TAATTGGTGG | GAAGAGTGCG | TACGAGAACT | TAGCTGCCTA | 350 |
|    | CGTGGACAAA | CTCTACTTAA | CTAGAGTACA | GCTCAACACA | CAACAAGACA | 400 |
|    | CTGAACTGGA | TTTATCCCTA | TTCAAGTCAT | GGAAACTCGT | ATCTGAGGTC | 450 |
| 10 | CCGACCATTA | CTGAAAACAA | AACAAAACCT | ATTTTCCAAA | TTTGGATTAA | 500 |
|    | CCCTAACCT  | ATTAGTGAGG | AACCCACATG | TTAG       |            | 534 |

## 15 2) INFORMATION FOR SEQ ID NO: 1500

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500

ATCGGGTTAT TGGCAATGGT CCTA

24

30

## 2) INFORMATION FOR SEQ ID NO: 1501

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501

GCGGTAGTTA GCTTGGCGTG AGATT

25

45

## 2) INFORMATION FOR SEQ ID NO: 1502

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 22 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502

5 GCGGGCGGAG CTGAGATATA CA 22

10 2) INFORMATION FOR SEQ ID NO: 1503

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503

AACGGAGTGG GTGTACGGAA TTACAG 26

25 2) INFORMATION FOR SEQ ID NO: 1504

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 498 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Escherichia coli*  
(B) STRAIN: TKS84  
(C) ACCESSION NUMBER: Z21672

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGAACTCGG | AATCAGTACG | CATTTATCTC | GTTGCTGCGA | TGGGAGCCAA | 50  |
|    | TCGGGTATT  | GGCAATGGTC | CTAATATCCC | CTGGAAAATT | CCGGGTGAGC | 100 |
| 45 | AGAAGATTTT | TCGCAGACTC | ACTGAGGGAA | AAGTCGTTGT | CATGGGGCGA | 150 |
|    | AAGACCTTTG | AGTCTATCGG | CAAGCCTCTA | CCGAACCGTC | ACACATTGGT | 200 |
|    | AATCTCACGC | CAAGCTAACT | ACCGCGCCAC | TGGCTGCGTA | GTTGTTTCAA | 250 |
|    | CGCTGTCGCA | CGCTATCGCT | TTGGCATCCG | AACTCGGCAA | TGAACTCTAC | 300 |
|    | GTCGCGGGCG | GAGCTGAGAT | ATACACTCTG | GCACTACCTC | ACGCCCACGG | 350 |
| 50 | CGTGTTTCTA | TCTGAGGTAC | ATCAAACCTT | CGAGGGTGAC | GCCTTCTTCC | 400 |
|    | CAATGCTCAA | CGAAACAGAA | TTCGAGCTTG | TCTCAACCGA | AACCATTCAA | 450 |
|    | GCTGTAATTC | CGTACACCCA | CTCCGTTTAT | GCGCGTCGAA | ACGGCTAA   | 498 |

## 2) INFORMATION FOR SEQ ID NO: 1505

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505

ATTTTTCGCA GGCTCACCGA GAGC

24

## 2) INFORMATION FOR SEQ ID NO: 1506

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506

CGGATGAGAC AACCTCGAAT TCTGCTG

27

## 2) INFORMATION FOR SEQ ID NO: 1507

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (B) STRAIN: RA33.2  
 (C) ACCESSION NUMBER: Z50802

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGAACCCGG | AATCGGTCCG | CATTTATCTG | GTCGCTGCCA | TGGGTGCCAA | 50  |
| TCGGGTTATT | GGCAATGGTC | CCGATATCCC | CTGGAAAATC | CCAGGTGAGC | 100 |
| AGAAGATTTT | TCGCAGGCTC | ACCGAGAGCA | AAGTGGTCGT | TATGGGCCGC | 150 |
| AAGACATTTG | AGTCCATAGG | CAAGCCCTTA | CCAAACCGCC | ACACAGTGGT | 200 |

|   |            |            |            |            |            |     |
|---|------------|------------|------------|------------|------------|-----|
|   | GCTCTCGCGC | CAAGCTGGTT | ATAGCGCTCC | TGGTTGTGCA | GTTGTTTCAA | 250 |
|   | CGCTGTCACA | CGTATCGCCA | TCGACAGCCG | AACACGGCAA | AGAACTCTAC | 300 |
|   | GTAGCGCGCG | GAGCCGAGGT | ATATGCGCTG | GCGCTACCGC | ATGCCAACGG | 350 |
|   | CGTCTTTCTA | TCTGAGGTAC | ATCAAACCTT | TGAGGGTGAC | GCCTTCTTCC | 400 |
| 5 | CAGTGCTTAA | CGCAGCAGAA | TTCGAGGTTG | TCTCATCCGA | AACCATTCAA | 450 |
|   | GGCACAATCA | CGTACACGCA | CTCCGTCTAT | GCGCGTCGTA | ACGGCTAA   | 498 |

## 10 2) INFORMATION FOR SEQ ID NO: 1508

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases  
(B) TYPE: Nucleic acid  
15 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508

AGAATGTATT GGTATTTCCA TCTATCG

27

## 25 2) INFORMATION FOR SEQ ID NO: 1509

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases  
30 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509

CAATGTCGAT TGTGAAATA TGTAATA

26

## 40 2) INFORMATION FOR SEQ ID NO: 1510

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
45 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## 50 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510

TGGAGTGCCA AAGGGGAACA AT

## 5 2) INFORMATION FOR SEQ ID NO: 1511

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511

CAGACACAAT CACATGATCC GTTATCG

27

20

## 2) INFORMATION FOR SEQ ID NO: 1512

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 bases  
 25 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (B) STRAIN: UI14  
 (C) ACCESSION NUMBER: Z83331

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | GTGAAACTAT | CACTAATGGC | AGCAATTTTCG | AAGAATGGAG | TTATCGGAAA | 50  |
|    | TGGCCCAGAT | ATTCCATGGA | GTGCCAAAGG  | GGAACAATTA | CTCTTCAAAG | 100 |
| 40 | CGATTACCTA | TAATCAGTGG | CTTTTGGTAG  | GCCGAAAGAC | TTTCGAGTCA | 150 |
|    | ATGGGGGCTT | TACCCAACCG | AAAATATGCC  | GTTGTAAGTC | GTTCAAGCTT | 200 |
|    | CACTTCCAGT | GATGAGAATG | TATTGGTATT  | TCCATCTATC | GATGAAGCGC | 250 |
|    | TAAATCATCT | GAAGACGATA | ACGGATCATG  | TGATTGTGTC | TGGTGGTGGT | 300 |
|    | GAAATATACA | AAAGCCTGAT | CGATAAAGTT  | GATACTTTAC | ATATTTCAAC | 350 |
| 45 | AATCGACATT | GAGCCAGAAG | GTGATGTCTA  | TTTTCCAGAA | ATCCCCAGTA | 400 |
|    | GTTTTAGGCC | AGTTTTTTCG | CAAGACTTCG  | TGTCTAACAT | AAATTATAGT | 450 |
|    | TACCAAATCT | GGCAAAGGG  | TTAA        |            |            | 474 |

50

## 2) INFORMATION FOR SEQ ID NO: 1513

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513

10 TTCAAGCTCA AATGAAAACG TCC

23

## 2) INFORMATION FOR SEQ ID NO: 1514

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514

25

GAAATTCTCA GGCATTATAG GGAAT

25

## 30 2) INFORMATION FOR SEQ ID NO: 1515

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515

GTGGTCAGTA AAAGGTGAGC AAC

23

45

## 2) INFORMATION FOR SEQ ID NO: 1516

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

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|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CTATGTCTCA | AGGCCGTGCA | ACATACTCTA | TGGAATTTGC | TAAATATGCT | 50  |
| GAAACTCCAC | GTAACGTGGC | TGAAGGCATC | ATTTCTAAAT | TTCAGTCTGG | 100 |
| CGGTAAAAAA | GGTGACGACG | AGTAA      |            |            | 125 |

5

## 2) INFORMATION FOR SEQ ID NO: 1519

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Acinetobacter lwoffii*
  - (B) STRAIN: CDCF 3697
- 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519

|               |            |             |            |            |    |
|---------------|------------|-------------|------------|------------|----|
| TCTTTCGATT    | ACTATAAGCC | CAAACATAATT | CATAGTTAAA | AACCAAGTGC | 50 |
| 25 TCATGCAGTG | ATCCTGCATG | AGTAGTTTAA  | AAAGGAAGAT | CTC        | 93 |

## 2) INFORMATION FOR SEQ ID NO: 1520

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1106 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Acinetobacter lwoffii*
  - (B) STRAIN: CDCF 3697
- 40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| 45 ATGGCTAAGG | CTAAGTTTGA | ACGTAATAAG | CCACACGTTA | ACGTGGGCAC | 50  |
| AATCGGTCAC    | GTTGACCATG | GTAAAACAAC | TTTAACAGCT | GCAATTGCAA | 100 |
| CTGTATGTGC    | GAAGAAATTC | GGTGGCGAAG | CGAAAGACTA | CGCTGCAATT | 150 |
| GACTCTGCAC    | CAGAAGAAAA | AGCACGTGGT | ATTACAATTA | ATACTTCACA | 200 |
| CGTAGAATAC    | GATTCTCCAA | CTCGTCACTA | CGCACACGTA | GACTGCCCCG | 250 |
| 50 GCCACGCCGA | TTATGTTAAA | AACATGATTA | CTGGTGCTGC | TCAGATGGAC | 300 |
| GGCGCGATCC    | TTGTATGTGC | TGCGACTGAT | GGTCCAATGC | CACAGACTCG | 350 |
| TGAACACATC    | CTTCTTTCTC | GTCAGGTTGG | TGTACCTTAC | ATTCTTGTAT | 400 |
| TCCTTAACAA    | GTGTGACCTT | GTTGATGATG | AAGAACTTCT | TGAGCTAGTG | 450 |

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | GAAATGGAAG | TTCGTGAACT | TCTTTCTACT | TATGACTTCC | CAGGTGATGA | 500  |
|    | CACTCCAGTT | ATCCGTGGTT | CAGCTCTTCT | TGCACTTAAC | GGTGACGCTG | 550  |
|    | GTCAGTATGG | CGAAGAAGCA | GTTGTTGCGC | TTGTTGACGC | ACTTGACACT | 600  |
|    | TACATTCCAG | AGCCAGTACG | TGCAATCGAC | CAAGCATTCT | TAATGCCAAT | 650  |
| 5  | CGAAGACGTA | TTCTCTATTT | CTGGTCGTGG | TACAGTAGTA | ACTGGCCGTG | 700  |
|    | TAGAAACTGG | TATTGTGAAA | GTAGGCGAAT | CAGTTGAAAT | CGTTGGTATC | 750  |
|    | CGTGATACTC | AAGTAACTAC | AGTTACTGGC | GTAGAAATGT | TCCGTAAATT | 800  |
|    | GCTTGACGAA | GGTCGTGCGG | GCGAGAACTG | TGGTGTTCTT | CTACGTGGTA | 850  |
|    | CTAAGCGTGA | AGACGTACAA | CGTGGTCAAG | TACTTGCTAA | ACCAGGTGCA | 900  |
| 10 | ATCAAGCCAC | ACACTAAATT | CGATGCAGAA | GTATACGTAC | TTTCTAAAGA | 950  |
|    | AGAAGGTGGT | CGTCACACTC | CATTCCTTAA | CGGTTACCGT | CCACAGTTCT | 1000 |
|    | ACTTCCGTAC | AACTGACGTA | ACTGGCGCGA | TCAAATTACA | AGATGGCGTT | 1050 |
|    | GAAATGGTTA | TGCCTGGTGA | CAACGTAGAA | ATGTCAGTAG | AATTAATCCA | 1100 |
|    | CCCAAT     |            |            |            |            | 1106 |

## 2) INFORMATION FOR SEQ ID NO: 1521

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*
- (B) STRAIN: ATCC 9006

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ACAAACTCAA | GGTCGTGCAT | CTTACTCAAT | GGAACCGTTA | AAATATGCTG | 50  |
| 35 | AAGCTCCAAC | AAGTGTTGCG | GCTGCAGTAA | TTGAAGCGCG | TAAAAAATAA | 100 |

## 2) INFORMATION FOR SEQ ID NO: 1522

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*
- (B) STRAIN: ATCC 9006

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522

TTTTTGTAAG CCAGCGGTGT AAAATATGAT TGTTTTATAC CGCACTTCTT 50  
 AGGAAACATT AGAA 64

5

## 2) INFORMATION FOR SEQ ID NO: 1523

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1098 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*  
 (B) STRAIN: ATCC 9006

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523

|    |            |             |            |            |            |      |
|----|------------|-------------|------------|------------|------------|------|
|    | ATGTCTAAAG | AAAAATTTGA  | ACGTACAAAA | CCGCACGTAA | ACGTGGGTAC | 50   |
|    | AATCGGCCAC | GTTGACCACG  | GTAAAACAAC | TTTAACAGCA | GCAATTACAA | 100  |
| 25 | CCGTATTAGC | AAAACACTAC  | GGTGGTGCAG | CGCGTGCATT | TGACCAAATC | 150  |
|    | GATAACGCGC | CAGAAGAAAA  | AGCGCGTGGT | ATTACCATCA | ACACTTCACA | 200  |
|    | TGTTGAATAC | GATACACCAA  | CTCGCCACTA | TGCACACGTA | GACTGTCCAG | 250  |
|    | GACACGCCGA | CTATGTTAAA  | AACATGATTA | CCGGTGCGGC | GCAAATGGAT | 300  |
|    | GGTGCTATTT | TAGTAGTAGC  | AGCAACAGAT | GGTCCTATGC | CACAACTCG  | 350  |
| 30 | TGAACATATC | TTATTAGGTC  | GCCAAGTAGG | TGTTCCATAC | ATCATCGTAT | 400  |
|    | TCTTAAACAA | ATGCGACATG  | GTAGATGATG | AAGAGTTATT | AGAATTAGTA | 450  |
|    | GAAATGGAAG | TGCGTGAACT  | TCTATCTCAA | TATGACTTCC | CAGGTGACGA | 500  |
|    | TACACCAATC | GTACGTGGTT  | CAGCATTACA | AGCATTGAAC | GGCGTAGCAG | 550  |
|    | AATGGGAAGA | AAAAATCCTT  | GAATTAGCTG | GTCACCTAGA | TACTTACATC | 600  |
| 35 | CCAGAACCAG | AACGTGCGAT  | TGACCAACCG | TTCCTTCTTC | CAATTGAAGA | 650  |
|    | CGTATTCTCA | ATTTTCAGGTG | GTGGTACAGT | AGTAACTGGT | CGTGTAGAAC | 700  |
|    | GTGGTATCAT | CCGTACTGGT  | GATGAAGTAG | AAATCGTCGG | TATCAAAGAT | 750  |
|    | ACAGCGAAAA | CTACTGTAAAC | AGGTGTTGAA | ATGTTCCGTA | AATTACTTGA | 800  |
|    | CGAAGGTCGT | GCAGGTGAAA  | ACATCGGTGC | ATTATTACGT | GGTACCAAAC | 850  |
| 40 | GTGAAGAAAT | CGAACGTGGT  | CAAGTATTAG | CGAAACCAGG | TTCAATCACA | 900  |
|    | CCACACACTG | ATTTTGAATC  | AGAAGTATAC | GTATTATCAA | AAGATGAAGG | 950  |
|    | TGGTCGTCAT | ACTCCATTCT  | TCAAAGGTTA | CCGTCCACAA | TTCTATTTCC | 1000 |
|    | GTACAACAGA | CGTAACTGGT  | ACAATTGAAT | TACCAGAAGG | CGTGGAATG  | 1050 |
| 45 | GTAATGCCAG | GCGATAACAT  | CAAGATGACA | GTAAGCTTAA | TCCACCCA   | 1098 |

## 2) INFORMATION FOR SEQ ID NO: 1524

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524

10 CAATGGAGTT CTTGAAGTAC AACGAAGCGC CTAGCAACGT CGCTCAGGCT 50  
ATTATCGAAG CTCGTAAAGC GAAATAA 77

15

2) INFORMATION FOR SEQ ID NO: 1525

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 67 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525

GATCCTTTCG AGTTCAATTT AGTTTACGCT CCCTCTGTGA GAGGGAGCGA 50  
TATTAAGGAA TATAGTC 67

35

2) INFORMATION FOR SEQ ID NO: 1526

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1112 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526

GTGTCTAAAG AAAAATTTGA ACGTTCAAAA CCGCACGTTA ACGTTGGTAC 50

|    |             |            |             |             |            |      |
|----|-------------|------------|-------------|-------------|------------|------|
|    | TATCGGCCAC  | GTTGACCACG | GTAACAACAAC | TCTGACTGCT  | GCAATCACTA | 100  |
|    | CAGTTTTTAGC | TAAAACTTAC | GGTGGTGCTG  | CTCGTGCAAT  | CGACCAAATC | 150  |
|    | GATAATGCAC  | CAGAAGAAAA | AGCGCGTGGT  | ATCACCATCT  | CTACTTCACA | 200  |
|    | CGTAGAATAC  | GATACTCCAA | CTCGCCACTA  | CGCACACGTA  | GACTGCCAG  | 250  |
| 5  | GTCACGCCGA  | CTATGTTAAA | AACATGATCA  | CTGGTGCTGC  | GCAAATGGAC | 300  |
|    | GGCGCTATTC  | TGGTAGTAGC | AGCAACTGAT  | GGTCCAATGC  | CACAACTCG  | 350  |
|    | TGAGCACATC  | CTGTTAGGTC | GTCAGGTTGG  | TGTTCCCTTAC | ATCATCGTAT | 400  |
|    | TCCTGAACAA  | ATGTGACATG | GATAGATGATG | AAGAGCTGTT  | AGAATTAGTT | 450  |
|    | GAAATGGAAG  | TTCGTGAACT | TCTGTCTCAA  | TACGATTTCC  | CAGGTGATGA | 500  |
| 10 | CACTCCAGTA  | ATCCGTGGTT | CAGCGCTGAA  | AGCACTGGAA  | GGCGAAGCAG | 550  |
|    | AGTGGAAGC   | AAAAATTGTT | GAATTAGCAG  | AAGCACTGGA  | TTCTTATATC | 600  |
|    | CCAGAGCCAG  | AGCGTGCAAT | TGACAAACCA  | TTCCTGTTAC  | CAATCGAAGA | 650  |
|    | TGTATTCTCA  | ATCTCAGGCC | GTGGTACAGT  | AGTTACTGGT  | CGTGTAGAGC | 700  |
|    | GTGGTATCAT  | CAAAGTAGGT | GATGAAGTTG  | AGATTGTTGG  | TATCAAAGAA | 750  |
| 15 | ACCACCAAAA  | CAACTTGTAC | TGGCGTTGAA  | ATGTTCCGTA  | AATTACTTGA | 800  |
|    | CGAAGGTCGT  | GCAGGTGAGA | ACGTAGGTGT  | TCTGCTGCGT  | GGTACAAAAC | 850  |
|    | GTGAAGAAAT  | CGAACGTGGA | CAAGTACTGG  | CAAACCCAGG  | CTCAATCAAC | 900  |
|    | CCACACAACA  | AATTTGAATC | AGAAGTTTAT  | ATTCTGAGCA  | AAGATGAAGG | 950  |
|    | TGGTCGTCAC  | ACACCATTCT | TCAAAGGCTA  | CCGTCCACAG  | TTCTACTTCC | 1000 |
| 20 | GTACAACCTGA | CGTAACTGGT | ACTATCGAAT  | TACCAGAAGG  | CGTAGAAATG | 1050 |
|    | GTAATGCCAG  | GCGACAACGT | GAACATGATC  | GTTGAACTGA  | TCCACCCAAT | 1100 |
|    | CGCAATGGAC  | GA         |             |             |            | 1112 |

25

## 2) INFORMATION FOR SEQ ID NO: 1527

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

35

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*  
 (B) STRAIN: ATCC 35224

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATCAACGAAG | CTATCGAGGT | TTATTTTGAG | GTTGAGGGCA | AGAAAAATAG | 50  |
|    | ATTGATCCTG | GAGGTCGCGG | CTCACTTGGG | TGATAACCGC | GTCAGAACGA | 100 |
|    | TCGCTATGGA | TATGAGTGAG | GGGCTTACTC | GCGGGCTTGA | AGCTACCGCT | 150 |
| 45 | CTTGGTGCGC | CTATTAGTGT | GCCGGTTGGC | GAGAAGGTTT | TGGGAAGAAT | 200 |
|    | TTTTAACGTC | GTCGGCGATC | TCATCGACGA | GGGCGAGGGC | GTAAATTTTG | 250 |
|    | ATAAACATTG | GTCTATCCAC | CGCGATCCGC | CACCATTTGA | AGAACAAAGC | 300 |
|    | ACGAAAAGTG | AAATTTTTGA | AACCGGTATA | AAGGTTGTGG | ATCTTCTTGC | 350 |
|    | GCCTTACGCA | AAGGGCGGTA | AGGTCGGACT | ATTTGGCGGT | GCAGGTGTGC | 400 |
| 50 | GTAAAACGGT | CATCATCATG | GAGCTCATCC | ACAATGTCGC | CTTCAAACAC | 450 |
|    | AGCGGATACT | CTGTATTTGC | AGGTGTTGGC | GAGAGGACGC | GCGAAGGAAA | 500 |
|    | CGACCTTTAT | CACGAGATGA | AAGAAAGTAA | CGTTTTGGAT | AAAGTCGCCT | 550 |
|    | TGTGCTACGG | ACAGATGAAC | GAGCCGCCAG | GGGCGAGAAA | TCGTATCGCA | 600 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CTGACTGGTC | TAACGATGGC | TGAGTATTTC | CGCGATGAGA | TGGGACTTGA | 650 |
| TGTGCTTATG | TTTATCGACA | ACATCTTCCG | CTTCTCTCAA | TCTGGTGCAG | 700 |
| AGATGTCGGC | ACTCCTCGGA | CGTATCCCAT | CAGCCGTTGG | TTACCAGCCG | 750 |
| ACGCTGGCAA | GCGAGATGGG | TAAATTTCAA | GAAAGGATCA | CATCGACTAA | 800 |

5

## 2) INFORMATION FOR SEQ ID NO: 1528

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528

20 AACTTGAGCG ATTTTCGGAT ACCCTG

26

## 2) INFORMATION FOR SEQ ID NO: 1529

25

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529

35

TTGCCGATGA AATAACCGCC GACT

24

## 40 2) INFORMATION FOR SEQ ID NO: 1530

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1035 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
(C) ACCESSION NUMBER: M11277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530

|    |             |            |            |            |             |      |
|----|-------------|------------|------------|------------|-------------|------|
|    | ATGCGATTGG  | TTTGAAATG  | TGGGGCGATT | CAGGCATCCC | GGTTATCTGA  | 50   |
|    | ATGGCTCAAC  | TCAACAGCCG | GTGCTCATGA | ACTTGAGCGA | TTTTTCGGATA | 100  |
| 5  | CCCTGACCTT  | TTCTGTGTAT | GGCTCAGTGC | TGATCTGGCT | GAAATCATAT  | 150  |
|    | CTCCGCGAAT  | CAGGAAGAAA | ACTGCAGTTA | GTCGGAATCG | CCTTACCCAA  | 200  |
|    | CACCCTGAAC  | CCAAGGGACG | ACCTAGCGCA | ATTGGCCGAA | ATTATCCAGC  | 250  |
|    | TCATCGATCA  | CCTCATGAAA | CCGCACGTTG | ATATGTTGAC | TCACTTGTTG  | 300  |
|    | GCGTCCATTG  | ATGGCCAGTC | GGCGGTTATT | TCATCGGCAA | AATGGGGGGA  | 350  |
| 10 | GCTAGAAACG  | GCTCGGCAGG | AGAAAGCTAT | CTCAGGGGTA | ACCAGATTGA  | 400  |
|    | AGCTCCGCTT  | GGCGTCGCTT | GCCCCGTCC  | TGAAAAACA  | CGTCAACAGC  | 450  |
|    | GATTTGTTCC  | GAAAAGCCTC | TGATCGAATA | GAGTCGATAG | AGTATACGTT  | 500  |
|    | GGAAACCTTG  | CGTATAATGA | AAACTTTCTT | CGATGGTACC | TCTCTTGAGG  | 550  |
|    | GAGATACTTC  | CGTACGTGAC | TCGTATATGG | CGGGCGTAGT | AGATGGAATG  | 600  |
| 15 | GTTTCGAGCGA | ATCCGGATGT | GAAGATAATT | CTGCTGGCGC | ACAACAATCA  | 650  |
|    | TCTACAAAAA  | ACTCCAGTCT | CCTTTTCAGG | CGAGCTTACG | GCTGTTCCCA  | 700  |
|    | TGGGGCAGCA  | CCTCGCAGAG | AGGGTGAATT | ACCGTGCGAT | TGCATTACACC | 750  |
|    | CATCTTGAC   | CCACCGTGCC | GGAAATGCAT | TTCCCATCGC | CAAAAAGTCC  | 800  |
|    | TCTTGATTTC  | TCTGTTGTGA | CCACGCCTGC | CGATGCAATC | CGTGAGGATA  | 850  |
| 20 | GTATGGAACA  | GTATGTCATC | GACGCCTGTG | GTACGGAGAA | TTCATGTCTG  | 900  |
|    | ACATTGACAG  | ATGCCCCCAT | GGAAGCAAAG | CGAATGCGGT | CTCAAAGCGC  | 950  |
|    | CTCTGTAGAA  | ACGAAATTGA | GCGAGGCATT | TGATGCCATC | GTCTGTGTTA  | 1000 |
|    | CAAGCGCCGG  | CAAGGACAGC | CTGGTTGCCC | TATAG      |             | 1035 |

25

2) INFORMATION FOR SEQ ID NO: 1531

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 25 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531

TCTTTTTGTT ACGACATACG CTTTT

40

25

2) INFORMATION FOR SEQ ID NO: 1532

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532

AGTGCTTCTT TATCCGCTGT TCTA

24

5

2) INFORMATION FOR SEQ ID NO: 1533

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533

CAGCGGATAA AGAAGCACTA CACATT

26

20

2) INFORMATION FOR SEQ ID NO: 1534

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534

CCTCCTGAAA TAAAGCCCGA CAT

23

35

2) INFORMATION FOR SEQ ID NO: 1535

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1260 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: A15097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535



|    |             |            |             |            |            |      |
|----|-------------|------------|-------------|------------|------------|------|
|    | ATGAGGTTTCG | AAGAATGGGT | CAAAGATAAG  | CATATTCCTT | NCAAACNGAA | 50   |
|    | TCACCCTGAT  | GATAATTACG | ATGATTTTAA  | GCCATTAAGA | AANATAATTG | 100  |
|    | GAGATACCCG  | AGTTGTAGCA | TTAGGTGAAA  | ATTCTCATTT | CATAAAAGAA | 150  |
|    | TTCTTTTTGT  | TACGACATAC | GCTTTTGCGT  | TTTTTTATCG | AAGATCTAGG | 200  |
| 5  | TTTTACTACG  | TTTGCTTTTG | AATTTGGTTT  | TGCTGAGGGT | CAAATCATCA | 250  |
|    | ATAACTGGAT  | ACATGGACAA | GGAAGTACG   | ATGAAATAGG | CAGATTCTTA | 300  |
|    | AAACACTTCT  | ATTATCCAGA | AGAGCTCAA   | ACCACATTC  | TATGGCTAAG | 350  |
|    | GGAGTACAAT  | AAAGCAGCAA | AAGAAAAAAT  | CACATTTCTT | GGCATTGATA | 400  |
|    | TACCCAGAAA  | TGGAGGTTCA | TACTTACCAA  | ATATGGAGAT | AGTGCATGAC | 450  |
| 10 | TTTTTTAGAA  | CAGCGGATAA | AGAAGCACTA  | CACATTATCG | ATGATGCATT | 500  |
|    | TAATATTGCA  | AAAAAGATTG | ATTACTTCTC  | CACATCACAG | GCAGCCTTAA | 550  |
|    | ATTTACATGA  | GCTAACAGAT | TCTGAGAAAT  | GCCGTTTAAC | TAGCCAATTA | 600  |
|    | GCTCGAGTAA  | AAGTTCGCCT | TGAAGCTATG  | GCTCCAATTC | ACATTGAAAA | 650  |
|    | ATATGGGATT  | GATAAATATG | AGACAATTCT  | GCATTATGCC | AACGGTATGA | 700  |
| 15 | TATACTTGA   | CTATAACATT | CAAGCTATGT  | CGGGCTTTAT | TTCAGGAGGC | 750  |
|    | GGAATGCAGG  | GCGATATGGG | TGCAAAAAGAC | AAATACATGG | CAGATTCTGT | 800  |
|    | GCTGTGGCAT  | TTAAAAAACC | CACAAAGTGA  | GCAGAAAGTG | ATAGTAGTAG | 850  |
|    | CACATAATGC  | ACATATTCAA | AAAACACCCA  | TTCTGTATGA | TGGATTTCTA | 900  |
|    | AGTTGCCTAC  | CAATGGGCCA | AAGACTTAAA  | AATGCCATTG | GTGATGATTA | 950  |
| 20 | TATGTCTTTA  | GGTATTACTT | CTTATAGTGG  | GCATACTGCA | GCCCTCTATC | 1000 |
|    | CGGAAGTTGA  | TACAAAATAT | GGTTTTTCGAG | TTGATAACTT | CCAACTGCAG | 1050 |
|    | GAACCAAATG  | AAGGTTCTGT | CGAGAAAGCT  | ATTTCTGGTT | GTGGAGTTAC | 1100 |
|    | TAATTCTTTT  | GTCTTTTTTA | GAAATATTCC  | TGAAGATTTA | CAATCCATCC | 1150 |
|    | CGAACATGAT  | TCGATTTGAN | TCTATTTACA  | TGAAAGCAGA | ACTCGAGAAA | 1200 |
| 25 | GCTTTCGATG  | GAATATTTCA | AATTGAAAAG  | TCATCTGTAT | CTGAGGTCGT | 1250 |
|    | TTATGAATAA  |            |             |            |            | 1260 |

## 30 2) INFORMATION FOR SEQ ID NO: 1536

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
 (B) TYPE: Nucleic acid  
 35 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536

AGATGTATTA ACTGGAAAAC AACAA

25

45

## 2) INFORMATION FOR SEQ ID NO: 1537

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
 50 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537

5 CTTTGTAATT AGTTTCTGAA AACCA

25

2) INFORMATION FOR SEQ ID NO: 1538

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538

20

TTAGAAGATA TAGGATACAA AATAGAAG

28

25 2) INFORMATION FOR SEQ ID NO: 1539

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539

GAATGAAAAA GAAGTTGAGC TT

22

40

2) INFORMATION FOR SEQ ID NO: 1540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

45

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*

(C) ACCESSION NUMBER: M14039

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGAAAAATA | ATAATGTAAC | AGAAAAAGAA | TTATTTTATA | TTTTAGATTT | 50  |
| 5  | ATTTGAACAC | ATGAAAGTAA | CTTATTGGTT | AGATGGTGGC | TGGGGGGTAG | 100 |
|    | ATGTATTAAC | TGGAAAACAA | CAAAGAGAAC | ACAGAGATAT | AGATATAGAT | 150 |
|    | TTTGACGCTC | AACACACTCA | AAAAGTTATA | CAAAAATTAG | AAGATATAGG | 200 |
|    | ATACAAAATA | GAAGTTCATT | GGATGCCTTC | ACGTATGGAA | CTTAAGCATG | 250 |
|    | AAGAATATGG | GTATTTAGAT | ATTCATCCTA | TAAATCTAAA | TGATGATGGA | 300 |
| 10 | TCAATTACCC | AAGCAAACCC | AGAAGGTGGT | AATTATGTTT | TCCAAAATGA | 350 |
|    | CTGGTTTTCA | GAACTAATT  | ACAAAGATCG | AAAAATACCA | TGTATTTCAA | 400 |
|    | AAGAAGCTCA | ACTTCTTTT  | CATTCTGGTT | ATGATTTAAC | AGAAACAGAC | 450 |
|    | CATTTTGATA | TAAAAAATTT | AAAATCAATA | ACATAA     |            | 486 |

15

## 2) INFORMATION FOR SEQ ID NO: 1541

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 25 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541

|    |            |            |       |    |
|----|------------|------------|-------|----|
| 30 | TGATAATCTT | ATACGTGGGG | AATTT | 25 |
|----|------------|------------|-------|----|

## 2) INFORMATION FOR SEQ ID NO: 1542

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542

|    |            |            |        |    |
|----|------------|------------|--------|----|
| 45 | ATAATTTTCT | AATTGCCCTG | TTTCAT | 26 |
|----|------------|------------|--------|----|

## 2) INFORMATION FOR SEQ ID NO: 1543

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases  
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543

GGGCAATTAG AAAATTATTT ATCAGA

26

10

2) INFORMATION FOR SEQ ID NO: 1544

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544

TTTTACTCAT GTTTAGCCAA TTATCA

26

25

2) INFORMATION FOR SEQ ID NO: 1545

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 804 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Enterococcus faecium*  
(C) ACCESSION NUMBER: AF110130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGTTAAAAC | AAAAAGAATT | AATTGCAAAC | GTTAAGAATC | TTACTGAGTC | 50  |
| 45 | AGATGAACGA | ATTACAGCTT | GTATGATGTA | TGGATCGTTT | ACCAAAGGAG | 100 |
|    | AAGGTGACCA | ATACTCTGAT | ATAGAGTTCT | ATATATTTTT | GAAACATAGT | 150 |
|    | ATAACCTCGA | ACTTTGATTC | ATCCAACCTG | TTGTTTGACG | TAGCTCCGTA | 200 |
|    | CTTGATGCTT | TATAAAAATG | AGTACGGAAC | AGAGGTAGTT | ATTTTTGATA | 250 |
|    | ATCTTATACG | TGGGGAATTT | CATTTCTTTT | CTGAAAAGA  | TATGAACATA | 300 |
| 50 | ATCCCCTCGT | TTAAAGATTC | AGGTTATATT | CCTGATACGA | AGGCTATGCT | 350 |
|    | TATTTACGAT | GAAACAGGGC | AATTAGAAAA | TTATTTATCA | GAGATAAGTG | 400 |
|    | GTGCAAGACC | AAATAGACTT | ACTGAAGAAA | ATGCTAATTT | TTTGTTGTGT | 450 |
|    | AATTTCTCTA | ATCTATGGTT | GATGGGAATC | AACGTTCTAA | AAAGAGGAGA | 500 |

ATATGCTCGT TCATTAGAAC TCTTATCACA ACTTCAAAAA AATACACTAC 550  
 AACTTATACG TATGGCAGAA AAAAATGCTG ATAATTGGCT AAACATGAGT 600  
 AAAAACCTTG AAAAAGAAAT TAGCCTTGAA AATTATAAAA AATTTGCAAA 650  
 GACCACTGCT CGATTAGATA AGGTAGAATT ATTTGAAGCC TATAAAAATT 700  
 5 CTTTGCTATT AGTTATGGAT TTGCAAAGTC ACCTTATTGA ACAATACAAC 750  
 TTAAAAGTTA CACATGACAT TTTAGAAAGA TTGTTGAATT ACATTAGTGA 800  
 ATAG 804

10

## 2) INFORMATION FOR SEQ ID NO: 1546

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546

CAAGAAGGAA TGGCTGTACT AC

22

25

## 2) INFORMATION FOR SEQ ID NO: 1547

## (i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1547

TAATTCCCAA ATAACCCTAA TAATAGA

27

40

## 2) INFORMATION FOR SEQ ID NO: 1548

## (i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(C) ACCESSION NUMBER: U70055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548

5  
ATGGAAAAAT ACAACAATTG GAAACTTAAG TTTTATACAA TATGGGCAGG 50  
GCAAGCAGTA TCATTAATCA CTAGTGCCAT CTTGCAAATG GCGATTATTT 100  
TTTACCTTAC AGAAAAAACT GGATCCGCGA TGGTCTTGTC TATGGCTTCA 150  
CTATTAGGTT TTTTACCCTA TCGGGTCTTT GGACCTGCAA TTGGTGTGCT 200  
10 AGTGGATCGT CATGATAGGA AGAAGATAAT GATTGGTGCT GATTTAATTA 250  
TCGCAGCAGC TGGTTCGGTG CTTACTATTG TTGCATTCTA TATGGAGCTA 300  
CCTGTCTGGA TGGTTATGAT AGTATTGTTT ATCCGTAGCA TTGGAACAGC 350  
TTTTACACACC CCGGCTCTCA ATGCGGTAC GCCACTTTTA GTACCAGAAG 400  
AACAGCTTAC GAAATGTGCA GGCTATAGTC AGTCTTTGCA GTCTATAAGC 450  
15 TATATTGTTA GTCCGGCGGT TGCAGCACTC TTATACTCCG TTTGGGAAGT 500  
AAATGCTATT ATTGCCATCG ATGTATTGGG TGCTGTGATT GCATCTATTA 550  
CGGTAGCAAT TGTACGTATT CCTAAGCTGG GTGATCGCGT GCAAAGTTTG 600  
GACCCAAATT TCATAAGAGA AATGCAAGAA GGAATGGCTG TACTACGGCA 650  
AAATAAAGGA TTATTTGCTT TATTACTCGT TGGAACATTA TATATGTTTG 700  
20 TTTATATGCC AATTAATGCA CTATTCCCTT TAATTAGCAT GGATTACTTT 750  
AATGGAACAC CTGTGCATAT TTCTATTACG GAAATTTCTT TTGCATCTGG 800  
AATGTTGATA GGGGGTCTAT TATTAGGGTT ATTTGGGAAT TACCAAAGC 850  
GAATCTTATT AATAACGGCA TCCATTTTTA TGATGGGGAT AAGCTTAACC 900  
ATTTCAGGAT TACTTCCCCA AAGTGGATTT TTCATTTTGT TAGTCTGCTG 950  
25 TGCAATAATG GGGCTTTCTG TTCCGTTTTA CAGCGGTGTG CAAACAGCTC 1000  
TTTTTCAGGA GAAAATTAAG CCTGAATATT TAGGACGTGT ATTTTCTTTA 1050  
ACTGGAAGTA TCATGTCTCT TGCTATGCCA ATTGGATTAA TTCTTTCTGC 1100  
ACTCTTTGCT GATAGAATCG GTGTAAATCA TTGGTTTTTA CTATCAGGTA 1150  
CTTTAATTAT TTGCATTGCA ATAGTTTGCC CAATGATAAA TGAGATTAGA 1200  
30 AAATTAGATT TAAAATAA 1218

2) INFORMATION FOR SEQ ID NO: 1549

35  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549

45  
GCTTATTATT AGGAAGATTA GGGGGC

26

50 2) INFORMATION FOR SEQ ID NO: 1550

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550

TAGCAAGTGA CATGATACTT CCGA

24

2) INFORMATION FOR SEQ ID NO: 1551

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (C) ACCESSION NUMBER: U83667

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551

|    |             |            |            |             |            |      |
|----|-------------|------------|------------|-------------|------------|------|
|    | ATGGAAAAAT  | ACAACAATTG | GAAACGAAAA | TTTTATGCAA  | TATGGGCAGG | 50   |
| 30 | GCAAGCAGTA  | TCATTAATCA | CTAGTGCCAT | CCTGCAAATG  | GCGATTATTT | 100  |
|    | TTTACCTTAC  | AGAAAAAACA | GGATCTGCGA | TGGTCTTGTC  | TATGGCTTCA | 150  |
|    | TTAGTAGGTT  | TTTTACCCTA | TGCGATTTTG | GGACCTGCCA  | TTGGTGTGCT | 200  |
|    | AGTGGATCGT  | CATGATAGGA | AGAAGATAAT | GATTGGTGCC  | GATTTAATTA | 250  |
|    | TCGCAGCAGC  | TGGTGCAGTG | CTTGCTATTG | TTGCATTCTG  | TATGGAGCTA | 300  |
| 35 | CCTGTCTGGA  | TGATTATGAT | AGTATTGTTT | ATCCGTAGCA  | TTGGAACAGC | 350  |
|    | TTTTCATACC  | CCAGCACTCA | ATGCGGTTAC | ACCACTTTTA  | GTACCAGAAG | 400  |
|    | AACAGCTAAC  | GAAATGCGCA | GGCTATAGTC | AGTCTTTGCA  | GTCTATAAGC | 450  |
|    | TATATTGTTA  | GTCCGGCAGT | TGCAGCACTC | TTATACTCCG  | TTTGGGATTT | 500  |
|    | AAATGCTATT  | ATTGCCATCG | ACGTATTGGG | TGCTGTGATT  | GCATCTATTA | 550  |
| 40 | CGGTAGCAAT  | TGTACGTATA | CCTAAGCTGG | GTAATCAAGT  | GCAAAGTTTA | 600  |
|    | GAACCAAATT  | TCATAAGGGA | GATGAAAGAA | GGAGTTGTGG  | TTCTGAGACA | 650  |
|    | AAACAAAGGA  | TTGTTTGCCT | TATTACTCTT | AGGAACACTA  | TATACTTTTG | 700  |
|    | TTTATATGCC  | AATCAATGCA | CTATTTCCCT | TAATAAGCAT  | GGAACACTTT | 750  |
|    | AATGGAACGC  | CTGTGCATAT | TTCTATTACG | GAAATTTCCCT | TTGCATTTGG | 800  |
| 45 | GATGCTAGCA  | GGAGGCTTAT | TATTAGGAAG | ATTAGGGGGC  | TTCGAAAAGC | 850  |
|    | ATGTATTACT  | AATAACAAGT | TCATTTTTTA | TAATGGGGAC  | CAGTTTAGCC | 900  |
|    | GTTTCGGGAA  | TACTTCCTCC | AAATGGATTT | GTAATATTCT  | TAGTTTGCTG | 950  |
|    | TGCAATAATG  | GGGCTTTTCG | TGCCATTTTA | TAGCGGTGTG  | CAAACAGCTC | 1000 |
|    | TTTTTTCAGGA | GAAATTAAG  | CCTGAATATT | TAGGACGTGT  | ATTTTCTTTG | 1050 |
| 50 | ATCGGAAGTA  | TCATGTCACT | TGCTATGCCA | ATTGGGTTAA  | TTCTTTCTGG | 1100 |
|    | ATTCTTTGCT  | GATAAAATCG | GTGTAAATCA | TTGGTTTTTA  | CTATCAGGTA | 1150 |
|    | TTTTAATTAT  | TGGCATTGCT | ATAGTTTGCC | AAATGATAAC  | TGAGGTTAGA | 1200 |
|    | AAATTAGATT  | TAAAATAA   |            |             |            | 1218 |

## 2) INFORMATION FOR SEQ ID NO: 1552

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552

GGCAAGCAGT ATCATTAATC ACTA

24

## 2) INFORMATION FOR SEQ ID NO: 1553

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553

CAATGCTACG GATAACAAT ACTATC

26

## 2) INFORMATION FOR SEQ ID NO: 1554

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554

AGAAAATTAA GCCTGAATAT TTAGGAC

27

## 2) INFORMATION FOR SEQ ID NO: 1555

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid



- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555

TAGTAAAAAC CAATGATTTA CACCG

25

10

2) INFORMATION FOR SEQ ID NO: 1556

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556

ACTGTACGCA CTTGCAGCCC GACAT

25

25

2) INFORMATION FOR SEQ ID NO: 1557

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557

40

GAACGGCAGG CGATTCTTGA GCAT

24

2) INFORMATION FOR SEQ ID NO: 1558

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558

GTGGTGGTGC ATGGCGATCT CT

22

5

2) INFORMATION FOR SEQ ID NO: 1559

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559

GCCGCAGCGA GGTACTCTTC GTTA

24

20

2) INFORMATION FOR SEQ ID NO: 1560

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 906 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Escherichia coli*  
 (C) ACCESSION NUMBER: D16251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGACCGTAG | TCACGACCGC | CGATACCTCC | CAACTGTACG | CACTTGCAGC | 50  |
| 40 | CCGACATGGG | CTCAAGCTCC | ATGGCCCCTG | GACTGTCAAT | GAGCTTGGGC | 100 |
|    | TCGACTATAG | GATCGTGATC | GCCACCGTCG | ACGATGGACG | TCGGTGGGTG | 150 |
|    | CTGCGCATCC | CGCGCCGAGC | CGAGGTAAGC | GCGAAGGTCG | AACCAGAGGC | 200 |
|    | GCGGGTGCTG | GCAATGCTCA | AGAATCGCCT | GCCGTTTCGG | GTGCCGGAAT | 250 |
|    | GGCGCGTGGC | CAACGCCGAG | CTCGTTGCCT | ATCCCATGCT | CGAAGACTCG | 300 |
| 45 | ACTGCGATGG | TCATCCAGCC | TGGTTCGTCC | ACGCCCCGCT | GGGTCGTGCC | 350 |
|    | GCAGGACTCG | GAGGTCTTCG | CGGAGAGCTT | CGCGACCGCG | CTCGCCGCCC | 400 |
|    | TGCATGCCGT | CCCCATTTCC | GCCGCCGTGG | ATGCGGGGAT | GCTCATCCGT | 450 |
|    | ACACCGACGC | AGGCCCGTCA | GAAGGTGGCC | GACGACGTTG | ACCGCGTCCG | 500 |
|    | ACGCGAGTTC | GTGGTGAACG | ACAAGCGCCT | CCACCGGTGG | CAGCGCTGGC | 550 |
| 50 | TCGACGACGA | TTCGTCGTGG | CCAGATTTCT | CCGTGGTGGT | GCATGGCGAT | 600 |
|    | CTCTACGTGG | GCCATGTGCT | CATCGACAAC | ACGGAGCGCG | TCAGCGGGAT | 650 |
|    | GATCGACTGG | AGCGAGGCCC | GCGTTGATGA | CCCTGCCATC | GACATGGCCG | 700 |
|    | CGCACCTTAT | GGTCTTTGGT | GAAGAGGGGC | TCGCGAAGCT | CCTCCTCACG | 750 |

|            |            |             |            |            |     |
|------------|------------|-------------|------------|------------|-----|
| TATGAAGCGG | CCGGTGGCCG | GGTGTGGCCG  | CGGCTCGCCC | ACCACATCGC | 800 |
| GGAGCGCCTT | GCGTTCGGGG | CGGTACACCTA | CGCACTCTTC | GCCCTCGACT | 850 |
| CGGGTAACGA | AGAGTACCTC | GCTGCGGCGA  | AGGCGCAGCT | CGCCGCAGCG | 900 |
| GAATGA     |            |             |            |            | 906 |

5

## 2) INFORMATION FOR SEQ ID NO: 1561

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: ATCC 18804

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1561

|               |            |            |            |             |      |
|---------------|------------|------------|------------|-------------|------|
| GATCATGGTA    | AAACTACATT | GACTGCTGCT | ATCACCAAAG | TTTTAGCCGA  | 50   |
| 25 ACAAGGTGGT | GCCAACTTCT | TGGATTAYGG | TTCTATTGAT | AGAGCTCCAG  | 100  |
| AAGAAAGAGC    | TAGAGGTATC | ACTATTTCCA | CTGCCCACGT | TGAATACGAA  | 150  |
| ACCAAGAACA    | GACACTATGC | CCACGTTGAT | TGTCCAGGAC | ACGCTGATTA  | 200  |
| TATCAAAAAT    | ATGATTACTG | GTGCCGCTCA | AATGGATGGT | GCTATCATTG  | 250  |
| TTGTTGCTGC    | CACTGATGGT | CAAATGCCTC | AAACCAGAGA | ACATTTGTTA  | 300  |
| 30 TTGGCCAGAC | AAGTTGGTGT | TCAAGACTTG | GTTGTGTTTG | TCAACAAAGT  | 350  |
| CGATACTATT    | GATGACCCTG | AAATGTTGGA | ATTAGTCGAA | ATGGAAATGA  | 400  |
| GAGAATTGTT    | ATCCACCTAC | GGTTTTGATG | GTGACAACAC | TCCAGTTATT  | 450  |
| ATGGGATCTG    | CTTTAATGGC | TTTGGAAGAC | AAGAAACCAG | AAATTGGTAA  | 500  |
| GGAAGCTATC    | TTGAAATTGT | TAGATGCTGT | CGATGAACAC | ATTCCAATCT  | 550  |
| 35 CATCAAGAGA | CTTGGAACAA | CCATTTTTGT | TACCAGTTGA | AGACGTGTTC  | 600  |
| TCCATCTCCG    | GTAGAGGAAC | TGTTGTCACT | GGTAGAGTTG | AAAGAGGTGT  | 650  |
| TTTGAAGAAG    | GGTGAAGAAA | TCGAAATTGT | TGGTGGTTTT | GACAAACCTT  | 700  |
| ACAAGACTAC    | TGTTACCGGT | ATTGAAATGT | TCAAAAAGA  | ATTAGACTCT  | 750  |
| GCTATGGCTG    | GTGACAACTG | TGGTGTTTTG | TTAAGAGGTG | TTAAAAGAGA  | 800  |
| 40 TGAAATCAAG | AGAGGTATGG | TTTTGGCCAA | ACCAGGTACT | GCCACTTCTC  | 850  |
| ACAAGAAGTT    | CTTGGCTTCC | TTGTATATTT | TGACTTCCGA | AGAAGGTGGY  | 900  |
| CGTTCCACTC    | CATTTGGTGA | AGGTTACAAG | CCTCAATGCT | TCTTCAGAAC  | 950  |
| TAACGATGTC    | ACTACCACAT | TTTCATTCCC | AGAAGGAGAA | GGTGTGTGACC | 1000 |
| 45 ATTCTCAAAT | GATCATGCCA | GGTGACAACA | TTGAAATGGT | TGGTGAAT    | 1048 |

## 2) INFORMATION FOR SEQ ID NO: 1562

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida dubliniensis*

(B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562

10  
 TGATCACGGT AAAACCACAT TAACTGCTGC CATTACCAAA GTATTAGCTG 50  
 AACAAAGGTGG TGCCAACCTT TTGGATTACG GTTCCATTGA TAGAGCTCCA 100  
 GAAGAAAGAG CCAGAGGTAT CACTATTTCC ACTGCCCACG TTGAATACGA 150  
 AACCAAGAAC AGACACTATG CCCACGTTGA TTGTCCAGGA CACGCTGATT 200  
 15 ATATCAAAAA CATGATTACT GGTGCTGCTC AAATGGATGG TGCTATCATT 250  
 GTTGTGCTG CTACTGACGG TCAAATGCCA CAAACCAGAG AACATTTATT 300  
 GTTGGCAAGA CAAGTTGGTG TTCAAGACTT GGTTGTCTTT GTCAACAAAG 350  
 TTGATACTAT TGATGACCCT GAGATGTTGG AATTAGTCGA AATGGAAATG 400  
 AGAGAATTGT TGTCCACCTA CGGTTTTGAT GGTGACAACA CTCCTGTTAT 450  
 20 TATGGGATCT GCTTTAATGG CCTTGGAAGG CAAAAAACCA GAAATTGGTA 500  
 AGGAAGCTAT TTTGAGATTG TTAGATGCTG TCGATGAACA CATTCCAAC 550  
 CCATCAAGAG ACTTGAACA ACCATTTTTG TTGCCAGTTG AAGACGTGTT 600  
 CTCCATCTCT GGTAGAGGAA CTGTTGTCAC CGGTAGAGTT GAAAGAGGTG 650  
 TCTTGAAGAA GGGTGAAGAA ATCGAAATTG TTGGTGGTTT TGACAAACCA 700  
 25 TACAAGACCA CTGTTACTGG TATTGAAATG TTCAAAAAGG AATTAGATTC 750  
 TGCTATAGCT GGTGACAAC GTGGTGT TTTT GTTGAGAGGT GTTAAAAGAG 800  
 ATGAAATCAA GAGAGGTATG GTTTTGGCCA AGCCAGGTAC TGCTACTTCT 850  
 CACAAGAAAT TTTTAGCATC TTTGTATATT TTGACTTCAG AAGAAGGTGG 900  
 TCGTTCCACT CCATTTGGAG AAGGTTACAA GCCTCAATGT TTCTTCAGAA 950  
 30 CTAATGACGT CACTACCACA TTTTCATTCC CAGAAGGAGA AGGTGTTGAC 1000  
 CACTCCCAA TGGTCATGCC AGGTGATAAC ATTGAAATGG TTGGTGAATT 1050  
 GATCAAATCA TGTCCATTGG AAGT 1074

35

2) INFORMATION FOR SEQ ID NO: 1563

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1033 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida famata*

(B) STRAIN: ATCC 62894

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563

GATCACGGGA AGACTACTTT GACCGCTGCC ATCACCAAAG TTTTAGCCGA 50  
 AAAAGGTGGT GCTAACTTCT TGGACTACGG TTCTATCGAT AAAGCTCCAG 100

|    |            |             |            |             |             |      |
|----|------------|-------------|------------|-------------|-------------|------|
|    | AAGAAAGAGC | CAGAGGTATT  | ACTATTTCTG | CTGCCCATGT  | TGAATACGAA  | 150  |
|    | ACTGACAAGA | GACACTATGC  | CCATGTTGAT | TGTCCAGGTC  | ACGCAGATTA  | 200  |
|    | TATCAAGAAT | ATGATTACTG  | GTGCTGCTCA | AATGGATGGT  | GCCATTATTG  | 250  |
|    | TTGTTGCTGC | TTCCGATGGT  | CAAATGCCTC | AAACCAGAGA  | ACATTTGTTA  | 300  |
| 5  | TTGGCCAGAC | AAGTTGGTGT  | TCAACACTTG | GTTGTTTTTCG | TCAACAAGGT  | 350  |
|    | CGACACCATT | GACGATCCAG  | AAATGTTGGA | ATTGGTTGAA  | ATGGAAATGA  | 400  |
|    | GAGATTTGTT | AACTACTTAC  | GGTTTTGATG | GTGATAACAC  | CCCAGTTATC  | 450  |
|    | ATGGGATCTG | CTTTGTGTGC  | TTTGGAATCC | AGAGAACCAG  | AAATTGGTCA  | 500  |
|    | AAAAGCCATT | GAAAAATTGT  | TAGATGCCGT | CGATGAATAC  | ATTCCAACCC  | 550  |
| 10 | CAGTCAGAGA | CTTGGAAACAA | CCATTCTTGA | TGCCAGTTGA  | AGAAGTTTTTC | 600  |
|    | TCCATTTCCG | GTAGAGGTAC  | CGTTGTTGCT | GGTAGAGTCG  | AAAGAGGTAC  | 650  |
|    | CTTGAAGAAG | GGTGAAGAAA  | TCGAAATTGT | TGGTGGTTTC  | GACAAGCCAT  | 700  |
|    | TCAAGGCCAC | TGTTACTGGT  | ATTGAAATGT | TCAAGAAGGA  | ATTGGACTCC  | 750  |
|    | GCTCTTGCTG | GTGACAACTG  | TGGTATCTTG | TTGAGAGGTG  | TCAAGAGAGA  | 800  |
| 15 | CGAAGTTAAG | AGAGGTATGG  | TCTTGACCAA | GCCAAACACC  | GTCATTCCC   | 850  |
|    | ACAAGAAGAT | CTTGGCCTCG  | TTGTATATCT | TGACCAAGGA  | AGAAGGTGGT  | 900  |
|    | AGACACTCTC | CATTTGGAGC  | CAACTACAAG | CCCCAATTGT  | TCATGAGAAC  | 950  |
|    | CACCGATGTT | ACCGGTACCA  | TGACCTTCCC | AGAAGGTGCC  | GACCAATCTG  | 1000 |
|    | CCATGGTCAT | GCCAGGTGAC  | AACGTTGAAA | TGC         |             | 1033 |
| 20 |            |             |            |             |             |      |

## 2) INFORMATION FOR SEQ ID NO: 1564

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*  
 (B) STRAIN: ATCC 66032

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GATCACGGTA | AGACTACATT | GACAGCTGCT | ATCACCAAGA | CATTGGCCAA | 50  |
| 40 | GAACGGTGGT | GCTGATTTCT | TGGACTACTC | TTCCATTGAC | AAAGCTCCAG | 100 |
|    | AGGAGAGAGC | CCGTGGTATC | ACTATCTCTA | CTGCCCATGT | CGAGTACGAG | 150 |
|    | ACCGCCAAGA | GACATTACTC | CCACGTCGAC | TGTCCAGGTC | ACGCCGACTA | 200 |
|    | CATCAAGAAC | ATGATTACTG | GTGCTGCCCA | AATGGACGGT | GCTATCATCG | 250 |
|    | TTGTCGCCGC | CACCGATGGT | CAAATGCCAC | AAACTAGAGA | GCATTTGCTG | 300 |
| 45 | TTGGCCAGAC | AAGTCGGTGT | TCAACGTATC | GTTGTCTTTG | TCAACAAGGT | 350 |
|    | GGACACCATC | GATGACCCTG | AAATGTTGGA | ATTAGTGGA  | ATGGAAATGA | 400 |
|    | GAGAATTGTT | GAACGAATAC | GGTTTTGACG | GTGACAATGC | CCCTATCATT | 450 |
|    | ATGGGTTCCG | CTTTGTGTGC | CCTAGAAGGT | CGTCAACCTG | AAATTGGTGA | 500 |
|    | GCAAGCTATC | ATGAAACTAT | TGGACGCTGT | TGATGAATAC | ATTCCAACCC | 550 |
| 50 | CAGAAAGAGA | CTTGAACAAG | CCATTCTTGA | TGCCTGTTGA | AGACATCTTC | 600 |
|    | TCCATCTCTG | GTAGAGGTAC | CGTCGTCACT | GGACGTGTCG | AAAGAGGTAA | 650 |
|    | CTTGAAGAAG | GGTGAAGAAG | TTGAAATTGT | TGGTCACAAC | ACTACCCCAT | 700 |
|    | TGAAGACCAC | CGTTACTGGT | ATCGAAATGT | TCAGAAAGGA | ATTGGACCAA | 750 |

|   |            |            |            |            |            |      |
|---|------------|------------|------------|------------|------------|------|
|   | GCTATGGCTG | GTGACAACGC | CGGTATCCTA | TTGAGAGGTA | TCAGAAGAGA | 800  |
|   | CCAATTGAAG | AGAGGTATGG | TCATGGCCAA | GCCAGGTACC | GTCAAGGCTC | 850  |
|   | ACACCAAGAT | TTTGGCTTCT | TTGTACATCT | TGTCTAAGGA | AGAAGGTGGT | 900  |
|   | AGACATTCTG | GTTTCGGTGA | AAACTACAGA | CCTCAGATGT | TTATCAGAAC | 950  |
| 5 | CGCAGATGTC | ACTGTTGTGA | TGAAGTTCCC | AGAATCTGTG | GAAGACCACT | 1000 |
|   | CTATGCAAGT | TATGCCAGGT | GACAACGTCG | AAATGGTCTG | TGAACTAGTC | 1050 |
|   | CACCCA     |            |            |            |            | 1056 |

10

## 2) INFORMATION FOR SEQ ID NO: 1565

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1061 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida guilliermondii*
- (B) STRAIN: ATCC 6260

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565

|    |            |            |            |            |             |      |
|----|------------|------------|------------|------------|-------------|------|
|    | GATCATGGTA | AGACCACTTT | GACCGCTGCT | ATCACCAAGG | TTTTGTTCGGA | 50   |
|    | AAAAGGAGGT | GCTAATTTCT | TGGATTACGG | CTCCATCGAC | AGAGCTCCAG  | 100  |
|    | AAGAGAGAGC | CAGAGGTATC | ACCATTTCCA | CTGCCCATGT | TGAGTACCAA  | 150  |
| 30 | ACTGATAAGA | GACATTATGC | CCACGTTGAC | TGTCCAGGTC | ACGCCGATTA  | 200  |
|    | CATTAAGAAT | ATGATTACTG | GTGCCGCCCA | GATGGACGGT | GCCATTATTG  | 250  |
|    | TTGTTGCTGC | CACTGACGGT | CAAATGCCTC | AGACCAGAGA | GCACTTGTTG  | 300  |
|    | TTGGCCAGAC | AAGTTGGTGT | GCAACACTTG | GTAGTTTTTG | TGAACAAGGT  | 350  |
|    | GGACACCATT | GACGATCCCG | AGATGTTGGA | ATTGGTCGAG | ATGGAAATGA  | 400  |
| 35 | GAGAATTGTT | GAGTCAGTAC | GGTTTCGATG | GTGACAACAC | CCCAGTTATC  | 450  |
|    | ATGGGATCTG | CTTTGTGTGC | TTTGGAAGT  | AAGCAGCCAG | AAATTGGTGT  | 500  |
|    | GCAAGCCATT | GAAAAATTGT | TGGACGCTGT | CGATGAGCAC | ATTCCTACTC  | 550  |
|    | CTACCCGTGA | CTTGGAACAG | CCATTCTTGT | TGCCTGTTGA | AGATGTGTTC  | 600  |
|    | TCCATTTCTG | GTAGAGGAAC | TGTGGTACT  | GGTAGAGTCG | AAAGAGGTTC  | 650  |
| 40 | GTTGAAGAAG | GGTGAGGAAA | TCGAGATTGT | TGGTGACTTT | GACAAGCCAT  | 700  |
|    | TCAAGACCAC | TGTGACTGGA | ATTGAAATGT | TCAAGAAGGA | ATTGGATGCT  | 750  |
|    | GCTATGGCTG | GTGACAATGC | TGGTATCTTG | TTGAGAGGTG | TCAAGAGAGA  | 800  |
|    | CGATGTCAAG | AGAGGTATGG | TTTTGGCCAA | GCCTTCCACC | GTCATTCTC   | 850  |
|    | ACAAGAAGGT | GTTGGCTTCC | TTGTACATCT | TGAGTAAGGA | AGAAGGTGGC  | 900  |
| 45 | CGTCACTCTC | CTTTTGGTGA | GAACTACAAG | CCTCAATTGT | TCATCAGAAC  | 950  |
|    | TACTGACGTT | ACCGGTACTT | TAAGATTCCC | AGCCGGCGAG | GGTGTCGACC  | 1000 |
|    | ACTCGCAAAT | GGTTATGCCA | GGTGACAATG | TTGAGATGGA | AATTGAGCTT  | 1050 |
|    | GTGAGAAAGA | C          |            |            |             | 1061 |

50

## 2) INFORMATION FOR SEQ ID NO: 1566

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*  
 (B) STRAIN: ATCC 22991

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566

```

15  GATCACGGTA AGACTACCTT GACTGCTGCT ATCACCAAGG TTTTGGCTTC      50
    TAAGGGTGGT GCTAGCTTCT TGGACTATGG TTCCATTGAC AGAGCCCCAG      100
    AGGAGAGAGC TAGAGGTATT ACTATTTCTA CTGCCCACGT TGAGTACCAA      150
    ACCGAAAAGA GACACTACGC CCACGTCGAC TGTCCAGGTC ACGCTGATTA      200
    CATTAGAAT  ATGATTACTG GTGCCGCCCA GATGGACGGT GCTATCATTTG      250
20  TTGTTGCTGC TTCTGATGGT CAGATGCCTC AGACCAGAGA GCACCTTTTG      300
    TTGGCCAGAC AGGTTGGTGT TCAGAACTTG GTTGTTTTCG TTAACAAGGT      350
    TGACACCATT GACGACCCTG AAATGTTGGA ATTGGTTGAG ATGGAAATGA      400
    GAGAATTGTT GACTACTTAC GGTTTTGACG GTGATGAGAC TCCTGTTATC      450
    ATGGGTTCTG CTTTGTGCGC TTTGGAAGAG AAGCAACCAG AGATTGGTGA      500
25  GCAGGCTATC ATGAAGTTGT TGGACGCTGT CGATGAGTAC ATTCCAACCC      550
    CACAGCGTGA CTTGGAGCAG CCATTCTTGA TGCCTGTTGA GGATGTTTTTC      600
    TCCATTTCTG GTAGAGGTAC TGTCGTTACT GGTAGAGTTG AGAGAGGTTC      650
    TTTGAAGAAG GGTGAGGAAA TCGAGATTGT CGGTGACTTC GCCAAGACTT      700
    TCAAGGCTAC CGTTACTGGT ATTGAGATGT TCAAGAAGGA ATTGGATGCT      750
30  GCTATGGCTG GTGACAACGC CGGTATCTTG TTGAGAGGTG TCAAGAGAGA      800
    TGAGATCTCC CGTGGTGATG TCTTGGCCAA GCCAGGTACT GTTACTCCAC      850
    ACAAGAAGAT CTTGGCTTCT TTGTACGTTT TGACCAAGGA AGAAGGTGGT      900
    CGTCACAACC CATTGCTGA  GAACTACAAG CCACAGTTGT TCCTCAGAAC      950
    CACCAACGTC ACTGGTACCA TGAGATTCCC AGAAGGTGAA GATGTTGACC      1000
35  ACTCTGCCAT GGTAAACCCA GGTGACAACG TTGAGATGGA AATCGAGTTG      1050
    GGTAGAAAGG CCCCACTTGA GTT                                1073
  
```

## 40 2) INFORMATION FOR SEQ ID NO: 1567

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida kefyr*  
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | CATGGTAAGA | CCACTTTGAC | TGCTGCCATC | ACCAAGACTC | TAGCTGAACG | 50   |
|    | TGGTGGTGCT | GACTTTTTGG | ACTACTCTTC | TATTGACAAG | GCTCCAGAAG | 100  |
| 5  | AAAGAGCYAG | AGGTATCACT | ATTTCTACTG | CTCATGTTGA | ATACGAGACT | 150  |
|    | GAAAAGAGAC | ATTACTCCCA | CGTTGACTGT | CCAGGTCACG | CTGATTACAT | 200  |
|    | CAAGAACATG | ATTACTGGTG | CTGCTCAAAT | GGACGGTGCT | ATTATTGTTG | 250  |
|    | TTGCTGCTAC | TGATGGTCAA | ATGCCTCAAA | CCAGAGAGCA | TTTGTTGTTG | 300  |
|    | GCCAGACAAG | TTGGTGTCCA | ACACATTGTT | GTTTTCGTTA | ACAAGGTTGA | 350  |
| 10 | CACCATCGAT | GATCCAGAAA | TGTTGGAATT | GGTTGAAATG | GAAATGAGAG | 400  |
|    | AATTRTTGAC | TCAATATGGC | TTTGACGGTG | ACAACACTCC | AGTGATCATG | 450  |
|    | GGTTCTGCTT | TGTGTGCCTT | GGAAGGTAAG | CAACCAGAAA | TTGGTGAGCA | 500  |
|    | AGCCATCATG | AAGTTGTTGG | ACGCTGTTGA | CGAATACATC | CCAACCCCAG | 550  |
|    | CCCGTGACTT | GGAAAIVCCA | TTCTTGATGC | CTGTTGAAGA | TATCTTCTCC | 600  |
| 15 | ATTTCCGGTA | GAGGTACTGT | CGTCACTGGT | AGAGTTGAAC | GTGGTAACTT | 650  |
|    | GAAGAAGGGT | GAAGAAATCG | AAATTGTTGG | TCACAACACC | ACTCCTTTCA | 700  |
|    | AGACTACTGT | TACTGGTATT | GAAATGTTCA | GAAAGGAATT | GGACCAAGCC | 750  |
|    | ATGGCTGGTG | ACAACGCTGG | TGTCCTTTTG | AGAGGTGTCA | GAAGAGACCA | 800  |
|    | ATTGAAGAGA | GGTATGGTTT | TGGCTAAGCC | AGGTACTGTT | AAGGCCCACA | 850  |
| 20 | CCAAGTTCTT | GGCTTCCTTG | TACATTTTGA | CCAAGGAAGA | AGGTGGTAGA | 900  |
|    | CACTCCGGTT | TCGGTGAAAA | CTACAGACCA | CAAATCTACG | TCAGAACTGC | 950  |
|    | TGACGTTACC | GTDGTCTTGA | AGTTCCCAGA | ATCTGTTGAA | GACCATTCCA | 1000 |
|    | TGCAAGTCAT | GCCAGGTGAC | AATGTCGAAA | TGGAGTGTGA | ATTGGTTCAC | 1050 |
|    | CCAACTCCAT | TG         |            |            |            | 1062 |
| 25 |            |            |            |            |            |      |

2) INFORMATION FOR SEQ ID NO: 1568

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitaniae*
- (B) STRAIN: ATCC 66035

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CGGAAAGACC | ACCTTGACCG | CCGCCATTAC | CAAGGTTTTG | GCTGACAAGG | 50  |
| 45 | GTGGCGCCAA | CTTCTTGAC  | TACGGTGCCA | TTGACAAGGC | TCCTGAAGAA | 100 |
|    | AGAGCACGTG | GTATCACCAT | TTCCACTGCC | CACGTTGAAT | ACGAGACCGA | 150 |
|    | CAACAGACAC | TACGCCACG  | TTGACTGTCC | AGGTCACGCC | GATTACATCA | 200 |
|    | AGAACATGAT | CACGGGTGCC | GCTCAAATGG | ACGGTGCCAT | TATTGTTGTT | 250 |
|    | GCAGCCACCG | ACGGCCAAAT | GCCTCAAACC | AGAGAGCACT | TGTTGTTGGC | 300 |
| 50 | CAGACAAGTT | GGTGTGCAAC | ACTTGTTTGT | TTTCGTGAAC | AAGGTTGATA | 350 |
|    | CCATCGACGA | CCCAGAAATG | TTGGAATTGG | TTGAAATGGA | AATGAGAGAA | 400 |
|    | TTGTTGACTC | AATACGGATT | TGACGGCGAT | GAAACCCCTG | TTGTTATGGG | 450 |
|    | CTCTGCTCTT | TGCGCTTTGG | AAGGTAGAGA | ACCAGAGATT | GGTGAGCAAG | 500 |



|    |            |             |            |             |            |      |
|----|------------|-------------|------------|-------------|------------|------|
|    | CCATCACCAA | GTTGTTGGAG  | GCTGTTGACG | AGTACATCCC  | AACCCACAA  | 550  |
|    | CGTGAATTGG | AACAACCAATT | CTTGATGCCT | GTTGAAGATG  | TTTTCTCCAT | 600  |
|    | TTCTGGTAGA | GGTACTGTTG  | TCACTGGTAG | AGTGGAGAGA  | GGTTCCTTGA | 650  |
|    | AGAAGGGTGA | GGAGATCGAG  | ATTGTTGGTG | ACTTTGACAA  | GCCTTTCAAG | 700  |
| 5  | ACTACTGTTA | CTGGTATTGA  | GATGTTCAAG | AAGGAATTGG  | ACGCTGCTAT | 750  |
|    | GGCTGGTGAC | AATGCTGGTA  | TCTTGTGAG  | AGGTGTCAAG  | AGAGAACAAG | 800  |
|    | TTTCCCGTGG | TATGGTTTTG  | GCCAAGCCAG | GCACTGTGAC  | CTCGCACAAG | 850  |
|    | AAGGTTTTTG | CTTCTTTGTA  | CATTTTGTCT | AAGGAAGAAG  | GTGGTCGTCA | 900  |
|    | CTCTCCATTT | GGCGAGAACT  | ACAAGCCTCA | ATTGTTTCCTT | AGAACTACCG | 950  |
| 10 | ATGTCACTGG | TACTTTGAGA  | TTCCCAGCAG | GTGAGGACGT  | TGACCACTCC | 1000 |
|    | GCTATGGTTT | CTCCAGGTGA  | CAATGTCGAG | ATGGAAATCG  | AGTTGGTCAG | 1050 |
|    | AAAGACTCCT | CT          |            |             |            | 1062 |

15 2) INFORMATION FOR SEQ ID NO: 1569

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 990 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida sphaerica*

(B) STRAIN: ATCC 2504

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569

|    |             |            |            |             |            |     |
|----|-------------|------------|------------|-------------|------------|-----|
|    | TCACCAAGAC  | TTTGGCTGAA | CGTGGTGGTG | CTGATTTCTT  | GGACTACTCT | 50  |
| 35 | TCCATTGACA  | AGGCTCCAGA | AGAAAGAGCR | AGAGGTATCA  | CTATTTCTAC | 100 |
|    | TGCACATGTT  | GAATATGAAA | CTGACAAGAG | ACATTACTCT  | CACGTCGACT | 150 |
|    | GTCCAGGTCA  | TGCTGATTAC | ATCAAGAATA | TGATTACTGG  | TGCTGCCCAA | 200 |
|    | ATGGATGGTG  | CTATCATTGT | TGTTGCTGCT | ACAGATGGTC  | AAATGCCTCA | 250 |
|    | AACCAGAGAA  | CATTTGTTGT | TGGCTAGACA | AGTTGGTGTT  | CAACAYATCG | 300 |
| 40 | TTGTTTTTCGT | TAACAAGGTT | GACACTATCG | ATGACCCCTGA | AATGTTAGAA | 350 |
|    | TTGGTTGAAA  | TGGAAATGAG | AGAATTATTG | ACCCAATACG  | GTTTCGATGG | 400 |
|    | TGACAACACT  | CCAGTCATCA | TGGGTTCTGC | TTTGTGTGCT  | TTAGAAGGTA | 450 |
|    | AGCAACCAGA  | AATTGGTGAA | CAAGCAATCA | TGAAGTTATT  | GGACGCTGTT | 500 |
|    | GACGAATACA  | TCCCAACTCC | AGCTCGTGAT | TTGGAAAAGC  | CTTTCTTGAT | 550 |
| 45 | GCCTGTTGAA  | GATATCTTCT | CCATCTCCGG | TAGAGGTACC  | GTCGTAAGTG | 600 |
|    | GTAGAGTTGA  | ACGTGGTAAC | TTGAAKAAGG | GTRAAGAAAT  | CGAAATCGTT | 650 |
|    | GGTCACAACA  | CCACTCCATT | CAAGACCACT | GTTACTGGTA  | TTGAAATGTT | 700 |
|    | CAGAAAGGAA  | TTGGACCAAG | CTATGGCTGG | TGATAACGCT  | GGTGTCWTGT | 750 |
|    | TGAGAGGTGT  | CAGAAGAGAC | CAATTAAAGA | GAGGTATGGT  | CTTGGCCAAG | 800 |
| 50 | CCAGGTACTG  | TCAAGGCTCA | CACCRAATTC | TTGGCCTCTT  | TGTATATCTT | 850 |
|    | GACCAAGGAA  | GAAGGTGGTA | GACATTCCGG | TTTCGGTGAA  | AATTACAGAC | 900 |
|    | CTCAAATCTA  | CGTTAGAACT | GCTGATGTCA | CCGTTGTTTT  | GAAGTTCCCA | 950 |
|    | GAAGCTGTTG  | AAGATCACTC | TATGCAAGTC | ATGCCAGGTG  |            | 990 |

## 2) INFORMATION FOR SEQ ID NO: 1570

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1184 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*  
 (B) STRAIN: ATCC 750

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | GATCATGGTA | AAACCACTTT | GACTGCTGCC | ATTACTAAAG | TCTTGGCTGA | 50   |
|    | TAAAGGTCAA | GCTAACTTCT | TAGATTACGG | TTCTATTGAT | AGAGCTCCAG | 100  |
|    | AAGAAAGAGC | CAGAGGTATC | ACCATCTCTA | CTGCCCACGT | TGAATATGAA | 150  |
| 20 | ACCGAAAAAA | GACATTACGC | CCATGTTGAG | TATGTATACT | TTTTTTTGT  | 200  |
|    | GTGTAATTGT | TTTAAAGATT | TTCTTTAAAG | CTGAAGAAGT | CAAATCAGTT | 250  |
|    | CTTTGATAAC | TTCTATTAAA | AAAAGGGAAA | AATTAACAAG | ATATACTAAC | 300  |
|    | ACTATAACAG | TTGTCCTGGA | CATCAAGATT | ATATCAAGAA | TATGATTACC | 350  |
|    | GGTGCCGCTC | AAATGGATGG | TGCTATTATT | GTTGTTGCTG | CCACTGATGG | 400  |
| 25 | TCAAATGCCA | CAAACCAGAG | AACATTTGTT | GTTGGCTAGA | CAAGTCGGTG | 450  |
|    | TTCAAGATTT | GGTTGTCTTT | GTTAACAAAG | TCGACACTAT | TGATGACCCA | 500  |
|    | GAAATGTTGG | AATTGGTTGA | AATGGAAATG | AGAGAATTAT | TGACTACTTA | 550  |
|    | CGGTTTTGAT | GGTGATAACA | CTCCTGTTAT | CATGGGTTCT | GCTTTGATGG | 600  |
|    | CCTTGCAAGG | TAAACAACCA | GAAATTGGTG | AACAAGCTAT | CATGAAATTG | 650  |
| 30 | ATGGACGCTA | TTGATGAACA | CATTCCAACC | CCAACCAGAG | ACTTGGAACA | 700  |
|    | ATCTTTCTTG | ATGCCAGTTG | AAGATGTTTT | CTCCATTTCT | GGTAGAGGTA | 750  |
|    | CTGTTGTTAC | TGGTAGAGTC | GAAAGAGGTG | TCTTAAAGAA | GGGTGAAGAA | 800  |
|    | ATTGAAATTG | TTGGTGGTTT | CGAAAAACCA | TTCAAGACCA | CTGTTACTGG | 850  |
|    | TATTGAAATG | TTCAAGAAAG | AATTAGATGC | TGCTATGGCT | GGTGACAAC  | 900  |
| 35 | GTGGTGTCTT | GTTGAGAGGT | GTCAAGAGAG | ACGAAATCAA | GAGAGGTATG | 950  |
|    | GTTTTGGCTA | AACCAGGTAC | TGCTACTTCC | CACAAGAAAT | TCTTGGCTTC | 1000 |
|    | CATGTATATC | TTAACTGCTG | AAGAAGGTGG | TCGTTCCACT | CCATTCGGTG | 1050 |
|    | AAGGTTACAA | GCCACAATGT | TTCTTCAGAA | CTAACGATGT | TACCACTTCC | 1100 |
|    | TTCTCTTTCC | CAGAAGGTGA | AGGTGTTGAC | CACTCCCAA  | TGGTTATGCC | 1150 |
| 40 | AGGTGACAAC | ATTGAAATGG | TCGGTGAATT | GATT       |            | 1184 |

## 2) INFORMATION FOR SEQ ID NO: 1571

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida viswanathii*

(B) STRAIN: ATCC 28269

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571

```

CGATCACGGT AAGACCACCT TGACCGCCGC CATCACCAAG GTCTTGGCCG      50
ACAAGGGTCA GGCTAACTTC TTGGACTACG GATCCATTGA CAGAGCCCCT      100
GAAGAAAGAG CAAGAGGTAT CACTATCTCC ACTGCCCACG TTGAATACGA      150
10 GACTGATAAG AGACACTATG CCCACGTTGA TTGCCCCGGC CATCAAGATT      200
ATATCAAGAA TATGATCACT GGTGCTGCCC AAATGGACGG TGCTATCATT      250
GTTGTTGCTG CTA CTGACGG TCAGATGCCA CAAACCAGAG AACACTTGTT      300
GTTGGCTAGA CAAGTTGGTG TCCAAGACTT GGTGTTTTTC GTTAACAAGG      350
TTGACACTAT CGATGACCCA GAAATGTTGG AATTGGTTGA AATGGAAATG      400
15 AGAGAATTAT TATCTTCTTA YGGCTTTGAC GGTGACAACA CCCAGTTGT      450
CATGGGTTCC GCTTTGATGG CTTTGCAAGG TAAGCAACCA GAAATTGGTG      500
AACAAGCTAT TATTAAGTTG ATGGACGCTA TTGATGAACA CATYCCAACC      550
CCAACCAGAG ACTTGGAACA ACCATTCTTG TTGCCAGTTG AAGATGTCTT      600
TTCTATTTCC GGTAGAGGTA CCGTCGTCAC TGGTAGAGTC GAAAGAGGTG      650
20 TCTTGAAGAA GGGTGAAGAA ATTGAAATTG TCGGTAAGT TGAAGGCCA      700
TTCAAGACCA CCGTTACTGG TATTGAAATG TTCAAGAAGG AATTGGATGC      750
TGCTATGGCT GGTGACAAC GTGGTGTCTT GTTGAGAGGT GTCAAGAGAG      800
ACGAAATCAG CAGAGGTATG GTTTTGGCCA AGCCAGGTAC CGTCACTTCC      850
CACAAGAAGT TCTTGGCCTC CATGTACATC TTGACTGGTG AAGAAGGTGG      900
25 TCGTCGTACC CCATTCGGTG AAGGTTACAA GCCACAATGT TTCTTCAGAA      950
CCAATGACAT CACCACCACT TTCACTTTCC CAGAAGGTGA AGGTGTCGAC      1000
CACTCCCAA TGTTATGCC AGGTGACAAC ATCGAAATGG TTGGTGAATT      1050
GTACAAGGCT TGTCCTTGA A                                1071

```

30

## 2) INFORMATION FOR SEQ ID NO: 1572

## (i) SEQUENCE CHARACTERISTICS:

```

35 (A) LENGTH: 817 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

## 40 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*

(B) STRAIN: ATCC 8750

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572

```

TATCTTGGTT WGCTCGGCCG CTGACGGCCC AATGCCTCAG ACTCGCGAGC      50
ACATCCTGCT GAGCCGTCAG GTTGGCGTTC CTTACATCAT CGTGTTCCCTG      100
50 AACAAAGGCCG ACATGGTTGA TGACGAAGAG CTGATCGAAC TGGTTGAAAT      150
GGAAGTTCGC GAGCTGTTGT CCAAGTACGA CTTCCCTGGC GACGACACCC      200
CGATCATCAA GGGTTCGGCC AAAGTGGCTC TGGAAGGCCG CGAAGGCCCA      250
CTGGGCAGCC AAGCCGTTCT GGCTCTGGCC GAAGCGCTGG ACAACTACAT      300

```

|    |             |            |            |             |            |     |
|----|-------------|------------|------------|-------------|------------|-----|
|    | TCCTACGCCT  | GAGCGTGCCG | TTGACGGTAC | G TTCCTGATG | CCTGTTGAAG | 350 |
|    | ACGTGTTCTC  | GATCTCCGGC | CGTGGTACGG | TTGTGACCGG  | TCGTATTGAG | 400 |
|    | CGCGGCATCA  | TCAAGGTCGG | CGAAGAAATC | GAAATCGTGG  | GTATCAAAGA | 450 |
|    | CACGGTCAAG  | ACCATTTGTA | CCGGCGTTGA | AATGTTCCGC  | AAACTGCTGG | 500 |
| 5  | ACCAGGGCGA  | AGCTGGCGAT | AACGTCGGTC | TGCTGCTGCG  | TGGTACCAAG | 550 |
|    | CGTGAAGACG  | TGGAACGTGG | TCAAGTTCTG | GCCAAGCCAG  | GCTCGATCAA | 600 |
|    | GCCACACACT  | GACTTCGACG | CCGAGGTGTA | CATTCTGTCC  | AAAGAAGAAG | 650 |
|    | GTGGTCGTCA  | CACTCCTTTC | TTCAAGGGCT | ACCGTCCTCA  | GTTCTACTTC | 700 |
|    | CGTACAAC TG | ACGTGACCGG | CACCATCGAG | CTGCCAGAAG  | ACAAGGAAAT | 750 |
| 10 | GGTTCTGCCA  | GGCGACAACA | TTTCGATGAA | AGTGTCCCTG  | ATCGCTCCTA | 800 |
|    | TCGCCATGGA  | AGAAGGT    |            |             |            | 817 |

## 15 2) INFORMATION FOR SEQ ID NO: 1573

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 bases  
 (B) TYPE: Nucleic acid  
 20 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella buccalis*  
 (B) STRAIN: ATCC 35310

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573

|    |             |             |             |            |             |     |
|----|-------------|-------------|-------------|------------|-------------|-----|
| 30 | TATCCTTGTA  | GTTGCTGCTA  | CTGATGGTCC  | TATGCCACAG | ACACGTGAGC  | 50  |
|    | ACGTGCTTTT  | GGCTCGTCAG  | GTAAACGTTT  | CTCGTTTGGT | TGTGTTTCATG | 100 |
|    | AACAAGTGTG  | ACTTGGTAGA  | AGACGAAGAG  | ATGCTTGAAC | TCGTTGAAAT  | 150 |
|    | GGAGTTGCGC  | GAAC TTCTTG | AGCAATACGA  | ATTCGAAGAG | GATACTCCAA  | 200 |
| 35 | TCGTTTCGTGG | TTCTGCACTG  | GGTGCAATTGA | ATGGTGTTGA | CAAGTGGGTT  | 250 |
|    | GACAGCGTGA  | TGACGTTGAT  | GGACACTGTT  | GACGAGTGGA | TTCAAGAGCC  | 300 |
|    | AGAGCGTGAC  | CTTGACAAAC  | CTTTCTTGAT  | GCCAGTAGAG | GACGTGTTCT  | 350 |
|    | CTATCACAGG  | TCGTGGTACC  | GTTGTAACAG  | GACGTATTGA | GACTGGTAAG  | 400 |
|    | GTAAAGGTTG  | GCGACGAGAT  | TCAGTTGCTC  | GGTCTTGGTG | AGGACAAGAA  | 450 |
| 40 | GTCTGTTGTA  | ACAGGCGTTG  | AAATGTTCCG  | TAAGATTCTT | TCTGAAGGTG  | 500 |
|    | AAGCAGGTGA  | TAACGTAGGA  | CTTTTGCTCC  | GCGGTATCGA | TAAGGATGAA  | 550 |
|    | GTAAAGCGTG  | GTATGGTTGT  | TGTACACCCA  | GGTGCCATCA | CTCCTCACGA  | 600 |
|    | TCACTTCAAG  | GCTTCCATCT  | ATGTATTGAA  | GAAGGAAGAG | GGTGGACGTC  | 650 |
|    | ATACTCCATT  | CGGAAACAAG  | TATCGTCCTC  | AGTTCTATCT | CCGTACAATG  | 700 |
| 45 | GACTGTACAG  | GTGAGATCAC  | TTTGCCAGAA  | GGCGTAGAGA | TGGTGATGCC  | 750 |
|    | TGGTGACAAC  | GTAGAGATTG  | AGGTTACCTT  | GATTTACAAG | GTTGCC      | 796 |

## 50 2) INFORMATION FOR SEQ ID NO: 1574

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases

- (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*  
 (B) STRAIN: ATCC 19716

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | GCTATTCTAG | TAGTAGCAGC | AACTGATGGT | CCTATGCCAC  | AGACCCGTGA | 50  |
|    | GCACATCCTA | TTAGCACGTC | AGGTAGGCGT | ACCATAACATC | ATCGTATTCC | 100 |
| 15 | TAAACAAGTG | CGATATGGTT | GACGACGAGG | AATTATTAGA  | GTTAGTTGAG | 150 |
|    | ATGGACGTAC | GTGATCTATT | AAATCAGTAC | CAGTTCCCAG  | GCGACGACAC | 200 |
|    | TCCAATCATC | CGTGGTTCAG | CACTAGGTGC | ATTAAACGGC  | GAAGAGAAGT | 250 |
|    | GGAAAGAGGC | AATCTATCAG | TTAGCAGACA | CTCTAGATTG  | ATACATTCCA | 300 |
|    | GAGCCAAAGC | GTGATATCGA | TGATCCATTC | CTATTACCAA  | TCGAAGATAT | 350 |
| 20 | CTTCTCAATC | TCAGGTCGTG | GTACTGTAGT | AACCGGCCGT  | GTAGAGCGTG | 400 |
|    | GTATTGTACA | CGTAGGTGAC | GAAGTTGAAA | TCGTTGGTAT  | TCGTCCAACC | 450 |
|    | ACCAAGACCA | CTGTAAGTGG | CGTTGAAATG | TTCCGTAAGT  | TACTAGACGA | 500 |
|    | AGGTCGTGCA | GGTGATAACG | TTGGTGTCT  | ACTACGTGGT  | ACCAAGCGTG | 550 |
|    | ATGAGGTTGA | GCGTGGTCAG | GTTCTAGCTG | CTCCAGGCAC  | AATCACTCCA | 600 |
| 25 | CACACCAAGT | TCAGTGGTCA | GGTTTACGTA | CTAAGCAAGG  | ATGAAGGTGG | 650 |
|    | TCGTCACACT | CCATTCTTCA | AGGGCTACCG | TCCACAGTTC  | TTCTTCCGTA | 700 |
|    | CAACCGATAT | TACCGGTTCT | ATCGATCTGA | AAGAGGGCGT  | AGAGATGGTA | 750 |
|    | ATGCCAGGTG | ATAACACCGA | CATGACCGTA | ACCCTAATCC  | ACCCAGTAGC | 800 |
| 30 | TATGGCTGAA | GGCGAGAGAT |            |             |            | 820 |

## 2) INFORMATION FOR SEQ ID NO: 1575

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*  
 (B) STRAIN: ATCC 33315

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GGTAGTGTCT | GCAGCTGACG | GCCCAATGCC | ACAAACTCGT | GAACATATCC | 50  |
| 50 | TATTGTCACG | TAACGTTGGT | GTACCATACA | TCGTTGTATT | CTTAAACAAA | 100 |
|    | ATGGATATGG | TTGACGATGA | AGAATTACTT | GAATTAGTTG | AAATGGAAGT | 150 |
|    | ACGTGATCTA | TAACTGAAT  | ACGACTTCCC | AGGTGATGAT | ACTCCTGTTA | 200 |
|    | TTTCTGGTTC | AGCTTTGAAA | GCTTTAGAAG | GCGACGAAGA | ATATGAACAA | 250 |

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | AAAGTCTTAG | ACTTAATGGC | AGCTGTAGAT | GATTTTCATCC | CAACTCCTGA | 300 |
|    | ACGTGACCAT | GACAAACCGT | TCATGATGCC | GATTGAAGAT  | GTTTTCTCAA | 350 |
|    | TCACTGGTCG | TGGAAGTGT  | GCTACAGGTC | GTGTTGAACG  | TGGAAGTATT | 400 |
|    | AAAGTCGGTG | ATGAAGTTGA | TATCATCGGT | ATTCATGAAA  | ATGTTAAAAA | 450 |
| 5  | GACAACTGTT | ACGGGTGTAG | AAATGTTCCG | TAAATTGTTG  | GATTACGCTG | 500 |
|    | AAGCTGGCGA | TAACATCGGT | ACATTATTGC | GTGGTGTTTC  | TCGTGATGAT | 550 |
|    | ATCGAACGTG | GTCAAGTGTT | GGCTAAACCA | GGCACAATCA  | CACCACATAC | 600 |
|    | AAAATTCTCA | GCTGAAGTTT | ATGTATTAAC | AAAAGAAGAA  | GGCGGACGTC | 650 |
|    | ATACTCCATT | CTTCTCAAAC | TATCGCCCAC | AATTTTACTT  | CCGTACAAC  | 700 |
| 10 | GACATCACTG | GTGTCATTGA | ATTGCCAGAA | GGTACTGAAA  | TGGTTATGCC | 750 |
|    | AGGTGATAAC | GTAGCAATGG | AAGTTGAATT | AATTCACCCT  | GTTGCTATTG | 800 |
|    | AAA        |            |            |             |            | 803 |

15

## 2) INFORMATION FOR SEQ ID NO: 1576

## (i) SEQUENCE CHARACTERISTICS:

- |    |                          |
|----|--------------------------|
|    | (A) LENGTH: 805 bases    |
| 20 | (B) TYPE: Nucleic acid   |
|    | (C) STRANDEDNESS: Double |
|    | (D) TOPOLOGY: Linear     |

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- |  |  |
|--|--|
|  | (A) ORGANISM: <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> |
|  | (B) STRAIN: ATCC 33292   |

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | TTAATGAAGC | AATTGTTGTA | AATTTTGAAA | GCGAAGGAAA | AAAACATAAA | 50  |
|    | CTTGTTTTAG | AAGTAGCAGC | TCATTTAGGA | GATAATAGAG | TTAGAACTAT | 100 |
|    | TGCTATGGAT | ATGACAGATG | GTTTGGTAAG | GGGCTTAAAA | GCTGAGGCTT | 150 |
| 35 | TAGGTGCTCC | TATTAGTGTT | CCTGTTGGTG | AGAAAGTTTT | AGGAAGAATT | 200 |
|    | TTCAATGTTA | CTGGAGATTT | GATCGATGAA | GGTGAAGAAA | TTTCTTTTGA | 250 |
|    | TAAAAAATGG | GCAATTCATA | GAGATCCGCC | AGCTTTTGAA | GATCAAAGCA | 300 |
|    | CAAAAAGTGA | GATTTTTGAA | ACAGGGATTA | AAGTTGTAGA | TTTGCTTGCT | 350 |
|    | CCTTATGCAA | AAGGTGGTAA | AGTAGGTCTT | TTTGGTGGTG | CAGGTGTTGG | 400 |
| 40 | TAAAAC     | TTGTTATGG  | AGCTTATTCA | CAATGTTGCA | TTTAAGCATA | 450 |
|    | GCGGCTATTC | TGTATTTGCA | GGTGTGGGTG | AGAGAACTCG | TGAAGGAAAT | 500 |
|    | GACCTTTATA | ATGAAATGAA | AGAAAGTAAT | GTTTTAGACA | AAGTTGCTCT | 550 |
|    | ATGTTATGGA | CAAATGAATG | AACCACCAGG | AGCAAGAAAT | CGTATTGCTT | 600 |
|    | TAACAGGTTT | AACAATGGCT | GAGTATTTTA | GAGATGAAAT | GGGTCTTGAT | 650 |
| 45 | GTGCTTATGT | TTATTGATAA | TATCTTTAGA | TTTTCACAAT | CAGGTTCTGA | 700 |
|    | AATGTCAGCA | CTTTTAGGAA | GAATTCCATC | AGCTGTGGGT | TATCAACCAA | 750 |
|    | CCCTAGCAAG | TGAAATGGGT | AAATTCCAAG | AAAGAATTAC | TTCAACTAAA | 800 |
|    | AAAGG      |            |            |            |            | 805 |

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## 2) INFORMATION FOR SEQ ID NO: 1577

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*  
 (B) STRAIN: ATCC 33238

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577

|    |            |             |            |             |            |     |
|----|------------|-------------|------------|-------------|------------|-----|
| 15 | ATTTACCCAA | GATCAACGAA  | GCCGTCGAAG | TAAATTTCTGA | GGTTGAGGGC | 50  |
|    | AAGCAAAACA | GACTTGTTGTT | AGAGGTTGCC | GCACACCTTG  | GCGATAACCG | 100 |
|    | CGTAAGAACG | ATCGCTATGG  | ATATGAGCGA | AGGCTTAACC  | AGAGGCCTTG | 150 |
|    | AGGCTACGGC | TCTTGCGCG   | CCTATTAGCG | TTCCGGTCGG  | CGAAAAAGTT | 200 |
|    | TTGGGAAGGA | TTTTTAACGT  | CGTCGGCGAT | CTGATCGACG  | AGGGTGAAGG | 250 |
| 20 | CATAGAATTT | GATAAAAAAT  | GGTCTATCCA | CCGCGATCCT  | CCGCCGTTTG | 300 |
|    | AAGAGCAAAG | CACGAAGAGT  | GAAATTTTTG | AAACGGGTAT  | AAAAGTGGTC | 350 |
|    | GATCTTCTAG | CCCCTTATGC  | AAAAGGCGGT | AAGGTCGGAT  | TATTCGGCGG | 400 |
|    | TGCCGGCGTC | GGTAAGACGG  | TTATTATCAT | GGAGCTTATC  | CACAACGTTG | 450 |
|    | CATTTAAGCA | TAGCGGTTAT  | TCCGTGTTTG | CCGGCGTGGG  | CGAGCGAACC | 500 |
| 25 | CGCGAAGGAA | ACGACCTTTA  | TCACGAGATG | AAAGAGAGTA  | ACGTTTTTGA | 550 |
|    | CAAAGTCGCC | TTGTGCTACG  | GCCAGATGAA | CGAGCCGCCG  | GGAGCAAGAA | 600 |
|    | ACCGCATCGC | TCTAACAGGC  | CTAACGATGG | CTGAATACTT  | CCGCGACGAG | 650 |
|    | ATGGGACTTG | ACGTTTTGAT  | GTTTATAGAC | AACATCTTCC  | GTTTCTCTCA | 700 |
|    | GTCTGGCGCT | GAGATGTCGG  | CGCTTCTTGG | ACGTATCCCG  | TCAGCCGTTG | 750 |
| 30 | GTTATCAGCC | GACTTTGGCG  | AGCGAAATGG | GCAAATTCCA  | AGAGAGAATT | 800 |
|    | ACATCAACC  |             |            |             |            | 809 |

## 35 2) INFORMATION FOR SEQ ID NO: 1578

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*  
 (B) STRAIN: ATCC 25788

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578

|    |            |             |            |              |            |     |
|----|------------|-------------|------------|--------------|------------|-----|
| 50 | AATCGAAGTG | CAACGTTTCAT | TGCGTGTA   | CTTGATGGTGCT | GTAAGTGTGT | 50  |
|    | TGGACTCACA | ATCAGGTGTA  | GAACCTCAA  | AAGAGAACAGT  | TTGGCGTCAA | 100 |
|    | GCGACAGATT | ACCGCGTACC  | GCGTGTTGTA | TTCTGTAACA   | AAATGGACAA | 150 |

|    |            |            |            |             |            |      |
|----|------------|------------|------------|-------------|------------|------|
|    | AATTGGTGCA | GACTTCTTAT | ACTCTGTATC | AACTTTACAT  | GATCGTTTAC | 200  |
|    | AAGCAAATGC | TCACCCAATC | CAATTACCAA | TTGGTGCGGA  | AGATGACTTT | 250  |
|    | ACTGGTATTA | TCGACTTAGT | AAAAATGAAA | GCTGAAATCT  | ACACAAATGA | 300  |
|    | CTTAGGAACT | GAAATCCAAG | AGACTGAAAT | TCCTGAAGAA  | TACGTAGAAT | 350  |
| 5  | TAGCTGAAGA | ATGGCGCGAA | AAATTAATTG | AAGCTGTTGC  | TGATACTGAT | 400  |
|    | GAAGAACTAA | TGATGAAATT | CTTGGAAGGT | GAAGAAATCA  | CTGAAGAAGA | 450  |
|    | ATTGAAAGCT | GGTATTCGTC | AAGCAACATT | GACTGTTGAC  | TTTTTCCCTG | 500  |
|    | TTCTTTGCGG | ATCTGCCTTT | AAAAACAAAG | GGGTTCAATT  | GATGTTGGAT | 550  |
|    | GCAGTCATCG | ACTACTTGCC | TTCACCACTT | GATGTTCCCTG | CGATTAAAGG | 600  |
| 10 | GATCAATCCT | AAAACAGACG | AAGAACTGA  | TCGTCCGGCT  | GACGATGAAG | 650  |
|    | CACCATTTCG | TTCATTAGCA | TTTAAAGTAA | TGACTGACCC  | ATTCGTARGT | 700  |
|    | CGTTTGACAT | TCTTYCGTGT | GTATTCARGT | ATCTTGAAC   | CTGGATCATA | 750  |
|    | CGTATTGAAT | GCTTCAAAAG | GCAAACGCGA | ACGTATCGGT  | CGGATCCTAC | 800  |
|    | AAATGCACGC | CAACACTCGT | GCTGAAATCC | AAACAGTATA  | CTCAGGCGAT | 850  |
| 15 | ATCGCCGCTG | CTGTTGGTTT | GAAAGACACA | ACAACAGTATA | ATCCACTATG | 900  |
|    | TGATGAAAAA | TCCCCAGTAA | TCCTTGAATC | AATCGAATTC  | CCAGAACCAG | 950  |
|    | TTATCGAAGT | CGCTGTTGAG | CTTAAATCAA | AAGCTGACCA  | AGATAAAATG | 1000 |
|    | GGGGTTGCTT | TACAAAAACT | TGCTGAAGAA | GATCCATCAT  | TCCGTGTGGA | 1050 |
|    | AMCAAACGCT | GAAACAGGCG | AACTGTTAT  | CGCTGGTATG  | GGAGAACTTC | 1100 |
| 20 | ACTTGGACGT | CTTAGTTGAC | CGTATGCGTC | GCGAATTTAA  | AGTTGAAGCA | 1150 |
|    | AACGTAGGTG | CGCCTCAAGT | TTCTTATCGT | GAAACATTCC  | GTGCAGCAAC | 1200 |
|    | ACAAGCGGAA | GGTAAATTTG | TACGTCAGTC | TGGTGGTAAA  | GGTCAATACG | 1250 |
|    | GTCACGTATG | GGTCGAATTT | ACACCAAACG | AAGAAGGTAA  | AGGCTTCGAA | 1300 |
|    | TTCGAAAACG | CGATTGTCGG | TGGTGTGGTT | CCTCGTGAAT  | ACATCCCAGC | 1350 |
| 25 | AGTTGAAAAA | GGACTTGAAG | AATCAATGGC | GAACGGTGTC  | TTAGCCGGTT | 1400 |
|    | ACCCATTAGT | AGACATCAAA | GCAAACTTTT | ATGATGGTTC  | ATACCATGAT | 1450 |
|    | GTCGATTCAA | GTGAAACTGC | CTTCCGTGTT | GCAGCTTCTA  | TGGCTTTACG | 1500 |
|    | TGCTGCAGCG | AAGAAAGCAA | ACCCAGTAAT | TCTTGAACCA  | ATGATGAAAG | 1550 |
|    | TAGTTATCAC | TGTACCAGAA | GATTACTTAG | GTGATGTTAT  | GGGTCACGTA | 1600 |
| 30 | ACTGCTCGTC | GTGGACGCGT | AGAAGGAATG | GAAGCACWCG  | GTAACTCACA | 1650 |
|    | AATCGTGAAC | GCAATCGTGC | C          |             |            | 1671 |

## 35 2) INFORMATION FOR SEQ ID NO: 1579

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases  
 (B) TYPE: Nucleic acid  
 40 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*  
 (B) STRAIN: ATCC 49573

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 50 | GAAGTACAAC | GTTCACTACG | GGTTCTTGAC | GGWGCTGTAA | CAGTATTGGA | 50  |
|    | CTCACAATCT | GGTGTAGAAC | CACAACTGA  | AACAGTTTGG | CGTCAAGCGA | 100 |
|    | CAGATTACCG | CGTACCACGT | ATCGTATTCT | GTAACAAAAT | GGATAAAATC | 150 |



|    |            |            |             |            |             |      |
|----|------------|------------|-------------|------------|-------------|------|
|    | GGTGCAGACT | TCTTATACTC | TGTATCTACT  | TTACATGATC | GCTTGCAAGC  | 200  |
|    | AAATGCTCAT | CCAATCCAAT | TACCAATTGG  | TGCGGAAGAT | GACTTTACTG  | 250  |
|    | GTATCATCGA | TCTAGTAAAA | ATGAAAGCTG  | AGATCTATAC | AAACGATTTA  | 300  |
|    | GGAACAGAGA | TTCAAGAAAC | TGAAATTCCT  | GAAGAGTACA | AAGAATTAGC  | 350  |
| 5  | TGAAGAATGG | CGCGAAAAAT | TAGTTGAAGC  | TGTTGCAGAT | ACTGACGAAG  | 400  |
|    | AGCTAATGAT | GAAATTCTTG | GAAGGTGAAG  | AAATCACTGA | AGAAGAATTG  | 450  |
|    | AAAGCTGGTA | TCCGTCAAGC | GACATTGACT  | GTTGAATTTT | TCCCAGTTCT  | 500  |
|    | TTGTGGTTCA | GCCTTCAAAA | ACAAAGGGGT  | TCAATTGATG | TTGGATGCAG  | 550  |
|    | TCATCGACTA | CCTTCCTTCA | CCACTTGATG  | TTCTTGCAAT | CAAAGGGATC  | 600  |
| 10 | AATCCTAAAA | CTGACGAAGA | AACTGATCGT  | CCTGCTGACG | ATGAAGCGCC  | 650  |
|    | TTTTGCTTCA | CTAGCATTTA | AAGTAATGAC  | TGACCCATTC | GTAGGTCGTT  | 700  |
|    | TGACATTCTT | CCGTGTGTAT | TCAGGTGTCT  | TGAACTCTGG | ATCATATGTC  | 750  |
|    | TTGAATGCTT | CAAAAGACAA | ACGCGAACGT  | ATCGGTCGTA | TTCTGCAAAT  | 800  |
|    | GCACGCGAAC | ACTTGTGCAG | AAATCCAAAC  | AGTTTATTCA | GGCGATATCG  | 850  |
| 15 | CTGCAGCTGT | TGGTTTGAAA | GATTCCACAA  | CAGGGGATAC | ATTGTGTGCG  | 900  |
|    | AAAAATCACC | CAGTAATCCT | TGAATCAATC  | GAATTCCCAG | AMCCAGTTAT  | 950  |
|    | CGAAGTAGCT | GTTGAACYTA | AATCAAAAAGC | TGACCAAGAT | AAAATGGGTG  | 1000 |
|    | TGGCTTTACA | AAAACCTGCT | GAAGAAGATC  | CTTCATTCCG | TGTAGAAMCA  | 1050 |
|    | AACGCTGAAA | CTGGCGAAAC | TGTTATCGCA  | GGGATGGGTG | AACTTCACTT  | 1100 |
| 20 | GGACGTCCTT | GTTGACCGTA | TGCGTCGCGA  | ATTTAAAGTT | GAAGCAAACG  | 1150 |
|    | TTGGTGCGCC | TCAAGTTTCT | TACCGCGAAA  | CATTCCGTGC | TTCTACGCAA  | 1200 |
|    | GCCGAAGGTA | AATTTGTACG | TCAGTCTGGT  | GGTAAAGGTC | AATACGGTCA  | 1250 |
|    | CGTATGGATC | GAATTTACAC | CAAACGAAGA  | AGGTAAAGGC | TTCGAATTCTG | 1300 |
|    | AAAACGCAAT | TGTCGGTGGT | GTGGTTCCAC  | GTGAATACAT | CCCAGCAGTT  | 1350 |
| 25 | GAAAAAGGAC | TTGAAGACTC | AATGGCTAAC  | GGTGTCTAG  | CTGGTTATCC  | 1400 |
|    | ATTGGTTGAC | ATCAAAGCCA | AGCTTTACGA  | TGGTTCATAC | CATGATGTCTG | 1450 |
|    | ATTCAAGTGA | AACAGCCTTC | CGTGTGGCAG  | CTTCAATGGC | TTTACGTGCT  | 1500 |
|    | GCAGCGAAGA | AAGCTAATCC | AGTGATTCTT  | GAACCAATGA | TGAAAGTTGT  | 1550 |
|    | TATCACTGTT | CCTGAAGATT | ACTTAGGTGA  | TATTATGGGA | CACGTAACCTG | 1600 |
| 30 | CTCGTCGTGG | ACGTGTTGAA | GGTATGGAAG  | CGCATGGTAA | CTCACAAATC  | 1650 |
|    | GTTAACGCGA | TT         |             |            |             | 1662 |

## 35 2) INFORMATION FOR SEQ ID NO: 1580

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1669 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*  
 (B) STRAIN: ATCC 49456

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 50 | CAATCGAAGT | ACAACGTTCT | CTTCGTGTAT | TGGATGGTGC | TGTTACCGTT | 50  |
|    | CTTGACTCAC | AATCAGGTGT | TGAGCCTCAA | ACTGAAACAG | TTTGGCGTCA | 100 |
|    | AGCAACTGAG | TATGGAGTTC | CACGTATCGT | ATTGCCAAC  | AAAATGGACA | 150 |

|    |             |            |            |            |            |      |
|----|-------------|------------|------------|------------|------------|------|
|    | AAATCGGTGC  | TGACTTCCTT | TACTCTGTAA | GCACACTTCA | CGATCGTCTT | 200  |
|    | CAAGCAAATG  | CACACCCAAT | CCAATTGCCA | ATCGGTTCTG | AAGATGACTT | 250  |
|    | CCGTGGTATC  | ATCGACTTGA | TCAAGATGAA | AGCTGAAATC | TATACTAACG | 300  |
|    | ACCTTGGTAC  | AGATATCCTT | GAAGAAGACA | TCCCAGCTGA | ATACCTTGAC | 350  |
| 5  | CAAGCTCAAG  | AATACCGTGA | AAAATTGATC | GAAGCAGTTG | CTGAAACTGA | 400  |
|    | CGAAGAATTG  | ATGATGAAAT | ACCTCGAAGG | TGAAGAAATC | ACTAACGAAG | 450  |
|    | AATTGAAAGC  | TGGTATCCGT | AAAGCGACTA | TCAACGTTGA | ATTCTTCCCA | 500  |
|    | GTATTGTGTG  | GCTCTGCCTT | CAAGAACAAA | GGTGTTCAAT | TGATGCTTGA | 550  |
|    | TGCGGTTATT  | GACTACCTTC | CAAGCCCCTT | TGACATCCCA | GCGATCAAAG | 600  |
| 10 | GTATCAACCC  | AGATWCAGAT | GAAGAAGAAA | CTCGTCCAGC | ATCTGATGAA | 650  |
|    | GAGCCATTG   | CAGCTCTTGC | CTTCAAGATC | ATGACAGACC | CATTGTAAG  | 700  |
|    | TCGTTTGACA  | TTCTTCCGTG | TTTACTCARG | TGKTCTTCAA | TCAGGTTTCA | 750  |
|    | ACGTATTGAA  | CACTTCTAAA | GGKAAACGTG | AGCGTATCGG | ACGTATCCTT | 800  |
|    | CAAATGCACG  | CCAACAGCCG | TCAAGAAATT | GACACTGGTT | ACTCAAGAGA | 850  |
| 15 | TATCGCTGCT  | GCCGTTGGTT | TGAAAGATAC | TCCAACGGT  | GACTCATTGC | 900  |
|    | CAGATGAAAA  | AGCTAAAATC | ATTCTTGAGT | CAATCAACGT | TCCAGAMCCA | 950  |
|    | GTTATCCAAT  | TGATGGTTGA | GCCAAAATCT | AAAGCTGACC | AAGCCAAGAT | 1000 |
|    | GGGTATCGCC  | CTTCAAAAAT | TGGCTGAAGA | AGATCCAACA | TTCCGCGTTG | 1050 |
|    | AAMCAAACGT  | TGAAACTGGT | GAAMCAGTTA | TCTCTGGTAT | GGGTGAGCTT | 1100 |
| 20 | CACCTTGACG  | TCCTTGTTGA | CCGTATGCGT | CGTGAGTTCA | AAGTTGAAGC | 1150 |
|    | AAACGTAGGT  | GCTCCTCAAG | TATCTTACCG | TGAAACATTC | CGCGCTTCTA | 1200 |
|    | CTCAAGCACG  | TGGATTCTTC | AAACGTCAGT | CTGGTGGTAA | AGGTCAATTC | 1250 |
|    | GGTGATGTAT  | GGATTGAATT | TACTCCAAC  | GAAGAAGGTA | AAGGATTCGA | 1300 |
|    | ATTCGAAAAC  | GCAATCGTCG | GTGGTGTGGT | TCCTCGTGAA | TTTATCCCAG | 1350 |
| 25 | CGGTTGAAAA  | AGGTTTGGTA | GAATCTATGG | CTAACGGTGT | ACTTGCAGGT | 1400 |
|    | TACCCAATGG  | TTGACGTTAA | AGCTAAGCTT | TACGATGGTT | CATACCACGA | 1450 |
|    | TGTCGACTCA  | TCTGAAACTG | CCTTCAAGAT | TGCGGCTTCA | CTTGCTCTTA | 1500 |
|    | AAGAAGCTGC  | TAAATCAGCA | CAACCAGCTA | TCCTTGAGCC | AATGATGCTT | 1550 |
|    | GTAACAATCA  | CTGTTCCAGA | AGAAAACCTT | GGTGATGTTA | TGGGTCACGT | 1600 |
| 30 | AACTGCTCGT  | CGTGGACGTG | TAGATGGTAT | GGAAGCACWC | GGTAACAGCC | 1650 |
|    | AAATCGTTTCG | TGCTTACGT  |            |            |            | 1669 |

## 35 2) INFORMATION FOR SEQ ID NO: 1581

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases  
 (B) TYPE: Nucleic acid  
 40 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581

AATTGGGGAC TACACCTATT ATGATG

26

50

## 2) INFORMATION FOR SEQ ID NO: 1582

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582

10 GGCAAATCAG TCAGTTCAGG AGT

23

## 2) INFORMATION FOR SEQ ID NO: 1583

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583

25

CGATTGGCAA CAATACACTC CTG

23

## 2) INFORMATION FOR SEQ ID NO: 1584

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584

40

TCACCTATTT TTACGCCTGG TAGGAC

26

## 2) INFORMATION FOR SEQ ID NO: 1585

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

5 (C) ACCESSION NUMBER: AF139725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGACTATAC | CTGACGCAAA | TGCAATCTAT | CCTAACTCAG | CCATCAAAGA | 50  |
| 10 | GGTTGTCTTT | ATCAAGAACG | TGATCAAAAG | TCCCAATATT | GAAATTGGGG | 100 |
|    | ACTACACCTA | TTATGATGAC | CCAGTAAATC | CCACCGATTT | TGAGAAACAC | 150 |
|    | GTTACCCATC | ACTATGAATT | TCTAGGCGAC | AAATTAATCA | TCGGTAAATT | 200 |
|    | TTGTTCTATC | GCCAGTGGCA | TTGAATTTAT | CATGAACGGT | GCCAACCACG | 250 |
|    | TAATGAAAGG | TATTTGACT  | TATCCATTTA | ATATTTTAGG | TGGCGATTGG | 300 |
| 15 | CAACAATACA | CTCCTGAACT | GACTGATTTG | CCGTTGAAAG | GTGATACTGT | 350 |
|    | AGTCGGAAAT | GACGTGTGGT | TTGGGCAAAA | TGTGACCGTC | CTACCAGGCG | 400 |
|    | TAAAAATAGG | TGACGGTGCC | ATTATCGGAG | CAAATAGTGT | TGTAACAAAA | 450 |
|    | GACGTCGCTC | CATATACAAT | TGTCGGTGGC | AATCCAATTC | AACTCATCGG | 500 |
|    | ACCAAGATTT | GAACCGGAAG | TTATTCAAGC | ATTAGAAAAT | CTGGCATGGT | 550 |
| 20 | GGAATAAAGA | TATTGAATGG | ATAACTGCTA | ATGTTCTCTA | ACTAATGCAA | 600 |
|    | ACAACACCCA | CACTTGAATT | GATAAACAGT | TTAATGGAAA | AATAA      | 645 |

25 2) INFORMATION FOR SEQ ID NO: 1586

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586

ATTCCCACAA TCTTTTTTAT CAATAA

26

40

2) INFORMATION FOR SEQ ID NO: 1587

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587

CATTGTTCAG ATTCGGTAAA GTTC

24

## 2) INFORMATION FOR SEQ ID NO: 1588

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588

GTTTTTGAAG TTAAATAGTG TTCTT

25

## 2) INFORMATION FOR SEQ ID NO: 1589

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589

CTTCCATTG TACTTTCCT A

21

## 2) INFORMATION FOR SEQ ID NO: 1590

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1920 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Cloning vector pFW16  
 (C) ACCESSION NUMBER: U50983

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1590

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGAAAATTA | TTAATATTGG | AGTTTTAGCT | CATGTTGATG | CAGGAAAAAC | 50  |
| TACCTTAACA | GAAAGCTTAT | TATATAACAG | TGGAGCGATT | ACAGAATTAG | 100 |
| GAAGCGTGGA | CAAAGGTACA | ACGAGGACGG | ATAATACGCT | TTTAGAACGT | 150 |
| CAGAGAGGAA | TTACAATTCA | GACAGGAATA | ACCTCTTTTC | AGTGGGAAAA | 200 |
| TACGAAGGTG | AACATCATAG | ACACGCCAGG | ACATATGGAT | TTCTTAGCAG | 250 |

|    |             |            |            |            |             |      |
|----|-------------|------------|------------|------------|-------------|------|
|    | AAGTATATCG  | TTCATTATCA | GTTTTAGATG | GGGCAATTCT | ACTGATTTCT  | 300  |
|    | GCAAAAGATG  | GCGTACAAGC | ACAAACTCGT | ATATTATTTT | ATGCACTTAG  | 350  |
|    | GAAATGGGG   | ATTCCCACAA | TCTTTTTTAT | CAATAAGATT | GACCAAAATG  | 400  |
|    | GAATTGATTT  | ATCAACGGTT | TATCAGGATA | TTAAAGAGAA | ACTTTCTGCC  | 450  |
| 5  | GAAATTGTAA  | TCAAACAGAA | GGTAGAACTG | TATCCTAATG | TGTGTGTGAC  | 500  |
|    | GAACCTTTACC | GAATCTGAAC | AATGGGATAC | GGTAATAGAG | GGAAACGATG  | 550  |
|    | ACCTTTTAGA  | GAAATATATG | TCCGGTAAAT | CATTAGAAGC | ATTGGAAGTC  | 600  |
|    | GAACAAGAGG  | AAAGCATAAG | ATTTCAGAAT | TGTTCTCTGT | TCCCTCTTTA  | 650  |
|    | TCATGGAAGT  | GCAAAAAGTA | ATATAGGGAT | TGATAACCTT | ATAGAAGTTA  | 700  |
| 10 | TTACTAATAA  | ATTTTATTCA | TCAACACATC | GAGGTCCGTC | TGAACTTTGC  | 750  |
|    | GGAAATGTTT  | TCAAATTTGA | ATATACAAAA | AAAAGACAAC | GTCTTGCATA  | 800  |
|    | TATACGCCTT  | TATAGTGGAG | TACTACATTT | ACGAGATTCT | GTTAGAGTAT  | 850  |
|    | CAGAAAAGGA  | AAAAATAAAA | GTTACAGAAA | TGTATACTTC | AATAAATGGT  | 900  |
|    | GAATTATGTA  | AGATTGATAG | AGCTTATTCT | GGAGAAATTG | TTATTTTGCA  | 950  |
| 15 | AAATGAGTTT  | TTGAAGTTAA | ATAGTGTTCT | TGGAGATACA | AAACTATTGC  | 1000 |
|    | CACAGAGAAA  | AAAGATTGAA | AATCCGCACC | CTCTACTACA | AACAACGTGT  | 1050 |
|    | GAACCGAGTA  | AACCTGAACA | GAGAGAAATG | TTGCTTGATG | CCCTTTTGGA  | 1100 |
|    | AATCTCAGAT  | AGTGATCCGC | TTCTACGATA | TTACGTGGAT | TCTACGACAC  | 1150 |
|    | ATGAAATTAT  | ACTTTCTTTC | TTAGGGAAAG | TACAAATGGA | AGTGATTAGT  | 1200 |
| 20 | GCACTGTTGC  | AAGAAAAGTA | TCATGTGGAG | ATAGAAATAA | CAGAGCCTAC  | 1250 |
|    | AGTCATTTAT  | ATGGAGAGAC | CGTTAAAAAA | TGCAGAATAT | ACCATTACAC  | 1300 |
|    | TCGAAGTGCC  | GCCAAATCCT | TTCTGGGCTT | CCATTGGTCT | ATCTGTATCA  | 1350 |
|    | CCGCTTCCGT  | TGGGAAGTGG | AATGCAGTAT | GAGAGCTCGG | TTTCTCTTGG  | 1400 |
|    | ATACTTAAAT  | CAATCATTTT | AAAATGCAGT | TATGGAAGGG | ATACGCTATG  | 1450 |
| 25 | GTTGTGAACA  | AGGATTGTAT | GGTTGGAATG | TGACGGACTG | TAAAATCTGT  | 1500 |
|    | TTTAAGTATG  | GCTTATACTA | TAGCCCTGTT | AGTACCCAG  | CAGATTTTTCG | 1550 |
|    | GATGCTTGCT  | CCTATTGTAT | TGGAACAAGT | CTTAAAAAAA | GCTGGAACAG  | 1600 |
|    | AATTGTTAGA  | GCCATATCTT | AGTTTTTAAA | TTTATGCGCC | ACAGGAATAT  | 1650 |
|    | CTTTCACGAG  | CATACAACGA | TGCTCCTAAA | TATTGTGCGA | ACATCGTAGA  | 1700 |
| 30 | CACTCAATTG  | AAAAATAATG | AGGTCATTCT | TAGTGGAGAA | ATCCCTGCTC  | 1750 |
|    | GGTGTATTCA  | AGAATATCGT | AGTGATTTAA | CTTTCTTTAC | AAATGGACGT  | 1800 |
|    | AGTGTTTGTT  | TAACAGAGTT | AAAAGGGTAC | CATGTTACTA | CCGGTGAACC  | 1850 |
|    | TGTTTGCCAG  | CCCCGTCGTC | CAAATAGTCG | GATAGATAAA | GTACGATATA  | 1900 |
|    | TGTTCAATAA  | AATAACTTAG |            |            |             | 1920 |
| 35 |             |            |            |            |             |      |

## 2) INFORMATION FOR SEQ ID NO: 1591

## 40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591

50 ATGAGGTAAT AGAACGGATT

20

## 2) INFORMATION FOR SEQ ID NO: 1592

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592

CAGTATTTCA GTAAGCGTAA A

21

## 2) INFORMATION FOR SEQ ID NO: 1593

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593

CCGAGCGATT TACCGGATAC TTGGCTGCIC GCTCGG

36

## 2) INFORMATION FOR SEQ ID NO: 1594

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: N97-330  
 (C) ACCESSION NUMBER: AF175293

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGTTTAGAA | TTAAAGTTGC | AGTTCGTGTT | GGGGGCTGTT | CAGAGGAACA | 50  |
| TAATGTTTCG | ATAAAATCTG | CGATGGAGAT | TGCCGCAAAC | ATAGATACAA | 100 |
| AAAAGTATCA | GCCTTATTAT | ATTGGAATCA | CAAAATCCGG | CGTTTGGAAA | 150 |
| ATGTGTGAAA | AACCTTGTTT | GGAGTGGGAA | CAATATGCGG | GGGATCCGGT | 200 |
| TGTTTTTTCA | CCGGACAGAA | GTACGCATGG | TCTGCTGATA | CAAAAAGACA | 250 |

|    |             |            |            |            |            |      |
|----|-------------|------------|------------|------------|------------|------|
|    | CTGGGTATGA  | AATCCAGCCT | GTGGATGTGG | GATTACCGAT | GATTCATGGC | 300  |
|    | AAGTTTGGCG  | AGGATGGCTC | CATACAAGGC | TTGCTTGAAT | TGTCAGGCAT | 350  |
|    | TCCGTATGTG  | GGATGCGATA | TTCAAAGCTC | CGTGACCTGC | ATGGATAAGG | 400  |
|    | CGCTTG CATA | TACCGTTGTG | AAAAATGCGG | GTATCGCTGT | GCCTGGGTTC | 450  |
| 5  | CGGATCCTTC  | AGGAGGGGGA | TCGCCTGGAA | ACAGAGGATT | TCGTATATCC | 500  |
|    | CGTTTTTGTA  | AAGCCTGCCC | GTTCCGGCTC | ATCCTTTGGC | GTAAACAAGG | 550  |
|    | TATGCAAGGC  | AGAAGAACTG | CAGGCAGCAA | TCGAAGATGC | AAGAAAATAT | 600  |
|    | GACAGCAAGA  | TTTTGATTGA | AGAGGCCGTT | ACCGGGAGTG | AGGTAGGCTG | 650  |
|    | CGCCATACTG  | GGAAACGGAA | ATGATCTCAT | GGCTGGCGAG | GTGGATCAGA | 700  |
| 10 | TTGAGCTGAG  | ACACGGCTTT | TTTAAGATTC | ATCAGGAAGC | ACAGCCGGAG | 750  |
|    | AAAGGATCTG  | AAAATGCAGT | CATCCGAGTT | CCAGCCGCCT | TACCGGATGA | 800  |
|    | GGTAATAGAA  | CGGATTCAGA | AAACAGCAAT | GAAGATTTAC | CGGATACTTG | 850  |
|    | GCTGCAGAGG  | ATTGGCCCGC | ATTGACCTGT | TTTTGCGGGA | GGACGGCTGC | 900  |
|    | ATTGTGTTGA  | ATGAAGTGAA | TACCATGCCG | GGTTTTACTT | CCTACAGCCG | 950  |
| 15 | TTATCCCCGC  | ATGATGACAG | CAGCCGGTTT | TACGCTTACT | GAAATACTGG | 1000 |
|    | ATCGCTTGAT  | TGAACTTTCA | CTTAGGAGGT | AA         |            | 1032 |

20 2) INFORMATION FOR SEQ ID NO: 1595

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595

AAATAATGCT CCATCAATTT GCTGA

25

35 2) INFORMATION FOR SEQ ID NO: 1596

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596

ATAGTCGAAA AAGCCATCCA CAAG

24

50

2) INFORMATION FOR SEQ ID NO: 1597



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597

GATGAATTTG CGAAAATACA TGGA

24

## 2) INFORMATION FOR SEQ ID NO: 1598

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598

CAGCCAATTT CTACCCCTTT CAC

23

## 2) INFORMATION FOR SEQ ID NO: 1599

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*  
 (B) STRAIN: BM4405  
 (C) ACCESSION NUMBER: AF136925

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CAGGGAGTAT | TTGAGTTATT | AGATATTCCA | TATGTAGGTT | GTGGTATCGG | 50  |
| AGCTGCAGCA | ATTTCCATGA | ATAAAATAAT | GCTCCATCAA | TTTGCTGAAA | 100 |
| TAGTTGGTGT | AAAAAGCACT | CCTAGTATGA | TTATAGAAAA | GGGACAAGAC | 150 |
| CTACAAAAAG | TCGATGAATT | TGCGAAAATA | CATGGATTTC | CTTTATATAT | 200 |
| CAAACCGAAT | GAGGCAGGCT | CATCAAAAGG | AATTAGCAAG | GTAGAACAAA | 250 |
| AAAGTGATTT | ATATAAAGCA | ATAGACGAAG | CTTCAAAATA | TGATAGCCGT | 300 |

|              |            |            |            |            |     |
|--------------|------------|------------|------------|------------|-----|
| ATTTTAATTC   | AAAAGGAAGT | GAAAGGGGTA | GAAATTGGCT | GTGGGATTTT | 350 |
| AGGGAATGAA   | CAATTGGTCG | TTGGAGAATG | TGATCAAATT | AGTCTTGTGG | 400 |
| ATGGCTTTTT   | CGACTATGAA | GAGAAATACA | ATTTAGTAAC | AGCAGAAATT | 450 |
| TTGTTACCAG   | CTAAACTATC | AATAGACAAA | AAAGAAGACA | TCCAGATAAA | 500 |
| 5 AGCAAAAAAA | CTATACAGAC | TATTAGGGTG | CAAAGGATTA | GCGAGAATCG | 550 |
| ACTTTTCTT    | AACGGATGAC | GGAGAAATTT | TATTAAATGA | GATCAACACC | 600 |
| CTCC         |            |            |            |            | 604 |

10

## 2) INFORMATION FOR SEQ ID NO: 1600

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 805 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*
- (B) STRAIN: ATCC 49349

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| ACCTCAAATT    | AATGAAGCAA | TTGTTGTAAA | TTTTGAAAGC | GAAGGAAAAA | 50  |
| AACATAAACT    | TGTTTTAGAA | GTAGCAGCTC | ATTTAGGAGA | TAATAGAGTT | 100 |
| AGAACTATTG    | CTATGGATAT | GACAGATGGT | TTGGTAAGGG | GCTTAAAAGC | 150 |
| 30 TGAGGCTTTA | GGTGCTCCTA | TTAGTGTTC  | TGTTGGTGAG | AAAGTTTTAG | 200 |
| GAAGAATTTT    | CAATGTTACT | GGAGATTTGA | TCGATGAAGG | TGAAGAAATT | 250 |
| CCTTTTGATA    | AAAAATGGGC | AATTCATAGA | GATCCGCCAG | CTTTTGAAGA | 300 |
| TCAAAGCACA    | AAAAGTGAGA | TTTTTGAAAC | AGGGATTAAA | GTTGTAGATT | 350 |
| TACTTGCTCC    | TTATGCAAAA | GGTGGTAAAG | TAGGTCTTTT | TGGTGGTGCA | 400 |
| 35 GGTGTTGGTA | AAACTGTTAT | TATTATGGAG | CTTATTCACA | ATGTTGCATT | 450 |
| TAAGCATAGC    | GGCTATTCTG | TATTTGCAGG | TGTGGGTGAG | AGAACTCGTG | 500 |
| AAGGAAATGA    | CCTTTATAAT | GAAATGAAAG | AAAGTAATGT | TTTAGACAAA | 550 |
| GTTGCTCTAT    | GTTATGGACA | AATGAATGAA | CCACCAGGAG | CAAGAAATCG | 600 |
| TATTGCTTTA    | ACAGGTTTAA | CAATGGCTGA | GTATTTTAGA | GATGAAATGG | 650 |
| 40 GTCTTGATGT | GCTTATGTTT | ATTGATAATA | TCTTTAGATT | TTCACAATCA | 700 |
| GGTTCTGAAA    | TGTCAGCACT | TTAGGAAGA  | ATTCCATCAG | CTGTGGGTTA | 750 |
| TCAACCAACC    | CTAGCAAGTG | AAATGGGTAA | ATTCCAAGAA | AGAATTACTT | 800 |
| CAACT         |            |            |            |            | 805 |

45

## 2) INFORMATION FOR SEQ ID NO: 1601

## (i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus sulfureus*  
(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
| 10 | CTCCTTACCA  | GATATCAACA | ATGCGCTGGT | TGTATATAAA | AATGATGCCA | 50  |
|    | ATAAAACAAA  | AGTTGTTTTA | GAAGCAGCGT | TAGAATTAGG | TGACGGAATC | 100 |
|    | ATTCGTGCGA  | TTGCAATGGA | ATCGACTGAT | GGATTGCAAC | GTGGGATGGA | 150 |
|    | AGTTGTTCGAT | ATGGGAGAAT | CTATTTCTGT | ACCAGTTGGA | ACAGAACTT  | 200 |
|    | TAGGACGTGT  | GTTTAATGTA | TTAGGAGATA | CGATTGACTT | AGAAGCTCCT | 250 |
| 15 | TTTCCTAAAG  | ATGCACCGCG | TAGTGGAATC | CATAAAAAAG | CCCCTAATTT | 300 |
|    | TGATGAATTA  | AGTACAAGCA | CAGAAATTCT | AGAAACAGGG | ATCAAAGTCA | 350 |
|    | TCGATCTATT  | AGCCCCTTAT | TTAAAAGGTG | GTAAAGTTGG | ATTGTTTGGG | 400 |
|    | GGAGCCGGTG  | TAGGAAAAAC | GGTATTGATT | CAAGAGTTGA | TTCACAATAT | 450 |
|    | CGCACAAGAA  | CACGGTGCGA | TTTCGGTCTT | TACTGGTGTT | GGTGAGCGTA | 500 |
| 20 | CACGTGAAGG  | AAACGATTTG | TATTATGAAA | TGAAAGATTC | AGGAGTCATT | 550 |
|    | GAAAAACAG   | CGATGGTGTT | TGGACAAATG | AATGAGCCAC | CTGGTGACCG | 600 |
|    | GATGCGTGTA  | GCCTTGACTG | GATTAACGAT | TGCTGAATAT | TTCCGTGATG | 650 |
|    | TTGAAGGACA  | GGATGTACTG | TTGTTTATCG | ACAATATCTT | CCGTTTACAA | 700 |
|    | CAAGCTGGTT  | CTGAAGTGTC | TGCCTTGTTA | GGTCGTATGC | CATCAGCTGT | 750 |
| 25 | GGGATATCAA  | CCAACATTAG | CTACCGAAAT | GGGGCAATTG | CAAGAGCGGA | 800 |
|    | TCACGTCAAC  | GAAAAAAGGA | TCGATC     |            |            | 826 |

30 2) INFORMATION FOR SEQ ID NO: 1602

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 833 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*  
(B) STRAIN: ATCC 49428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 45 | TGATACTTTA | CCAGATATTA | ATAATGCATT | AGTAGTATAT | AAAAAGGACG | 50  |
|    | AGGACAAGAC | ACGCGTTGTC | TTAGAAGCCA | CCTTGGAAC  | TGGAGATGGC | 100 |
|    | ATGATTCGTG | CAATCTCTAT | GGGATCGACT | GATGGCTTGC | AACGGGGAAT | 150 |
|    | GGAAGTTGTG | GACACACAAG | CACCTATTTT | TGTTCCAGTA | GGAAATGAAA | 200 |
| 50 | CCTTAGGACG | TGTTTTTAAT | GTCTTAGGAG | AAACGATTGA | TAAACAGGCA | 250 |
|    | CCGTTTCCTG | AAGATGCCAA | AAAAAGTGGT | ATTCATAAAA | AAGCACCCGC | 300 |
|    | TTTTGATGAA | TTAAGTACCA | GTTCTGAAAT | ATTGGAAACC | GGGATTAAAG | 350 |
|    | TAATCGATTT | GCTAGCTCCT | TATTTACGAG | GTGGTAAAGT | TGGATTATTT | 400 |

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GGCGGTGCTG GCGTGGGTAA AACGGTATTA ATTCAAGAAT TAATTCATAA      450
CGTTGCCCAA GAACATGGGG GAATTTCTGT TTTTACGGGT GTCGGAGAGC      500
GTA CTCTGTA AGGAAATGAC CTATATTATG AAATGCAGGA TTCAGGCGTT      550
ATTGAAAAAA CGGCTATGGT ATTTGGACAA ATGAACGAAC CCCCTGGTGC      600
5  ACGTATGCGT GTAGCGTTAA CTGGTTTGAC ACTTGCTGAG TACTTCCGTG      650
ATGTACAAGG TCAAGACGTA TTATTATTTA TAGATAATAT TTTCCGCTTT      700
ACTCAAGCAG GAACAGAAGT ATCTGCTTTA TTAGGACGGA TGCCGTCTGC      750
CGTTGGTTAC CAACCAACTC TAGCAACGGA AATGGGACAG TTGCAAGAAC      800
GAATCACATC GACAGATAAA GGATCAATTA CCT                          833
10

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## 2) INFORMATION FOR SEQ ID NO: 1603

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15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 806 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
      (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Campylobacter sputorum subsp. sputorum
25  (B) STRAIN: ATCC 35980

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603

```

30  ATCAGCCTAA AATTAACGAA GCAATAGAAG TTAATTATGA ATTAGATGGT      50
      AAAAAAATAA GACTTATTCT TGAAGTAGCT GGACATCTTG GCGATAATAG      100
      AGCAAGAACC ATTGCTATGG ATATGAGTGA TGGTTTACAA AGAGGATTAG      150
      AAGTTACGGC TCTTGGTGCT CCTATAACAG TTCCTGTTGG AGATAAAGTT      200
      TTAGGTAGAA TGTTTAATGT TGTAGGTGAC TTAATAGATG AAGGTGAAGT      250
      AACAGATTTT GATAAAAGAT GGGCTATCCA TAGAGATCCT CCTTCGTTTG      300
35  AAGATCAAAG TACAAAAAGT GAAATTTTGG AAACAGGTAT AAAAGTAGTT      350
      GATCTTCTTG CACCTTATGC AAAAGGTGGT AAAGTTGGCT TATTTGGTGG      400
      TGCTGGCGTT GGAAAAACAG TTATCATAAT GGAGCTTATA CATAATGTTG      450
      CATTTAAACA CAGCGGTTAT TCAATTTTGG CCGGTGTTGG AGAGAGAACA      500
      AGAGAGGGAA ATGATCTTTA TAATGAGATG AAAGAGTCTG GTGTTTGGGA      550
40  TAAAGTTGCC TTATGTTATG GACAAATGAA TGAACCACCA GGAGCAAGAA      600
      ACCGTATAGC ATTAACAGGT CTTACAATGG CTGAATATTT CCGTGATGAA      650
      ATGGGGCTTG ATGTGTTGAT GTTTATAGAT AATATTTTGA GATTTTCTCA      700
      ATCAGGTTCT GAAATGTCAG CGCTGCTTGG TAGAATTCCA TCTGCTGTTG      750
      GTTATCAACC AACATTAGCA AGTGAGATGG GAAAACCTCA AGAAAGAATT      800
45  ACTTCC                          806

```

## 2) INFORMATION FOR SEQ ID NO: 1604

```

50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 738 bases
      (B) TYPE: Nucleic acid

```

- (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*  
(B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604

|    |             |            |            |             |            |     |
|----|-------------|------------|------------|-------------|------------|-----|
|    | GGTGTATATCC | GCACAATCGC | TATGGAATCT | ACAGATGGAT  | TGCAACGGGG | 50  |
|    | GATGGAAGTT  | GTCGATACCG | GCAAACCAAT | CTCTGTTCCCT | GTAGGTAAAG | 100 |
|    | AAACATTAGG  | TCGTGTGTTT | AACGTATTAG | GTGAAACGAT  | CGACAAAGAA | 150 |
| 15 | GCACCTTTTC  | CAGAAGATGT | AGAAAAGAGC | GGTATTACACA | AAAAGGCCCC | 200 |
|    | CGCTTTTGAA  | GACCTTAGCA | CCAGTAATGA | GATTTTAGAA  | ACTGGGATCA | 250 |
|    | AGGTTATCGA  | CTTATTAGCC | CCTTACTTAA | AAGGTGGTAA  | AGTTGGACTA | 300 |
|    | TTCGGTGGTG  | CCGGTGTGTT | TAAACCGTC  | TTAATTCAAG  | AACTGATTCA | 350 |
|    | TAATATCGCC  | CAAGAACACG | GTGGGATTTC | TGCTTTTACC  | GGGGTTGGGG | 400 |
| 20 | AACGGACTCG  | TGAAGGGAAC | GACCTTTATT | ATGAAATGAA  | AGAATCCGGC | 450 |
|    | GTTATTGAAA  | AAACAGCGAT | GGTCTTCGGA | CAAATGAATG  | AGCCACCAGG | 500 |
|    | TGCGCGGATG  | CGCGTTGCCT | TGACTGGTTT | GACATTAGCT  | GAATATTTCC | 550 |
|    | GTGATGAAGA  | AGGTCAAGAT | GTGTTGCTAT | TTATCGATAA  | CATTTTCCGC | 600 |
|    | TTCACACAAG  | CCGGATCAGA | AGTTTCGGCG | CTATTAGGTC  | GGATGCCATC | 650 |
| 25 | TGCCGTTGGT  | TATCAACCAA | CCTTGGCAAC | AGAAATGGGT  | CAATTACAAG | 700 |
|    | AACGAATCAC  | TTCAACGAAA | AAAGGCTCAA | TTACATCG    |            | 738 |

2) INFORMATION FOR SEQ ID NO: 1605

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605

ATYATYGAAR TITAYGCICC

20

2) INFORMATION FOR SEQ ID NO: 1606

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606

5 CCRAACATIA YICCIAC TTT TTC

23

## 2) INFORMATION FOR SEQ ID NO: 1607

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Klebsiella ornithinolytica*

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607

|    |   |     |
|----|---|-----|
| 25 | CTGGATTATG CGATGTCGGT CATTGTTGGC CGTGCGCTGC CGGATGTCCG  | 50  |
|    | AGATGGCCTG AAACCGGTAC ACCGTCGCGT ACTTTACGCC ATGAACGTAT  | 100 |
|    | TGGGCAATGA CTGGAACAAA GCCTATAAAA AATCCGCCCC TGTCGTTGGT  | 150 |
|    | GACGTAATCG GTAAATACCA CCCTCATGGT GATACCGCCG TTTATGACAC  | 200 |
|    | CATTGTACGT ATGGCACAGC CATTCTCCTT GCGTTATATG CTGGTCGATG  | 250 |
| 30 | GCCAGGGTAA CTTTCGGTTCT GTCGATGGCG ACTCCGCCGC AGCGATGCGT | 300 |
|    | TATACGGAAA TCCGTATGTC GAAAATCGCC CACGAG                 | 336 |

## 35 2) INFORMATION FOR SEQ ID NO: 1608

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 bases

(B) TYPE: Nucleic acid

40

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608

50

|  |     |
|--|-----|
| CTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG CTGCCGGATG | 50  |
| TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTATA CGCCATGAAC | 100 |
| GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCTG CCCGTGTCGT | 150 |

GGGTGACGTC ATCGGTAAAT ACCACCCTCA TGGTGATACT GCCGTATACG 200  
ACACCATTGT ACGTATGGCG CAGCCATTCT CCCTGCGTTA CATGCTGGTA 250  
GATGGCCAGG GTAACCTTGG TTCGGTCGAC GGC GACTCCG CCGCAGCGAT 300  
GCGTTATACG GAAATCCGTA TGTCGAAGAT CGCCCATGAA C 341

5

## 2) INFORMATION FOR SEQ ID NO: 1609

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609

20 GCCCTGATCC AAATAGCATA TA

22

## 2) INFORMATION FOR SEQ ID NO: 1610

25

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610

35

CCTGGCATAA CAGTAACATT CTG

23

## 40 2) INFORMATION FOR SEQ ID NO: 1611

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
45 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611

TGGGAAAAAG CAACTCCATC TC

22

## 2) INFORMATION FOR SEQ ID NO: 1612

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612

ACAACTGAAT TCGCAGCAAC AAT

23

## 2) INFORMATION FOR SEQ ID NO: 1613

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*  
 (C) ACCESSION NUMBER: U19459

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGAAATATG | GCCCTGATCC | AAATAGCATA | TATCCACATG | AAGAAATAAA | 50  |
| AAGTGTTTGT | TTTATTAAAA | ATACAATTAC | CAATCCAAAT | ATTATAGTTG | 100 |
| GAGATTATAC | TTACTATTCC | GATGTTAACG | GAGCTGAAAA | ATTTGAAGAA | 150 |
| CATGTGACAC | ATCATTATGA | ATTTAGGGGT | GATAAACTTG | TAATTGGCAA | 200 |
| GTTTTGTGCA | ATAGCTGAAG | GTATAGAATT | TATTATGAAT | GGAGCAAACC | 250 |
| ATAGAATGAA | TTCAATAACA | ACTTATCCTT | TTAATATAAT | GGGAAATGGT | 300 |
| TGGGAAAAAG | CAACTCCATC | TCTTGAAGAT | TTACCATTTA | AGGGAGATAC | 350 |
| TGTTGTTGGA | AATGATGTGT | GGATTGGTCA | GAATGTTACT | GTTATGCCAG | 400 |
| GAATTCAAAT | AGGAGATGGA | GCAATTGTTG | CTGCGAATTC | AGTTGTTACA | 450 |
| AAAGATGTAC | CACCATATCG | TATTATTGGT | GGAAATCCGA | GTAGAATTAT | 500 |
| AAAGAAAAGG | TTTGAAGATG | AATTGATAGA | TTATTTATTG | CAAATAAAAT | 550 |
| GGTGGGATTG | GTCAGCACAA | AAAATATTTT | CTAATCTTGA | AACACTTTGT | 600 |
| AGCTCTGATT | TAGAGAAAAT | AAAATCTATT | CGAGATTAG  |            | 639 |

## 2) INFORMATION FOR SEQ ID NO: 1614

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
 (B) TYPE: Nucleic acid



- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614

CCAATCCAGA AGAAATATAC CC

22

10

2) INFORMATION FOR SEQ ID NO: 1615

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615

ATTAGTTTAT CCCCAATCAA TTCA

24

25

2) INFORMATION FOR SEQ ID NO: 1616

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616

40 ATAATGAATG GGGCTAATCA TCGTAT

26

2) INFORMATION FOR SEQ ID NO: 1617

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617

GCCAACAAC GAATAAGGAT CAAC

24

5

2) INFORMATION FOR SEQ ID NO: 1618

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 639 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*  
(C) ACCESSION NUMBER: AF015628

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGAAATGGC | AAAATCAGCA | AGGCCCCAAT | CCAGAAGAAA | TATACCCTAT | 50  |
|    | AGAAGGTAAT | AAACATGTTT | AATTTATTAA | ACCATCTATA | ACAAAGCCCA | 100 |
| 25 | ATATTTTAGT | TGGGGAATAT | TCATATTACG | ATAGTAAAGA | TGGTGAATCT | 150 |
|    | TTTGAAAGCC | AAGTTCTTTA | TCACTATGAA | TTGATTGGGG | ATAAACTAAT | 200 |
|    | ATTAGGGAAG | TTTTGTTCTA | TTGGACCCGG | AACGACATTT | ATAATGAATG | 250 |
|    | GGGCTAATCA | TCGTATGGAT | GGTTCAACAT | TTCCATTCAA | TCTTTTCGGA | 300 |
|    | AATGGTTGGG | AGAAGCATAC | CCCTACATTG | GAAGACCTTC | CTTATAAGGG | 350 |
| 30 | TAACACGGAA | ATTGGGAACG | ATGTTTGGAT | TGGACGAGAT | GTGACAATTA | 400 |
|    | TGCCCCGGTG | AAAATAGGA  | AACGGGGCTA | TTATTGCAGC | AAAATCGGTT | 450 |
|    | GTGACAAAGA | ACGTTGATCC | TTATTAGTTT | GTTGGCGGTA | ATCCTTCACG | 500 |
|    | ATTAATTAAG | ATAAGGTTTT | CCAAGGAAAA | AATCGCAGCA | TTACTAAAAG | 550 |
|    | TAAGGTGGTG | GGACCTAGAG | ATAGAGACGA | TAAATGAAAA | TATTGATTGC | 600 |
| 35 | ATCCTGAATG | GTGATATAAA | AAAGGTTAAA | AGAAGTTAG  |            | 639 |

2) INFORMATION FOR SEQ ID NO: 1619

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619

50

AAGGCAAAAT AAAAGGAGCA AAGC

24

## 2) INFORMATION FOR SEQ ID NO: 1620

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620

TGTACCCGAG ACATCTTCAC CAC

23

## 2) INFORMATION FOR SEQ ID NO: 1621

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621

AATTGAAGGA CGGGTATTGT GGAAAG

26

## 2) INFORMATION FOR SEQ ID NO: 1622

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622

CGATTTTGAC AGATGGCGAT AATGAA

26

## 2) INFORMATION FOR SEQ ID NO: 1623

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1569 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*  
(C) ACCESSION NUMBER: M90056

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623

|    |            |             |             |            |            |      |
|----|------------|-------------|-------------|------------|------------|------|
|    | ATGAAAATAA | TGTTAGAGGG  | ACTTAATATA  | AAACATTATG | TTCAAGATCG | 50   |
|    | TTTATTGTTG | AACATAAATC  | GCCTAAAGAT  | TTATCAGAAT | GATCGTATTG | 100  |
|    | GTTTAATTGG | TAAAAATGGA  | AGTGGAAAAA  | CAACGTTACT | TCACATATTA | 150  |
| 15 | TATAAAAAAA | TTGTGCCTGA  | AGAAGGTATT  | GTAAAACAAT | TTTCACATTG | 200  |
|    | TGAACCTATT | CCTCAATTGA  | AGCTCATAGA  | ATCAACTAAA | AGTGGTGGTG | 250  |
|    | AAGTAACACG | AAACTATATT  | CGGCAAGCGC  | TTGATAAAAA | TCCAGAACTG | 300  |
|    | CTATTAGCAG | ATGAACCAAC  | AACTAECTTA  | GATAATAACT | ATATAGAAAA | 350  |
|    | ATTAGAACAG | GATTTAAAAA  | ATTGGCATGG  | AGCATTATTT | ATAGTTTCAC | 400  |
| 20 | ATGATCGCGC | TTTTTTTAGAT | AACTTGTGTA  | CTACTATATG | GGAAATTGAC | 450  |
|    | GAGGGAAGAA | TAAGTGAATA  | TAAGGGGAAT  | TATAGTAACT | ATGTTGAACA | 500  |
|    | AAAAGAATTA | GAAAGACATC  | GAGAAGAATT  | AGAATATGAA | AAATATGAAA | 550  |
|    | AAGAAAAGAA | ACGATTGGAA  | AAAGCTATAA  | ATATAAAAAG | ACAGAAAGCT | 600  |
|    | CAACGAGCAA | CTAAAAAACC  | GAAAAACTTA  | AGTTTATCTG | AAGGCAAAAT | 650  |
| 25 | AAAAGGAGCA | AAGCCATACT  | TTGCAGGTAA  | GCAAAAGAAG | TTACGAAAAA | 700  |
|    | CTGTAAAATC | TCTAGAAACC  | AGACTAGAAA  | AACTTGAAAG | CGTCGAAAG  | 750  |
|    | AGAAACGAAC | TTCCTCCACT  | TAAAATGGAT  | TTAGTGAACT | TAGAAAGTGT | 800  |
|    | AAAAAATAGA | ACTATAATAC  | GTGGTGAAGA  | TGTCTCGGGT | ACAATTGAAG | 850  |
|    | GACGGGTATT | GTGGAAAGCA  | AAAAGTTTTA  | GTATTTCGCG | AGGAGACAAG | 900  |
| 30 | ATGGCAATTA | TCGGATCTAA  | TGGTACAGGA  | AAGACAACGT | TTATTAAAAA | 950  |
|    | AATTGTGCAT | GGGAATCCTG  | GTATTTTCATT | ATCGCCATCT | GTCAAAATCG | 1000 |
|    | GTTATTTTAT | CCAAAAAATA  | GATACATTAG  | AATTAGATAA | GAGCATTTTA | 1050 |
|    | GAAAATGTTC | AATCTTCTTC  | ACAACAAAAT  | GAAACTCTTA | TTCGAACTAT | 1100 |
|    | TCTAGCTAGA | ATGCATTTTT  | TTAGAGATGA  | TGTTTATAAA | CCAATAAGTG | 1150 |
| 35 | TCTTAAGTGG | TGGAGAGCGA  | GTTAAAGTAG  | CACTAACTAA | AGTATTCTTA | 1200 |
|    | AGTGAAGTTA | ATACGTTGGT  | ACTAGATGAA  | CCAACAAACT | TTCTTGATAT | 1250 |
|    | GGAAGCTATA | GAGGCGTTTG  | AATCTTTGTT  | AAAGGAATAT | AATGGCAGTA | 1300 |
|    | TAATCTTTGT | ATCTCACGAT  | CGTAAATTTA  | TCGAAAAAGT | AGCCACTCGA | 1350 |
|    | ATAATGACAA | TTGATAATAA  | AGAAATAAAA  | ATATTTGATG | GCACATATGA | 1400 |
| 40 | ACAATTTAAA | CAAGCTGAAA  | AGCCAACAAG  | GAATATTAAA | GAAGATAAAA | 1450 |
|    | AACTTTTACT | TGAGACAAAA  | ATTACAGAAG  | TACTCAGTCG | ATTGAGTATT | 1500 |
|    | GAACCTTCGG | AAGAATTAGA  | ACAAGAGTTT  | CAAAACTTAA | TAAATGAAAA | 1550 |
|    | AAGAAATTTG | GATAAATAA   |             |            |            | 1569 |

45

2) INFORMATION FOR SEQ ID NO: 1624

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624

5 TTCTTTAATG CTCGTAGATG AACCTA 26

10 2) INFORMATION FOR SEQ ID NO: 1625

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1625

TTTTTCGTATT CTTCTTGTTG CTTTC 25

25 2) INFORMATION FOR SEQ ID NO: 1626

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626

AGGAATGATT AAGCCCCCTT CAAAAA 26

40 2) INFORMATION FOR SEQ ID NO: 1627

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627

TTACATTGCG ACCATGAAAT TGCTCT

26

## 2) INFORMATION FOR SEQ ID NO: 1628

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1658 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*  
 (C) ACCESSION NUMBER: U82085

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628

|    |             |            |             |            |             |      |
|----|-------------|------------|-------------|------------|-------------|------|
| 20 | ATGCTTAAAA  | TCGACATGAA | GAATGTAAAA  | AAATATTATG | CAGATAAATT  | 50   |
|    | AATTTTAAAT  | ATAAAAGAAC | TAAAGATTTA  | TAGTGGGGAT | AAAATAGGTA  | 100  |
|    | TTGTAGGTAA  | GAATGGAGTT | GGCAAAACAA  | CACTTTAAA  | AATAATAAAA  | 150  |
|    | GGACTAATAG  | AGATTGACGA | AGGAAATATA  | ATTATAAGTG | AAAAACAAC   | 200  |
|    | TATTAAATAT  | ATCTCTCAAT | TAGAAGAACC  | ACATAGTAAG | ATAATTGATG  | 250  |
| 25 | GAAAATATGC  | TTCAATATTT | CAAGTTGAAA  | ATAAGTGGA  | TGACAATATG  | 300  |
|    | AGTGGTGGTG  | AAAAAACTAG | ATTTAACTA   | GCAGAGGGAT | TTCAAGATCA  | 350  |
|    | ATGTTCTTTA  | ATGCTCGTAG | ATGAACCTAC  | AAGTAATTTA | GATATCGAAG  | 400  |
|    | GAATAGAGTT  | GATAACAAAT | ACTTTTAAAG  | AGTACCGTGA | TACTTTTTTG  | 450  |
|    | GTAGTATCTC  | ATGATAGAAT | TTTTTTAGAT  | CAAGTTTGTA | CAAAAATTTT  | 500  |
| 30 | TGAAATTGAA  | AATGGATATA | TTAGAGAATT  | CATCGGTAAT | TATACAAACT  | 550  |
|    | ATATAGAGCA  | AAAAGAAATG | CTTCTACGAA  | AGCAACAAGA | AGAATACGAA  | 600  |
|    | AAGTATAATT  | CTAAAAGAAA | GCAATTGGAG  | CAAGCTATAA | AGCTAAAAGA  | 650  |
|    | GAATAAGGCG  | CAAGGAATGA | TTAAGCCCCC  | TTCAAAAACA | ATGGGAACAT  | 700  |
|    | CTGAATCTAG  | AATATGGAAA | ATGCAACATG  | CTACTAAACA | AAAAAGATG   | 750  |
| 35 | CATAGAAATA  | CGAAATCGTT | GGAAACACGA  | ATAGATAAAT | TAAATCATGT  | 800  |
|    | AGAAAAAATA  | AAAGAGCTTC | CTTCTATTAA  | AATGGATTTA | CCTAATAGAG  | 850  |
|    | AGCAATTTCA  | TGGTCGCAAT | GTAATTAGTT  | TAAAAAACTT | ATCTATAAAA  | 900  |
|    | TTTAATAATC  | AATTTCTTTG | GAGAGATGCT  | TCATTTGTCA | TTAAAGGTGG  | 950  |
|    | AGAAAAGGTT  | GCTATAATTG | GTAACAATGG  | TGTAGGAAAA | ACAACATTGT  | 1000 |
| 40 | TGAAGCTGAT  | TCTAGAAAAA | GTAGAATCAG  | TAATAATATC | ACCATCAGTT  | 1050 |
|    | AAAATTGGAT  | ACGTCAGTCA | AAACTTAGAT  | GTTCTACAAT | CTCATAAATC  | 1100 |
|    | TATCTTAGAA  | AATGTTATGT | CTACCTCCAT  | TCAAGATGAA | ACAATAGCAA  | 1150 |
|    | GAATTGTTCT  | AGCAAGATTA | CATTTTTTATC | GCAATGATGT | TCATAAAGAA  | 1200 |
|    | ATAAATGTTT  | TGAGTGGTGG | AGAACAAATA  | AAGGTTGCTT | TTGCCAAGCT  | 1250 |
| 45 | ATTTGTTAGC  | GATTGTAATA | CATTAATTCT  | TGATGAACCA | ACAACTATT   | 1300 |
|    | TGGATATCGA  | TGCTGTTGAG | GCATTAGAAG  | AATTGTTAAT | TACCTATGAA  | 1350 |
|    | GGTGTGTGTG  | TATTTGCTTC | CCATGATAAA  | AAATTTATAC | AAAACCTAGC  | 1400 |
|    | TGAACAATTG  | TTAATAATAG | AAAATAATAA  | AGTGAAAAAA | TTCGAAGGAA  | 1450 |
|    | CATATATAGA  | ATATTTAAAA | ATTAAAGATA  | AACCAAATTT | AAATACAAAT  | 1500 |
| 50 | GAAAAAGAAC  | TCAAAGAAAA | AAAGATGATA  | CTAGAAATGC | AAATTTTCATC | 1550 |
|    | ATTATTAAAGT | AAAATCTCAA | TGGAAGAAAA  | TGAAGAAAAA | AACAAAGAAT  | 1600 |
|    | TAGATGAAAA  | GTACAAATTG | AAATTAAAAG  | AATTGAAAAG | CCTAAATAAA  | 1650 |
|    | AATATTTA    |            |             |            |             | 1658 |

## 2) INFORMATION FOR SEQ ID NO: 1629

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629

AAGGGGAAAG TTTGGATTAC ACAACA

26

## 2) INFORMATION FOR SEQ ID NO: 1630

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630

GAACCACAGG GCATTATCAG AACC

24

## 2) INFORMATION FOR SEQ ID NO: 1631

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631

CGACGATGCT TTATGGTTTG T

21

## 2) INFORMATION FOR SEQ ID NO: 1632

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632

GTTAATTTGC CTATCTTGTC ACACTC

26

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2) INFORMATION FOR SEQ ID NO: 1633

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 900 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*  
(C) ACCESSION NUMBER: M36022

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGGAATTTA | AATTACAAGA | ATTAAATCTT | ACTAACCAAG | ATACAGGACC | 50  |
|    | ATATGGTATA | ACCGTTTCAG | ATAAGGGGAA | AGTTTGGATT | ACACAACATA | 100 |
|    | AAGCAAATAT | GATAAGTTGC | ATCAATTTAG | ATGGAAAAAT | TACAGAGTAC | 150 |
| 30 | CCACTACCGA | CACCAGATGC | AAAAGTCATG | TGTTTAACTA | TATCCTCAGA | 200 |
|    | TGGGGAAGTT | TGGTTTACTG | AGAATGCAGC | AAACAAAATA | GGGAGGATTA | 250 |
|    | CAAAAAAAGG | GATTATTAAG | GAATATACAT | TGCCTAACCC | AGATTCAGCA | 300 |
|    | CCCTACGGTA | TTACAGAAGG | ACCAAATGGA | GATATATGGT | TTACAGAAAT | 350 |
|    | GAATGGCAAC | CGTATTGGAC | GTATTACGGA | CGACGGTAAA | ATTCGTGAAT | 400 |
| 35 | ACGAGCTGCC | TAATAAAGGA | TCTTACCCTT | CTTTTATCAC | TTTGGGTTCT | 450 |
|    | GATAATGCCC | TGTGGTTCAC | AGAAAATCAA | AATAATGCTA | TTGGTAGAAT | 500 |
|    | TACAGAAAGT | GGGGATATTA | CAGAGTTTAA | AATTCCTACA | CCTGCATCAG | 550 |
|    | GACCAGTTGG | TATTACAAAG | GGGAACGACG | ATGCTTTATG | GTTTGTGGAA | 600 |
|    | ATTATCGGTA | ATAAGATAGG | GCGAATAACT | CCTCTGGGGG | AAATTACCGA | 650 |
| 40 | ATTCAAAATT | CCAACGCCAA | ACGCTCGACC | TCATGCAATT | ACTGCTGGAG | 700 |
|    | CAGGAATTGA | TTTATGGTTT | ACTGAATGGG | GGGCTAATAA | AATAGGAAGG | 750 |
|    | CTGACAAGCA | ATAATATAAT | TGAGGAATAC | CCAATTCAAA | TCAAAAGTGG | 800 |
|    | TGAACCACAT | GGCATTGTGT | TCGATGGTGA | AACAATTTGG | TTTGCAATGG | 850 |
|    | AGTGTGACAA | GATAGGCAAA | TTAACTCTCA | TTAAGGATAA | TATGGAGTGA | 900 |

45

2) INFORMATION FOR SEQ ID NO: 1634

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single



(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634

TTAACTTGTC TATTCCCGAT TCAGG

25

10

2) INFORMATION FOR SEQ ID NO: 1635

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635

GCTGTGGCAA TGGATATTCT GTA

23

25

2) INFORMATION FOR SEQ ID NO: 1636

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636

TTCCTACCCC TGATGCTAAA GTGA

24

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2) INFORMATION FOR SEQ ID NO: 1637

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637

CAAAGTGCGT TATCCGAACC TAA

23

5

## 2) INFORMATION FOR SEQ ID NO: 1638

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 527 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: WSA-172

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GGTGGGGAAG | ACTGTCTTCA | TCCAGGAATT | GATTGTGAGT | CGTTCCACAT | 50  |
|    | GCTCACCTAG | TTTTCGCTCG | ATCTTTTCAC | TAACGCAAAC | CATGTAGAAC | 100 |
|    | AACATTGCCA | AGGCCACGG  | TGGTTACTCC | GTCTTCACTG | GTGTTGGTGA | 150 |
| 25 | GCGTACTCGT | GAGGGTAACG | ATCTGTACCA | CGAAATGCAG | GAGACTGGTG | 200 |
|    | TCATTACGCT | CGAGGGTGAA | TCCAAGGTCG | CACTGGTGTT | CGGACAGATG | 250 |
|    | AACGAGCCCC | CCGGTGCCCG | TGCCCGTGTC | GCCCTTACCG | GTCTGACCAT | 300 |
|    | TGCCGAGTAC | TTCCGTGACG | AGGAGGGTCA | GGACGTGCTG | CTCTTCATTG | 350 |
|    | ACAACATTTT | CCGTTTCACC | CAGGCCGGTT | CTGAGGTGTC | TGCCCTTCTC | 400 |
| 30 | GGTCGTATCC | CCTCTGCCGT | CGGTTACCAG | CCCACCCTGG | CCGTCGACAT | 450 |
|    | GGGTGGTATG | CAGGAGCGTA | TCACCACCAC | CAAGAAGGGT | TCTATTACCT | 500 |
|    | CCGTCCARGC | CGTCTACGTC | CCCGCGA    |            |            | 527 |

35

## 2) INFORMATION FOR SEQ ID NO: 1639

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 452 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

45

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: ATCC 64746

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639

|  |            |            |            |            |            |     |
|--|------------|------------|------------|------------|------------|-----|
|  | ACTGTCTTGA | TTCAAGAACT | TATTAACAAC | ATTGCTAAAG | CCCATGGTGG | 50  |
|  | TTACTCTATT | TTCTGTGGTG | TTGGTGAACG | TACTCGTGAA | GGTAACGATT | 100 |

|   |            |            |            |            |            |     |
|---|------------|------------|------------|------------|------------|-----|
|   | TATACCACGA | AATGATGGAA | ACTGGTGTCA | TTAAACTTGA | AGGTGACTCC | 150 |
|   | AAGTGTGCTC | TTGTATTCGG | TCAAATGAAC | GAACCTCCTG | GTGCTCGTGC | 200 |
|   | CCGTGTTGCT | TTAACTGGTT | TAACCATTGC | TGAATACTTC | CGTGATGAAG | 250 |
|   | AAGGTCAAGA | TGTGTTACTT | TTCATTGATA | ACATTTTCCG | TTTCACTCAA | 300 |
| 5 | GCTGGTTCTG | AAGTATCTGC | CCTTTTAGGT | CGTATTCCAT | CTGCTGTAGG | 350 |
|   | TTACCAACCC | ACTTTATCTA | CTGATATGGG | TGGTATGCAA | GAACGTATTA | 400 |
|   | CTACTACCAA | GAATGGTTCC | ATTACCTCTG | TACARGCCGT | CTACGTCCCC | 450 |
|   | GC         |            |            |            |            | 452 |

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## 2) INFORMATION FOR SEQ ID NO: 1640

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 783 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*  
 (B) STRAIN: ATCC 6462  
 25 (C) ACCESSION NUMBER:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | ACGCCCTTAC | GGTAAAACAA | AGCAACGAAA | ACGGAAGCAT  | GAAGTTAACA | 50  |
| 30 | TTTGAAGTTG | CACTTCATTT | AGGTGATGAT | ACAGTTCGTA  | CAGTTGCGAT | 100 |
|    | GTCTTCCACA | GATGGACTTG | TTCGTGGCAC | AGAAGTAGAA  | GATACTGGTA | 150 |
|    | AAGCAATCTC | TGTACCAGTT | GGTGATGCAA | CACTTGGTCG  | TGTATTCAAC | 200 |
|    | GTATTAGGTG | ATGCAATTGA | CTTAGATGGT | GAAGTTCCCTG | CGGATGTACA | 250 |
|    | CCGTGATCCA | ATTCACCGTC | AAGCACCTGC | ATTCGAAGAA  | TTATCTACTA | 300 |
| 35 | AAGTAGAAAT | TCTTGAAACT | GGTATTAAAG | TAGTAGACTT  | ACTTGCTCCT | 350 |
|    | TACATTAAGG | GTGGTAAGAT | CGGCCTATTC | GGTGGTGCCG  | GCGTAGGTAA | 400 |
|    | AACAGTATTA | ATTCAGAAGT | TAATTAACAA | CATCGCACAA  | GAGCACGGTG | 450 |
|    | GTATCTCTGT | ATTCGCTGGT | GTAGGTGAGC | GTAATCGTGA  | GGGTAATGAC | 500 |
|    | TTATACCATG | AAATGAGCGA | TTCTGGCGTA | ATCAAGAAAA  | CTGCGATGGT | 550 |
| 40 | ATTCGGACAA | ATGAATGAGC | CACCTGGAGC | ACGTCAACGT  | GTTGCATTAA | 600 |
|    | CAGGTTTAAC | AATGGCTGAG | CATTTCCGTG | ATGAGCAAGG  | ACAAGACGTA | 650 |
|    | CTTCTGTTCA | TCGATAACAT | CTTCCGTTTC | ACGCAAGCGG  | GTTCTGAAGT | 700 |
|    | ATCTGCCCTT | CTTGGTCTGA | TGCCATCTGC | GGTAGGTTAC  | CAACCAACAC | 750 |
|    | TTGCAACAGA | AATGGGTCAA | TTACAAGAGC | GTA         |            | 783 |

45

## 2) INFORMATION FOR SEQ ID NO: 1641

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 823 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL NRS-319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641

10 ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAGCAAGCAT 50  
 TAACTTAACA TTTGAAGTTG CACTTCATTT AGGTGATGAC ACAGTTCGTA 100  
 CAGTTGCAAT GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA 150  
 GATACTGGTA AAGCAATCTC TGTACCAGTT GGTGATGCAA CACTTGGTCG 200  
 15 TGTATTCAAC GTATTAGGTG ATGCAATTGA CTTAGATGGT GATGTTCTTG 250  
 CGGATGTACG TCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCGAAGAA 300  
 CTATCTACTA AAGTAGAAAT TCTTGAAACT GGTATTAAAG TAGTAGACTT 350  
 ACTTGCTCCT TACATTAAGG GTGGTAAGAT CGGTCTATTC GGTGGTGCCG 400  
 GTGTAGGTAA AACAGTATTA ATTCAGGAAT TAATTAACAA CATCGCACAA 450  
 20 GAACACGGTG GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTACTCGTGA 500  
 GGGTAACGAC TTATACCATG AAATGAGCGA TTCTGGCGTA ATTAAGAAAA 550  
 CTGCGATGGT ATTCGGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT 600  
 GTTGCAATTA CAGGTTTAAC AATGGCTGAA CATTTCCGTG ATGAGCAAGG 650  
 ACAAGACGTA CTATTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCAG 700  
 25 GTTCTGAAGT ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC 750  
 CAACCAACAC TTGCAACAGA AATGGGTCAA TTACAAGAGC GTATTACATC 800  
 TACAAATAAA GGATCTATCA CGT 823

30

2) INFORMATION FOR SEQ ID NO: 1642

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL BD-15

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642

50 GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAAAG 50  
 CAACGAAAAC GGAGCAAACA TTAACCTAAC ATTTGAAGTT GCACTTCATT 100  
 TAGGTGATGA TACAGTTCGT ACAGTTGCGA TGTCTTCCAC AGATGGACTT 150  
 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT 200  
 TGGTGATGTA ACACTTGGTC GTGTATTCAA CGTATTAGGT GATGCAATTG 250  
 ACTTAGATGG TGAAGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT 300  
 CAAGCACCTG CATTCGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC 350

|    |             |            |            |             |            |     |
|----|-------------|------------|------------|-------------|------------|-----|
|    | TTGGTATTAAA | GTAGTAGACT | TACTTGCTCC | TTACATTAAAG | GGTGGTAAGA | 400 |
|    | TTGGTCTATT  | CGGTGGTGCC | GGTGTAGGTA | AAACAGTATT  | AATTCAGGAA | 450 |
|    | TTAATTAACA  | ACATCGCACA | AGAACACGGT | GGTATCTCTG  | TATTCGCCGG | 500 |
|    | TGTAGGTGAG  | CGTACTCGTG | AAGGTAACGA | CTTATACCAC  | GAAATGAGCG | 550 |
| 5  | ATTCTGGCGT  | AATTAAGAAA | ACTGCGATGG | TATTCGGACA  | AATGAACGAG | 600 |
|    | CCACCTGGAG  | CACGTCAACG | TGTTGCATTA | ACAGGTTTAA  | CAATGGCTGA | 650 |
|    | GCATTTCCGT  | GATGAGCAAG | GACAAGACGT | ACTACTGTTC  | ATCGATAACA | 700 |
|    | TCTTCCGTTT  | CACGCAAGCA | GGTTCTGAAG | TATCTGCCCT  | TCTTGGTCGT | 750 |
|    | ATGCCATCTG  | CGGTAGGTTA | CCAGCCAACA | CTTGCAACAG  | AAATGGGTCA | 800 |
| 10 | ATTACAAGAG  | CGTATTACAT | CTACAAATA  |             |            | 829 |

## 2) INFORMATION FOR SEQ ID NO: 1643

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycooides*  
 (B) STRAIN: NRRL BD-10

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 30 | AATCTACAAT | GCCCTTACGG | TAAAACAAAG | CAACGAAAAC | GGAGCAAGCA | 50  |
|    | TTAACTTAAC | ATTTGAAGTT | GCACTTCATT | TAGGTGATGA | CACAGTTCGT | 100 |
|    | ACAGTTGCGA | TGTCTTCCAC | AGATGGACTT | GTTCTGTGCA | CAGAAGTAGA | 150 |
|    | AGATACTGGT | AAACCAATCT | CTGTACCGGT | TGGTGATGCA | ACACTTGGTC | 200 |
|    | GTGTATTTAA | CGTATTAGGT | GATGCAATTG | ACTTAGATGG | TGAAGTTCCT | 250 |
| 35 | GCGGATGTAC | GCCGTGATCC | AATTCACCGT | CAAGCACCTG | CGTTCGAAGA | 300 |
|    | GTTATCTACG | AAAGTAGAAA | TTCTTGAAAC | TGGTATTAAA | GTAGTAGACT | 350 |
|    | TACTTGCTCC | TTACATTAAA | GGTGGTAAAA | TCGGTCTATT | CGGTGGTGCC | 400 |
|    | GGTGTAGGTA | AAACAGTATT | AATCCAGGAA | TTAATTAACA | ACATCGCACA | 450 |
|    | AGAGCACGGT | GGTATTTCTG | TATTCGCTGG | TGTAGGTGAG | CGTACTCGTG | 500 |
| 40 | AAGGTAATGA | CTTATACCAC | GAAATGAGCG | ATTCTGGCGT | AATCAAGAAA | 550 |
|    | ACAGCGATGG | TATTCGGACA | AATGAACGAG | CCACCTGGTG | CACGTCAACG | 600 |
|    | TGTTGCATTA | ACAGGATTAA | CAATGGCTGA | ACATTTCCGT | GATGAGCAAG | 650 |
|    | GACAAGACGT | ACTATTGTTC | ATCGATAACA | TCTTCCGTTT | CACGCAAGCG | 700 |
|    | GGTTCTGAAG | TATCTGCCCT | TCTTGGTCGT | ATGCCATCTG | CGGTAGGTTA | 750 |
| 45 | CCAACCAACT | CTTGCAACAG | AAATGGGTCA | ATTACAAGAG | CGTATTACAT | 800 |
|    | CTACAAATAA | AGGATCTATC | ACG        |            |            | 823 |

## 50 2) INFORMATION FOR SEQ ID NO: 1644

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
- (B) STRAIN: NRRL B-617

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | GGAAAGCTAC | CTGAAATCTA | CAATGCCCTT | AGAATTAAAC | AAGACGCAGT  | 50  |
|    | TAACTTAACT | TTAGAAGTTG | CACTTCACTT | AGGTGATGAT | ACAGTTCGTA  | 100 |
| 15 | CAGTTGCGAT | GTCTTCCACA | GACGGACTTG | TTCGTGGTAC | TGCAGTAGAA  | 150 |
|    | GATACTGGCA | AAGCGATTTC | TGTTCCAGTT | GGTGATGCAA | CACTTGGTTCG | 200 |
|    | TGTATTTAAC | GTATTAGGTG | ATGCAATTGA | CTTAGATGGT | GAGGTTCCAG  | 250 |
|    | CAGATGTACG | CCGTGATCCA | ATTCACCGTC | AAGCACCTGC | ATTCGAAGAG  | 300 |
|    | TTATCTACAA | AAGTAGAAAT | TCTTGAAACT | GGTATTAAAG | TAGTAGACTT  | 350 |
| 20 | ACTTGCTCCT | TACATTAAAG | GTGGTAAAAT | CGGTCTATTC | GGTGGTGCCG  | 400 |
|    | GTGTAGGTAA | AACAGTATTA | ATTCAGGAAT | TAATTAACAA | CATCGCACAA  | 450 |
|    | GAGCACGGTG | GTATCTCTGT | ATTCGCTGGT | GTAGGTGAGC | GTACTCGTGA  | 500 |
|    | AGGTAACGAC | TTATACCATG | AAATGAGCGA | TTCTGGCGTA | ATCAAGAAAA  | 550 |
|    | CTGCGATGGT | ATTCGGACAA | ATGAACGAGC | CACCTGGTGC | ACGTCAACGT  | 600 |
| 25 | GTTGCATTAA | CAGGTTTAAC | AATGGCTGAA | CATTTCCGTG | ATGAGCAAGG  | 650 |
|    | ACAAGACGTA | CTATTGTTCA | TCGATAACAT | CTTCCGTTTC | ACGCAAGCGG  | 700 |
|    | GTTCTGAA   |            |            |            |             | 708 |

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2) INFORMATION FOR SEQ ID NO: 1645

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- 35 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
- (B) STRAIN: ATCC 35567

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | GTACGATGCG | CTTGAAGTTC | AAAACGATGT | CAAAC TAGTG | CTGGAAGTTC | 50  |
|    | AACAGCAGCT | CGGTGGTGGT | GTCGTTCTGT | GTATCGCTAT  | GGGTACCTCA | 100 |
|    | GATGGCCTAA | GCCGCGGTCT | GAAAGTACTT | GATTTAGAAC  | ACCCTATCGA | 150 |
| 50 | AGTTCCTGTC | GGTGTGGCAA | CTCTGGGCCG | TATTATGAAC  | GTGCTTGGTG | 200 |
|    | AGCCTATCGA | TATGAAGGGT | GACATTGGTG | AAGAAGAGCG  | TTGGGCTATC | 250 |
|    | CATCGCGCTG | CACCAAGCTA | CGAAGATTTA | TCCAGTGCTA  | ACGAACTGCT | 300 |
|    | GGAAACGGGC | ATCAAGGTTA | TCGACCTGAT | TTGTCCGTTT  | GCCAAAGGCG | 350 |

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GTAAAGTTGG TCTGTTTGGT GGTGCCGGCG TAGGTAAAC GGTAAACATG 400
ATGGAGCTGA TTCGTAATAT TGCGACTGAG CACTCAGGT ACTCTGTATT 450
TGCCGGCGTT GGTGAGCGTA CTCGTGAGGG TAATGACTTC TACCACGAAA 500
TGACAGAATC TAACGTATTA GACAAAGTAT CTCTGGTTTA TGGCCAAATG 550
5 AATGAGCCAC CGGGAAACCG TCTGCGCGTT GCGTTAACCG GCCTGACCAT 600
GGCGGAAAAA TTCCGTGATG AAGGCCGTGA CGTTCTGCTG TTTATCGATA 650
ACATTTATCG TTATACCTTA GCCGGTACAG AAGTATCAGC ACTGTTAGGT 700
CGTATGCCAT CAGCGGTAGG TTACCAACCA ACGCTGGCGG AAGAGATGGG 750
TACACTGCAA GAACGTATCA CYTCAACC 778
10

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## 2) INFORMATION FOR SEQ ID NO: 1646

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15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 806 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
20
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Buttiauxella agrestis
25 (B) STRAIN: ATCC 33320

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646

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GATGCCGTAC CAAAAGTGTA CGACGCTCTT GAGGTTACAA ATGGTAAAGA 50
30 CCGTCTGGTG CTGGAAGTTC AGCAACAGTT AGGTGGTGGC GTAGTGCGTA 100
CTATCGCCAT GGGTACTTCT GATGGTTTGC GTCGTGGTCT GGAAGTTTCT 150
AACCTCGATC ACCCAATTGA AGTGCCAGTA GGTAAAGCAA CTCTGGGCCG 200
TATCATGAAC GTCCTGGGCG AGCCTATCGA CATGAAAGGC GATATCGGCG 250
AAGAAGAGCG TTGGGCGATT CACCGTGCTG CTCCTAGCTA CGAAGAACTG 300
35 TCTAGCTCCC AGGATCTGCT GGAAACCGGC ATCAAAGTAA TGGACCTGAT 350
TTGCCCGTTC GCTAAGGGTG GTAAAGTCGG TCTGTTTCGGT GGTGCGGGTG 400
TGGGTAAAAC TGTAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ACTCAGTGTT TGCAGGCGTG GGGGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCATGAAA TGACCGATTC CAACGTTCTG GACAAAGTAT 550
40 CACTGGTTTA TGGCCAGATG AACGAGCCAC CAGGTAACCG TCTGCGCGTT 600
GCGTTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA 650
CGTTCTGCTG TTCGTTGATA ACATTTACCG TTATACCCTG GCCGGTACAG 700
AAGTATCTGC GCTGCTGGGT CGTATGCCAT CTGCGGTAGG TTACCAGCCA 750
ACTCTGGCAG AAGAGATGGG TGTTTTGCAG GAGCGTATTA CCTCCACCAA 800
45 AACTGG 806

```

## 2) INFORMATION FOR SEQ ID NO: 1647

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50 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1122 bases
    (B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegica*  
(B) STRAIN: ATCC 36586

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | GAAACCGTTG | TTGACACTGG | TTCCCCAATC | ACCGTCCCAG | TTGGTCGTGA | 50   |
|    | AACCTTGGGT | CGTATCATTA | ACGTTATCGG | TGAACCAATC | GATGAACGTG | 100  |
|    | GTCCAATCAA | CACCAAGCAA | AGAAACCCAA | TCCATGCTGA | TCCTCCTTCA | 150  |
| 15 | TTTGCTGAAC | AATCCACTTC | TGCTGAAGTT | TTAGAAACCG | GTATTAAAGT | 200  |
|    | TGTCGATTTA | TTGGCTCCTT | ATGCCAGAGG | TGGTAAAATT | GGTTTATTCG | 250  |
|    | GTGGTGCCGG | TGTCGGTAAA | ACCGTCTTTA | TCCAAGAATT | GATTAACAAC | 300  |
|    | ATTGCTAAAG | CTCATGGTGG | TTTCTCAGTC | TTCACCGGTG | TCGGTGAAAG | 350  |
|    | AACCAGAGAA | GGTAACGATT | TATACCGTGA | AATGAAAGAA | ACCGGTGTCA | 400  |
| 20 | TTAACTTGGA | AGGTGACTCT | AAAGTCGCTT | TAGTCTTCGG | TCAAATGAAC | 450  |
|    | GAACCTCCAG | GTGCTAGAGC | CCGTGTTGCC | TTAACCGGTC | TAACCATTGC | 500  |
|    | TGAATACTTC | AGAGATGAAG | AAGGTCAAGA | TGTCTTGTTA | TTCGTTGATA | 550  |
|    | ACATTTTCAG | ATTCACCCAA | GCTGGTTCAG | AAGTCTCTGC | CTTATTAGGT | 600  |
|    | CGTATTCCAT | CTGCTGTCGG | TTATCAACCA | ACCTTGGCCA | CTGATATGGG | 650  |
| 25 | TTTGTTGCAA | GAACGTATCA | CCACCACCAG | AAAAGGTTCC | GTCACTTCTG | 700  |
|    | TCCAAGCTGT | TTATGTCCCA | GCTGATGATT | TGACTGATCC | TGCCCCAGCC | 750  |
|    | ACCACTTTCG | CGCATTTGGA | TGCTACTACT | GTCTTGTCTC | GTGGTATCTC | 800  |
|    | AGAATTGGGT | ATCTACCCAG | CTGTGCATCC | ATTGGATTCC | AAATCAAGAT | 850  |
|    | TATTAGATGC | CGCTGTTGTT | GGTCAAGAAC | ATTACGATGT | TGCTACTCAA | 900  |
| 30 | GTTCAACAAA | CTTTACAAGC | CTACAAATCT | TTACAAGATA | TTATCGCTAT | 950  |
|    | TTTAGGTATG | GATGAATTAT | CAGAACAAGA | TAAATTGACC | GTTGAAAGAG | 1000 |
|    | CTAGAAAGAT | CCAACGTTTC | TTATCTCAAC | CATTTGCTGT | CGCTGAAGTT | 1050 |
|    | TTCACTGGTA | TTCCAGGTAG | ATTAGTTAGA | TTGAAAGAAA | CCGTTGCTTC | 1100 |
| 35 | ATTCAGAGAC | GTTTTAGCTG | GT         |            |            | 1122 |

## 2) INFORMATION FOR SEQ ID NO: 1648

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
(B) STRAIN: ATCC 700677

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648



|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | TACGTCTCTT | ACCCTGACGA | TGATTTGCAA  | GTCGCATCTA | CGGTCGTAGA | 50  |
|    | TGTTTCAAAT | GGTAAAGTCA | TCGCCCAACT  | TGGAGCTCGT | CACCAAGCAA | 100 |
|    | GTAACGTTTC | ATTTGGTACC | AACCAAGCTG  | TGGAAACCAA | TCGTGACTGG | 150 |
|    | GGATCAACTA | TGAAACCAAT | CACAGACTAT  | GCTCCTGCCT | TGGAGTACGG | 200 |
| 5  | TGTCTACGAT | TCAACTGCTA | CTATCGTTCA  | CGATGAGCCC | TATAACTACC | 250 |
|    | CTGGGACAGA | TATCCCTCTC | TATAACTGGG  | ATCGAGCATA | TTTCGGTAAT | 300 |
|    | ATTACTCTGC | AATATGCCCT | TCAACAATCT  | CGTAACGTAC | CTGCCGTTGA | 350 |
|    | AACACTAAAC | AAGGTCGGTC | TAGATAAGGC  | TAAAACCTTC | CTTAATGGTC | 400 |
|    | TTGGTATCGA | CTATCCAAGC | ATGCATTATG  | CAAACGCCAT | TTCAAGTAAT | 450 |
| 10 | ACAACTGAAT | CCAACAAAAA | ATATGGTGCA  | AGTAGTGAAA | AAATAGCTAC | 500 |
|    | CGCCTATGCC | GCATTCGCAA | ATGGTGGTAT  | TTACCACAAA | CCAATGTACA | 550 |
|    | TCAATAAAGT | TGTCTTTAGC | GATGGTAGCG  | AAAAAGAATT | TTCTGACCCT | 600 |
|    | GGCACAAGAG | CCATGAAAGA | AACGACTGCT  | TACATGATGA | CAGAAATGAT | 650 |
|    | GAAAACAGTC | TGGACGTACG | GAAC TGGTCG | TGGTGCCTAC | CTGCCTTGGC | 700 |
| 15 | TTCCTCAAGC | TGGTAAAACA | GGTACCTCTA  | ACTATACTGA | CGAAGAAATT | 750 |
|    | GAAAAGTATA | TCAAGAACAC | TGGTTACGTA  | GCTCCAGATG | AAATGTTTGT | 800 |
|    | GGGTTATACC | CGT        |             |            |            | 813 |

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## 2) INFORMATION FOR SEQ ID NO: 1649

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter lari*  
 (B) STRAIN: ATCC 43675

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATTAATGAAG | CTATTGTTGT | TAATTATGAA | TTAGAAGGAA | AAGAATGCAA | 50  |
|    | GCTAGTTCTT | GAAGTAGCTG | CACATTTAGG | CGATAATAAA | GTAAGAACCA | 100 |
|    | TCGCTATGGA | TATGACAGAT | GGTCTTGTTA | GAGGTTTAAC | AGCCGTCGCA | 150 |
| 40 | ACTGGAAATC | CAATTAGTGT | TCCAGTAGGC | GAAAAAGTTC | TTGGAAGAAT | 200 |
|    | TTTTAATGTA | ACGGGTGATT | TGATTGATGA | GGGCGAAGAA | ATCAATTTTG | 250 |
|    | ATAAGCACTG | GTCAATTCAT | AGAGATCCAC | CTCCATTTGA | AGAACAAAGT | 300 |
|    | ACAAAAAGCG | AAATCTTTGA | AACAGGTATA | AAGTTTGTTG | ATTTGCTAGC | 350 |
|    | TCCTTATGCT | AAAGGTGGAA | AAGTTGGTCT | TTTTGGTGGT | GCAGGTGTTG | 400 |
| 45 | GTAAAACCGT | TATTATTATG | GAATTAATTC | ACAATGTTGC | ATTTAAACAT | 450 |
|    | AGCGGATATT | CTGTTTTTGC | AGGTGTTGGC | GAAAGAAGTC | GTGAGGGTAA | 500 |
|    | TGACCTTTAC | AATGAAATGA | AAGAAAGTAA | TGTATTAGAT | AAAGTTGCAT | 550 |
|    | TGTGTTATGG | TCAAATGAAT | GAACCACCAG | GGGCAAGAAA | TCGTATAGCT | 600 |
|    | TTAACAGGTC | TTACTATGGC | TGAGTATTTT | AGAGATGAAA | TGGGACTTGA | 650 |
| 50 | TGTTTTAATG | ATTATTGATA | ATATTTTCAG | ATTTTCTCAA | TCAGGCTCAG | 700 |
|    | AAATGTCAGC | ACTTTTAGGA | AGAATTCCTT | CAGCTGTTGG | TTATCAACCA | 750 |
|    | ACCTTAGCTA | GTGAAATGGG | TAAGTTCCAA | GAAAGAATTA | CTTCAACCAA | 800 |
|    | GAAAGGATCT | ATT        |            |            |            | 813 |

## 2) INFORMATION FOR SEQ ID NO: 1650

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*  
 (B) STRAIN: WSA-222

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GGTGGGGAAG | ACTGTGTTCA | TTCAGGAATT | GATTGTAAGT | TCTGTTATCA | 50  |
| ACTAAAGCCG | ACAGCGGTTG | CTGATATGCT | CTAGAACAAC | ATTGCTAAGG | 100 |
| CTCACGGTGG | TTACTCCGTG | TTCAGTGGTG | TCGGTGAGCG | TACCCGTGAG | 150 |
| GGTAACGATT | TGTACCATGA | AATGCAAGAG | ACCCGTGTCA | TTCAACTCGA | 200 |
| CGGAGAGTCC | AAGGTCGCTC | TTGTCTTCGG | TCAAATGAAC | GAGCCCCCTG | 250 |
| GTGCCCCGTG | CCGTGTTGCC | CTTACCGGTT | TGACCATTGC | TGAATACTTC | 300 |
| CGTGACGAGG | AAGGCCAAGA | CGGTAGGCTT | CATGCTTCTA | TCGCTAGGGG | 350 |
| CGTGTGATAC | AGGAGGCTAA | TCGCTTTTCT | AGTGCTTCTC | TTTATTGACA | 400 |
| ACATTTTCCG | TTTCACTCAA | GCTGGTTCTG | AAGTGTCTGC | CTTGCTCGGT | 450 |
| CGTATTCCTT | CCGCTGTCGG | TTACCAACCT | ACTCTCGCCG | TCGACATGGG | 500 |
| TGTTATGCAG | GAACGTATCA | CCACCACCAC | CAAGGGATCC | ATTACTTCAG | 550 |
| TGCARGCCGT | CTACGTCCCC |            |            |            | 570 |

## 2) INFORMATION FOR SEQ ID NO: 1651

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*  
 (B) STRAIN: ATCC 10784

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TGTCTTCATC | CAGGAGTTAA | TTGTACGTTT | TTTGTCTGCC | TACTATAATA | 50  |
| GACGAAGAAA | TATTTTGATT | TATTTTCTA  | ATAATTCAA  | TAGAACAACA | 100 |
| TTGCCAAAGC | CCACGGTGGT | TACTCTGTCT | TCAGTGGTGT | TGGCGAGCGG | 150 |
| ACCCGTGAAG | GAAACGATCT | GTACCACGAA | ATGCAGGAGA | CCCGTGTCT  | 200 |
| CCAGCTCGAT | GGCGAGTCCA | AGGTCGCCCT | CGTCTTCGGT | CAAATGAACG | 250 |
| AACCCCCCGG | AGCCCGTGCC | CGTGTTGCCC | TCAGTGGTCT | GACCGTTGCT | 300 |

|   |            |            |            |            |             |     |
|---|------------|------------|------------|------------|-------------|-----|
|   | GAATACTTCC | GTGACGAGGA | AGGTCAAGAT | GGTGCGTATA | TATATATTCTG | 350 |
|   | CCAGTAATTT | GACTCGAAGC | TCCACTCACA | CATATATTAG | TGCTCCTCTT  | 400 |
|   | CATCGACAAC | ATTTTCCGCT | TCACCCAGGC | AGGTTCCGAA | GTGTCCGCCC  | 450 |
|   | TGCTCGGCCG | TATCCCCTCC | GCCGTCGGTT | ACCAGCCCAC | CCTCGCTGTC  | 500 |
| 5 | GACATGGGTA | TGATGCAGGA | ACGTATCACC | ACCACCACCA | AGGGCTCCAT  | 550 |
|   | CACCTCCGTG |            |            |            |             | 560 |

10 2) INFORMATION FOR SEQ ID NO: 1652

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*  
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 25 | CCACAAGTGT | ACAGCGCCCT | TGAGGTTAAA | AATGGTGATG | CTCGTCTGGT | 50  |
|    | GCTGGAAGTT | CAGCAGCAGC | TGGGCGGTGG | CGTGGTTCGT | ACCATCGCCA | 100 |
|    | TGGGTTCTTC | AGACGGCCTT | AAGCGTGGTC | TGGAAGCCGT | TGACCTTCAG | 150 |
|    | CACCCAATTG | AAGTACCGGT | AGGTACTGCC | ACACTTGGCC | GTATCATGAA | 200 |
| 30 | CGTGCTGGGT | GAGCCGATCG | ATATGAAAGG | CGACATTGGC | GAAGAAGAGC | 250 |
|    | GCTGGGCGAT | TCACCGCTCT | GCACCTTCTT | ACGAAGATCA | GTCGAACTCT | 300 |
|    | CAGGATCTGC | TGGAAACCGG | CATCAAGGTG | ATTGACCTGA | TGTGTCCGTT | 350 |
|    | CGCCAAGGGC | GGTAAAGTCG | GCTTGTTTCG | TGGTGCGGGC | GTAGGTAAAA | 400 |
|    | CCGTCAACAT | GATGGAGCTT | ATTCGTAACA | TTGCGGCTGA | GCACTCAGGT | 450 |
| 35 | TTCTCGGTAT | TTGCCGGTGT | GGGTGAGCGT | ACCCGTGAAG | GTAACGACTT | 500 |
|    | CTACCACGAA | ATGACCGACT | CCAACGTTAT | CGACAAAGTT | TCGCTGGTCT | 550 |
|    | ATGGTCAGAT | GAACGAGCCA | CCGGGTAAAC | GTCTGCGCGT | TGCGCTGACC | 600 |
|    | GGTCTGACCA | TGGCGGAGAA | GTTCCGTGAC | GAAGGTCGTG | ACGTACTGCT | 650 |
|    | GTTTATCGAT | AACATCTATC | GTTACACCCT | GGCCGGTACT | GAAGTCTCCG | 700 |
| 40 | CTCTGCTGGG | TCGTATGCCT | TCTGCGGTAG | GTTACCAGCC | AACGCTGGCG | 750 |
|    | GAAGAGATGG | GCGTTCTGCA | GGAACGTATC |            |            | 780 |

45 2) INFORMATION FOR SEQ ID NO: 1653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 bases  
 (B) TYPE: Nucleic acid  
 50 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
|    | TGTGTTTCATT | CAGGAGCTGA | TTGTGAGTAC | CCCGGAGATT | TTCCTGCGAT | 50  |
|    | TGCGCATGAA  | GCAAGCGCTG | ACGTCCATCT | AGAACAACAT | CGCCAAGGCT | 100 |
| 10 | CACGGTGGTT  | ACTCCGTGTT | CTGCGGTGTC | GGCGAGCGTA | CTCGTGAGGG | 150 |
|    | TAACGATTTG  | TACCACGAAA | TGCAGGAGAC | CGGTGTCATC | AACCTCGAGG | 200 |
|    | GCGAGTCCAA  | GGTCGCCCTT | GTCTTCGGTC | AGATGAACGA | GCCCCCGGGA | 250 |
|    | GCCCGTGCCC  | GTGTCGCCCT | TACTGGTCTT | ACCGTCGCTG | AGTAAGTTTT | 300 |
|    | GACAACCAGA  | AGCGAGTATT | GCCACAATTA | CTGACTAAAA | ATCAAGATAT | 350 |
| 15 | TTCCGTGACG  | AGGAGGGCCA | GGATGTGCTT | CTCTTCATTG | ACAACATTTT | 400 |
|    | CCGTTTCACC  | CAGGCCGGTT | CTGAGGTGTC | CGCTCTTCTC | GGCCGTATTC | 450 |
|    | CCTCTGCCGT  | CGGTTACCAG | CCCCTCTCG  | CCGTCGACAT | GGGTATGATG | 500 |
|    | CAGGAGCGTA  | TCACCACCAC | CCAGAAGGGT | TCCATCACTT | CCGTC      | 545 |

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## 2) INFORMATION FOR SEQ ID NO: 1654

## (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 564 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium moniliiforme*

(B) STRAIN: WSA-213

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654

|    |             |             |            |            |            |     |
|----|-------------|-------------|------------|------------|------------|-----|
|    | TGTGTTTATT  | CAGGAGCTCA  | TCAACAACAT | CGCCAAGGCC | CACGGTGGTT | 50  |
|    | ACTCTGTCTT  | CACTGGTGTC  | GGTGAGCGAA | CCCGTGAGGG | TAACGATCTG | 100 |
| 40 | TACCACGAAA  | TGCAGGAGAC  | TTCCGTTATT | CAGCTTGATG | GCGAGTCCAA | 150 |
|    | GGTTGCCCTG  | GTTTTTCGGTC | AGATGAACGA | GCCCCCTGGA | GCTCGTGCCC | 200 |
|    | GTGTCGCTCT  | TACCGGGTAA  | GTTGATAGAT | AGTGCCTTCC | CTTCCTGTTT | 250 |
|    | CAACACCTCA  | ACACCACCAC  | TCCCCAAGAC | ATTGCTACTC | ATACTGCACC | 300 |
|    | ATGATATTAT  | ATTTACGCCT  | CTTGGACGCT | AGCTAATGTT | GTATCGACAG | 350 |
| 45 | TTTGACTGTT  | GCTGAGTACT  | TCAGAGACGA | GGAGGGTCAG | GACGTGCTGC | 400 |
|    | TTTTTCATTGA | CAACATTTTC  | CGATTCACTC | AGGCCGGTTC | CGAGGTGTCT | 450 |
|    | GCCCTTCTCG  | GTCGTATCCC  | CTCTGCCGTC | GGTTACCAGC | CCACTCTGGC | 500 |
|    | CGTCGACATG  | GGTGGTATGC  | AGGAGCGTAT | TACCACCACC | ACCAAGGGTT | 550 |
|    | CCATTACCTC  | AGTC        |            |            |            | 564 |

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## 2) INFORMATION FOR SEQ ID NO: 1655

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 776 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Klebsiella oxytoca*  
 (B) STRAIN: ATCC 13182

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655

15 CGTACCGCGC GTGTACGAGG CTCTTGAGGT ACAAATGGT AGTGAGAATC 50  
 TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATTGT TCGTACCATC 100  
 GCCATGGGTT CTTCCGACGG TCTGCGTCGC GGTCTGGAAG TCAAAGACCT 150  
 CGAGCATCCG ATCGAAGTCC CGGTAGGTAA AGCAACGCTG GGTTCGTATCA 200  
 20 TGAACGTACT GGGCCAACCG GTAGACATGA AAGGCGACAT CGGCGAAGAA 250  
 GAGCGTTGGG CGATTCACCG CGCAGCGCCT TCCTACGAAG AGTTGTCAAA 300  
 CTCTCAGGAA CTGCTGGAAA CCGGCATCAA AGTTATCGAC CTGATGTGTC 350  
 CGTTTGCGAA GGGCGGTAAA GTTGGTCTGT TCGGTGGTGC GGGTGTAGGT 400  
 AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA TCGAGCACTC 450  
 25 CGGTTACTCC GTGTTTGC GGCTAGGTGA ACGTACTCGT GAGGGTAACG 500  
 ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGATAA AGTATCCCTG 550  
 GTGTATGGCC AGATGAACGA GCCGCCGGGA AACCGTCTGC GCGTTGCGCT 600  
 GACCGGCCTG ACCATGGCTG AGAAGTTCCG TGACGAAGGT CGTGACGTTT 650  
 TGCTGTTCGT CGATAACATC TATCGTTACA CCCTGGCCGG TACTGAAGTA 700  
 30 TCCGCACTGC TGGGTCGTAT GCCTTCAGCG GTAGGTTACC AGCCGACTCT 750  
 GGCGGAAGAG ATGGGCGTTC TGCAGG 776

## 35 2) INFORMATION FOR SEQ ID NO: 1656

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 572 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Microsporum audouinii*  
 (B) STRAIN: ATCC 11347

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656

50 GTGTTTCATCC AGGAGTTGAT TGTAAGTGAT TATATTCCCC TAGAAAGAAA 50  
 TGTTTTGAAC AAAAGTCTCG AATTAGAAAA TTCTTTTCAG ATACTAATTT 100  
 ACTATAGAAC AACATTGCCA AGGCTCACGG TGGTTACTCC GTCTTCACCG 150

GTGTCGGAGA GCGAACCCGT GAAGGAAACG ATCTGTACCA TGAAATGCAG 200  
 GAAACTCGTG TCATCCAAC T GATGGCGAG TCCAAGGTCG CCCTGGTCTT 250  
 CGGTCAGATG AACGAGCCCC CAGGTGCCCCG TGCCCGTGTT GCTCTTACTG 300  
 GTTTGACCAT TGCTGAGTAC TTCCGTGATG AGGAAGGTCA AGACGGTATG 350  
 5 TTCTTTAAAT TAGATATCTT CTGGAGAAAC AGCGTCTAAC AAATTCTTCC 400  
 AGTGCTTCTC TTCATCGACA ACATCTTCCG TTTCACTCAG GCTGGTTCCG 450  
 AAGTGTCTGC CCTGCTTGGT CGTATTCCAT CTGCCGTCGG TTACCAACCC 500  
 ACTCTTGCCG TCGACATGGG TGGTATGCAG GAACGTATTA CCACCACCAA 550  
 GAAGGGATCC ATTACCTCCG TC 572  
 10

## 2) INFORMATION FOR SEQ ID NO: 1657

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 790 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear  
 20  
 (ii) MOLECULE TYPE: Genomic DNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Obesumbacterium proteus*  
 25 (B) STRAIN: ATCC 12841

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657

GCCTAAAGTG TATAACGCAC TTGAGGTGAA AGGCGGTGCC ACTAAACTGG 50  
 30 TACTGGAAGT TCAGCAGCAG CTAGGCGGCG GCGTTGTACG CTGTATCGCT 100  
 ATGGGTACTT CTGACGGTCT GCGTCGCGGA CTGGACGTTG TTGACCTGGA 150  
 GCACCCGATT GAAGTCCCGAG TAGGTAAAGC GACCTTAGGC CGCATTATGA 200  
 ACGTACTGGG TGAGCCAATT GATATGAAGG GTGATATCGG CGAAGAAGAT 250  
 CGCTGGGCTA TTCACCGTGA AGCTCCAAGC TACGAAGAAC TGTCTAACTC 300  
 35 GCAAGAACTG CTGGAAACCG GTATCAAGGT AATGGACTTG ATTTGTCCGT 350  
 TCGCTAAGGG CGGTAAAGTC GGTCTGTTCG GTGGTGCGGG TGTTGGTAAA 400  
 ACAGTAAACA TGATGGAGCT GATCCGTAAAC ATCGCGATCG AGCACTCAGG 450  
 TTA CTCTGTA TTTGCCGGCG TGGGTGAACG TACTCGTGAG GGTAACGACT 500  
 TCTACCACGA AATGACCGAC TCCAACGTAT TGGACAAAGT ATCACTGGTT 550  
 40 TATGGCCAGA TGAACGAGCC ACCAGGAAAC CGTCTGCGCG TTGCGCTGAC 600  
 CGGTCTGACT ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT GACGTACTGC 650  
 TGTTTCATCGA TAACATCTAC CGTTATACCT TGGCCGGTAC CGAAGTATCT 700  
 GCACTGCTGG GTCGTATGCC TTCTGCGGTA GGTTATCAGC CAACGCTGGC 750  
 GGAAGAGATG GGTGTTCTGC AAGAACGTAT CACCTCTACC 790  
 45

## 2) INFORMATION FOR SEQ ID NO: 1658

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 622 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paracoccidioides brasiliensis*

(B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658

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10 TGTCTTCATT CAGGAGCTTA TCAACAACAT CGCCAAGGCC CACGGTGGTT      50
   ACTCCGTCTT CACTGGTGTG GGAGAGCGCA CTCGTGAGGG AAACGACTTG      100
   TATCACGAGA TGCAAGAGAC TTCCGTTATC CAGCTCGAAG GCGAATCCAA      150
   GGTGCCCCTC GTCTTCGGTC AAATGAACGA GCCTCCGGGT GCTCGTGCTC      200
15 GTGTTGCTCT CACCGGTCGT AAGTGCTCCT TCCCAGATTT CTCTTCCCCA      250
   GTTCTGAC CCACCTTTTTC CTTCCACCAC CATTCTACTG GGTAGGACCA      300
   AGATAGCACT GCCTATTCTG GTGCCTTCCT ACCGCCTACT CTACTGCCTA      350
   TTCCACCACC TTTTCTACCG CCTCTTCTAC TTGCTATTGT ATACTAACTT      400
   ACTCAAACAG TTACTATTGC TGAGTACTTC CGTGACGCTG AGGGCCAGGA      450
20 TGTGCTTCTC TTCATCGACA ACATTTTCCG TTTCACCCAG GCCGGTTCCG      500
   AGGTGTCCGC TCTTCTCGGT CGTATCCCCT CCGCCGTCGG TTACCAGCCC      550
   ACCCTTGCCG TCGACATGGG TGGTATGCAG GAGCGTATCA CCACCACCAA      600
   GAAGGGATCC ATTACCTCCG TC                                     622

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2) INFORMATION FOR SEQ ID NO: 1659

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 794 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Plesiomonas shigelloides*

(B) STRAIN: ATCC 14029

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659

```

   GACGCTGTAC CTCAGGTGTA CGATGCACTG ACAGTTGAGG GTGCTGAGCT      50
   GGTACTGGAA GTGCAGCAGC AGCTGGGTGG TGGTGTGTT CGCTGTATCG      100
45 CGATGGGTGC CTCTGATGGC CTCAAGCGCG GTCTGAAAGC GCACAATACT      150
   GGTGCTCCTA TCACTGTACC GGTGGGTGTG GAAACACTGG GCCGGATCAT      200
   GGATGTGTTG GGTAACCCGA TTGACCAGAA AGGTCCAATC GGTGAACAAG      250
   ATCGCTGGGT GATCCACCGT GAAGCACCAA GCTACGAAGA TCAGGCTAAC      300
   AGCACTGAAC TGCTGGAAAC CGGTATCAAG GTTATCGACC TGGTATGCCC      350
50 GTTTGCGAAA GCGGGTAAAG TCGGTCTGTT CGGTGGTGCC GGTGTAGGTA      400
   AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC      450
   GGTTATTCCG TGTTTGCGGG CGTGGGTGAG CGTACCCGTG AAGGTAACGA      500
   CTTCTACCAC GAAATGACAG ACTCCAACGT ACTGGACAAA GTATCCCTGG      550

```

|   |            |            |            |            |            |     |
|---|------------|------------|------------|------------|------------|-----|
|   | TGTACGGTCA | GATGAACGAG | CCGCCAGGTA | ACCGTCTGCG | CGTAGCACTG | 600 |
|   | ACCGGCCTGA | CCATTGCGGA | GAAATTCCGT | GATGAAGGTC | GTGACGTACT | 650 |
|   | GCTGTTCATC | GATAACATCT | ACCGTTATAC | CCTGGCGGGG | ACCGAAGTAT | 700 |
|   | CGGCACTGCT | GGGCCGTATG | CCTTCTGCGG | TAGGTTATCA | GCCAACGCTG | 750 |
| 5 | CGGGAAGAGA | TGGGTGTACT | GCAAGAGCGT | ATTACCTCTA | CCCG       | 794 |

## 2) INFORMATION FOR SEQ ID NO: 1660

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*  
 (B) STRAIN: ATCC 8071

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 25 | AGGTATATGA | CGCTSTGAAG | ATCACAGGTG | AAGGCGCCTG | TAATGGTTTG | 50  |
|    | GTGCTGGAAG | TTCAGCAACA | GCTAGGCGGT | GGTGTAGTTC | GTACTATCGC | 100 |
|    | TATGGGTTCT | TCTGATGGTC | TGCGTCGTGG | TCTTGAGGTT | GTAACTCAG  | 150 |
|    | GTTACCTAT  | TTCTGTTTCT | GTTGGTACCG | CCACGCTTGG | CCGTATCATG | 200 |
|    | AACGTATTAG | GTGAGCCTAT | TGATGAAGCG | GGTCCAATCG | GTGAAGAAGA | 250 |
| 30 | GCGTTATGTT | ATTCACCGTG | CAGCACCTTC | ATATGAAGAT | CAATCGAACA | 300 |
|    | CTACTGAACT | GTTAGAGACA | GGTATCAAGG | TTATTGACCT | TGTTTGTCCA | 350 |
|    | TTCGCTAAGG | GTGGTAAAGT | AGGTCTGTTC | GGTGGTGCGG | GTGTTGGTAA | 400 |
|    | AACAGTTAAC | ATGATGGAAC | TGATTAACAA | CATCGCTAAA | GCTCACTCGG | 450 |
|    | GTCTTTCCGT | GTTCGCCGGT | GTGGGTGAAC | GTACTCGTGA | AGGTAACGAC | 500 |
| 35 | TTCTACTACG | AGATGAAAGA | TTCTGGCGTT | CTCGACAAAG | TGGCCATGGT | 550 |
|    | TTATGGTCAG | ATGAACGAGC | CACCAGGAAA | CCGTTTACGC | GTAGCACTGT | 600 |
|    | CAGGTCTGAC | AATGGCTGAG | AAGTTCCGTG | ACGAAGGTCG | TGACGTATTG | 650 |
|    | TTGTTTCGTT | ACAACATCTA | CCGTTATACC | TTAGCCGGTA | CTGAAGTATC | 700 |
|    | TGCACTGTTA | GGCCGTATGC | CTTCTGCGGT | AGGTTATCAA | CCAACATTGG | 750 |
| 40 | CTGAAGAAAT | GGGCGTTCTG | CAAGAGCGTA | TTACTTCAAC | TAAGACGGG  | 799 |

## 2) INFORMATION FOR SEQ ID NO: 1661

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661

TGGGAAGCGA AAATCCTG

18

5.

2) INFORMATION FOR SEQ ID NO: 1662

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 774 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*  
 (B) STRAIN: ATCC 35224

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CTATGCCTCA | AACTAGAGAG | CATATCTTGC | TATCTCGCCA | AGTAGGCGTT | 50  |
|    | CCATATATCG | TTGTATTTAT | GAACAAAGCC | GATATGGTCG | ATGACGCTGA | 100 |
| 25 | GCTTCTTGAG | CTAGTCGAGA | TGGAAATTCG | CGAGCTTCTT | AACGAGTACA | 150 |
|    | ACTTCCCTGG | CGATGATACT | CCTATCATAT | CAGGTTCTGC | TCTTAAAGCC | 200 |
|    | CTCGAAGAGG | CTAAAGCAGG | CGTTGATGGC | GAGTGGTCAG | CAAAAGTTCT | 250 |
|    | TGAGCTTATG | GATAAAGTCG | ATGAGTATAT | CCCAACTCCA | GTTCGTGCTA | 300 |
|    | CCGATAAAGA | CTTCCTGATG | CCTATCGAAG | ACGTTTTCTC | TATCTCAGGT | 350 |
| 30 | CGTGGAACGG | TCGTTACTGG | TAGGATCGAA | AAAGGTGTCG | TAAAAGTTGG | 400 |
|    | CGATACTATC | GAGATCGTTG | GTATCAAACC | TACTCAAAC  | ACGACAGTTA | 450 |
|    | CTGGCGTTGA | GATGTTTAGG | AAAGAGATGG | AACAAGCGCA | GGCCGGTGAT | 500 |
|    | AACGTAGGTG | TTCTTTTAAG | AGGTACTAAA | AAAGAAGACG | TCGAGCGCGG | 550 |
|    | CATGGTTCTT | TGTAAGCCAA | AATCAATCAC | TCCTCATACA | AAATTTGAGG | 600 |
| 35 | GTGAGGTTTA | TATCCTAACA | AAAGAGGAAG | GCGGACGCCA | CACTCCATTC | 650 |
|    | TTTAACAAC  | ATAGACCACA | ATTTTATGTA | AGAACAACAG | ACGTTACAGG | 700 |
|    | TTCTATCACA | CTTCAGAAAG | GAAGTGAAG  | GGTTATGCCT | GGAGATAATG | 750 |
|    | TCAGAATTTT | CGTTGAACTC | ATCG       |            |            | 774 |

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2) INFORMATION FOR SEQ ID NO: 1663

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 791 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*

(B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
| 5  | TTCTGCGGCT | GACGGCCCAA | TGCCACAAAC | TAGAGAGCAC  | ATCTTGCTAT | 50  |
|    | CTCGCCAAGT | AGGCGTTCCG | TATATCGTTG | TTTTTATGAA  | CAAAGCCGAT | 100 |
|    | ATGGTCGATG | ATGCCGAGCT | TCTTGAGCTG | GTTGAGATGG  | AGATTCGCGA | 150 |
|    | GCTTCTAAAC | GAGTATGATT | TCCCTGGTGA | CGATACTCCA  | ATCGTAGCAG | 200 |
|    | GCTCTGCTCT | TCAAGCTCTT | AATGAAGCCA | AAGCCGGAAC  | AGAAGGCGAG | 250 |
| 10 | TGGTCTGCAA | AAATTCTTGA | GCTTATGGCT | AAAGTTGACG  | AGTATATCCC | 300 |
|    | GACTCCGGTT | CGTGCAACGG | ATAAAGACTT | CTTGATGCCT  | ATTGAGGACG | 350 |
|    | TTTTCTCTAT | CTCCGGTCGC | GGCACCGTCG | TTACCGGCAG  | AATCGAAAAA | 400 |
|    | GGTATCGTAA | AAGTCGGTGA | TACTATCGAG | ATCGTAGGTA  | TCCGCGATAC | 450 |
|    | TCAAACAAC  | ACCGTTACCG | GCGTTGAGAT | GTTTCAGAAAA | GAGATGGATC | 500 |
| 15 | AAGGCGAAGC | GGGCGATAAC | GTAGGCGTTC | TTCTAAGAGG  | CACTAAAAAA | 550 |
|    | GAAGACGTTG | AGCGCGGTAT | GGTTCTTTGC | AAACCTAAAT  | CAATCACTCC | 600 |
|    | TCACACTAAA | TTTGAGGGAG | AGGTTTATAT | CTTAACATAA  | GAGGAAGGCG | 650 |
|    | GACGCCATAC | TCCATTCTTT | AATAACTATA | GACCGCAGTT  | TTATGTAAGA | 700 |
|    | ACTACCGACG | TTACCGGTTT | TATCACTCTT | CCGGAAGGAA  | CAGAGATGGT | 750 |
| 20 | TATGCCTGGC | GATAACTTAA | AGATAAGCGT | TGAGCTTATC  | G          | 791 |

2) INFORMATION FOR SEQ ID NO: 1664

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
| 40 | CGACGGACAG  | ATGCCCCAGA | CCAGGGAGCA | CTTGCTCCTC | GCCCGCCAGG | 50  |
|    | TCGGTGTCAA  | GCGCATTGTC | GTCTTCGTCA | ACAAGGTCGA | TGCCATTGAG | 100 |
|    | GACAAGGAGA  | TGTTGGAGCT | CGTCGAGATG | GAGATGCGTG | AGCTTCTCTC | 150 |
|    | CAGCTACGGC  | TTCGAGGGTG | ACGACACTCC | CATCGTCATG | GGTTCCGCCC | 200 |
|    | TTTGCGCCAT  | TGAGGGCCGC | GAGCCCGACA | TTGGTGTCGA | GAAGATTGAC | 250 |
| 45 | GAGCTCCTCG  | AGCACGTCGA | CACCTGGATC | CCCACCCCCG | AGCGTGACAT | 300 |
|    | CGCCAAGCCT  | TTCTTCATGT | CCGTTGAGGA | CGTCTTCTCC | ATTCCCGGCC | 350 |
|    | GTGGTACCGT  | CGCTTCTGGC | CGTGTCGAGC | GTGGTGTCCT | GAAGAAGGAT | 400 |
|    | TCCGAAGTCG  | AGCTTGTCGG | CAAGAACAAG | AACCCCATCA | AGACCAAGGT | 450 |
|    | TACCGACATC  | GAGACCTTCA | AGAAGTCTTG | CGACGAGTCC | CGCGCTGGTG | 500 |
| 50 | ACAACCTCCGG | TCTCCTTCTC | CGTGGTGTCA | AGCGTGACGA | TGTCCTCCGT | 550 |
|    | GGCATGGTTCG | TTGTCCAGCC | CGGCACCACC | AAGGCCACA  | AGAAGTTCCT | 600 |
|    | TGCCTCCATG  | TACGTCCTCA | CCAAGGAGGA | GGGTGGCCGC | CACACTGGTT | 650 |
|    | TCGCCAACAA  | CTACAAGCCC | CAGATGTTCA | TCCGTACCGC | CGATGAGGCC | 700 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GCCACTCTTA | CCTGGCCCGA | GGGTACCGAG | GAGGACAAGA | TGGTCATGCC | 750 |
| CGGTGACAAT | GTCGAGATGA | TCTGCGAGAT | CCACAAGCCC | ATTGCCGTCG | 800 |
| AGCAAGGCCA |            |            |            |            | 810 |

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## 2) INFORMATION FOR SEQ ID NO: 1665

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 19 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665

CAGTACAGGT AGACTTCTG

19

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## 2) INFORMATION FOR SEQ ID NO: 1666

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 888 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Microsporum audouinii*  
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666

|               |            |            |             |            |     |
|---------------|------------|------------|-------------|------------|-----|
| ATGATTGCGA    | AACCTACTTG | CTGTGGAAGA | ATTTGGATAT  | TCTAACATTT | 50  |
| CTCTAGGCCT    | CAAACCAGAG | AGCATCTGCT | CCTTGCCCGC  | CAGGTCGGTG | 100 |
| TTCAGAAGCT    | CGTCGTTTTT | GTTAACAAGG | TCGACGCTGT  | TGAGGACCCA | 150 |
| GAGATGTTGG    | AACTTGTCGA | GCTAGAGATG | CGTGAGCTGC  | TCAGCCACTA | 200 |
| TGGTTTCGAG    | GGTGAGGAGA | CCCCAATCAT | TTTTGGCTCT  | GCTCTCTGCG | 250 |
| CCCTTGAATC    | TCGACGACCA | GAATTGGGTG | TTGAGAAGAT  | CGATGAGCTA | 300 |
| 45 TTGAACGCTG | TGGATACCTG | GATTCCCACC | CCAGAGCGTG  | CCACTGATAA | 350 |
| GCCTTTCCTT    | ATGTCCATTG | AGGAAGTTTT | CTCCATCTCT  | GGTCGTGGTA | 400 |
| CCGTCGTTTT    | CGGTCGTGTC | GAGCGTGGTA | TCCTCAAGAA  | GGACTCTGAT | 450 |
| GTCGAAATTG    | TGGGTGGATC | TGATACACCC | ATCAAGACGA  | AGGTCACCGA | 500 |
| CATTGAAACC    | TTCAAGAAGT | CTTGTGACGA | ATCCCAGAGCT | GGTGACAACT | 550 |
| 50 CCGGTCTACT | TCTCCGAGGT | GTCAAGCGTG | AGGACTTGAG  | ACGTGGAATG | 600 |
| GTTGTTGCTG    | CTCCCGGATC | GACCAAGGCT | CATACCGACT  | TCATGGTCTC | 650 |
| CCTTTATGTT    | CTGACCGAGG | CTGAGGGTGG | CCGTTCCAAT  | GGATTACACC | 700 |
| ACAAGTACCG    | CCCACAGATG | TTCATCCGTA | CTGCCGGTAT  | GTAAACCCTT | 750 |

|            |             |            |            |            |     |
|------------|-------------|------------|------------|------------|-----|
| TTTCTACCAT | TCACTTTGTT  | TCACCACTGA | CTTGTATACT | TTACCGCAGA | 800 |
| CGAAGCCGCA | TCTTTCAGCT  | GGCCTGGAGA | GGATCAAGAC | AAGAAGGCCA | 850 |
| TGCCTGGTGA | CAATGTCTGAG | ATGATTTGCA | AGACCCTC   |            | 888 |

5

## 2) INFORMATION FOR SEQ ID NO: 1667

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 793 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*  
 (B) STRAIN: ATCC 24292

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667

|               |             |            |            |             |     |
|---------------|-------------|------------|------------|-------------|-----|
| ATGCCGCAGA    | CCCGCGAGCA  | CTTGCTGCTC | GCCCGTCAGG | TCGGTGTCCA  | 50  |
| GAAGATCGTT    | GTTTTCGTCA  | ACAAGGTTGA | TGCTATCGAC | GACCCGGAGA  | 100 |
| 25 TGCTGGAGCT | TGTCGAGATG  | GAGATGCGTG | AACTTCTCAG | CACATACGGT  | 150 |
| TTCGAGGGTG    | ACGAGACCCC  | TGTTATTATG | GGCTCCGCGC | TCATGGCTCT  | 200 |
| CAACAACCAG    | CGCCCCGAGA  | TTGGTCAACA | GAAGATTGAT | GAACTCATGG  | 250 |
| CCGCTGTCGA    | CGAGTGAGATC | CCTACTCCCC | AGCGTGACCT | CGACAAGCCT  | 300 |
| TTCCTGATGT    | CTGTTGAGGA  | TGTCTTCTCC | ATTGCTGGCC | GTGGTACCGT  | 350 |
| 30 TGTGTCCGGC | CGTGTGGAGC  | GCGGTACCCT | CAAGCGTGAT | GAGGAAGTCG  | 400 |
| AGCTTGTCGG    | CAAGGGTGTC  | GACCCCATCA | AGACCAAGGT | CACCGATATC  | 450 |
| GAGACTTTCA    | AGAAGTCCTG  | CGAGGAGGCT | CAGGCTGGTG | ACAACCTCTGG | 500 |
| TCTTCTGATC    | CGTGGTGTCC  | GCCGCGAGGA | TGTTCTGTCG | GGTATGGTTG  | 550 |
| TCTCCAAGCC    | CGGCACCGTC  | AAGTCTCACA | CTCAGTTCCT | GGCCTCGCTT  | 600 |
| 35 TACGTTCTCA | CCAAGGAGGA  | GGGTGGTCGC | CACACTGGTT | TCGGCGAGCA  | 650 |
| CTACCGTCCC    | CAGCTCTACC  | TCCGTACCTC | AGACGAGTCT | GTCGATCTGA  | 700 |
| CCTTCCCCGA    | GGGAAGTGAG  | GATCACCCT  | CCAAGATCGT | CATGCCTGGT  | 750 |
| GACAACATCG    | AGATGGTTCGT | CACGATGACT | CACGCCAACG | CTA         | 793 |

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## 2) INFORMATION FOR SEQ ID NO: 1668

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 891 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(B) STRAIN: K-12 KL1699  
(C) ACCESSION NUMBER: J01717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668

```

5 AACATGATCA CCGGTGCTGC GCAGATGGAC GGCGCGATCC TGGTAGTTGC      50
  TGCGACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC      100
  GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA ATGCGACATG      150
  GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG TTCGTGAACT      200
10 TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC GTTCGTGGTT      250
  CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCCTG      300
  GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG AGCGTGCGAT      350
  TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC      400
  GTGGTACCGT TGTTACCGGT CGTGTAGAAG GCGGTATCAT CAAAGTTGGT      450
15 GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACTCAGAAGT CTACCTGTAC      500
  TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT GCTGGTGAGA      550
  ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT      600
  CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC      650
  TGAAGTGATC ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT      700
20 TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA CGTGACTGGT      750
  ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG GCGACAACAT      800
  CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC GACGGTCTGC      850
  GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C              891

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2) INFORMATION FOR SEQ ID NO: 1669

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 805 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Saksenaea vasiformis
    (B) STRAIN: ATCC 60625

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669

```

  TCCTCGTGGT CGCCGCCACC GACGGCCCGA TGCCGCAGAC CAAGGAGCAC      50
  GTGCTCCTGG CCCGCCAGGT CGGCGTTCCG TACATCGTCG TCGCCCTCAA      100
45 CAAGGCCGAC ATGGTGGACG ACGAGGAGAT CCTGGAGCTC GTCGAGCTCG      150
  AGGTCCGTGA GCTCCTCTCC GAGTACGAGT TCCCGGGCGA CGACGTTCCC      200
  GTCGTCAAGG TCTCCGCTCT GAAGGCCCTC GAGGGCGACA AGGAGTGGGG      250
  CAACTCGGTT CTCGAGCTCA TGAACGCCGT CGACACGGCG ATCCCCGAGC      300
  CCGAGCGTGA CGTCGACAAG CCGTTCCTCA TGCCGATCGA GGACGTCTTC      350
50 ACGATCACCG GTCGCGGTAC GGTCGTCACC GGCCGTATCG AGCGTGGTGT      400
  CCTGAAGGTC AACGAGACCG TCGACATCAT CGGCATCAAG ACCGAGAAGA      450
  CCACCACCAC GGTACCCGGC ATCGAGATGT TCCGGAAGCT CCTCGACGAG      500
  GGCCAGGCCG GTGAGAACGT CGGTCTGCTC CTCCGTGGCA TCAAGCGCGA      550

```

|   |            |            |            |            |            |     |
|---|------------|------------|------------|------------|------------|-----|
|   | GGACGTCGAG | CGCGGCCAGG | TCATCATCAA | GCCGGGCTCG | GTCACGCCGC | 600 |
|   | ACACGGAGTT | CGAGGCGCAG | GCCTACATCC | TGTCCAAGGA | CGAGGGTGGC | 650 |
|   | CGCCACACGC | CGTTCTTCAA | CAACTACCGC | CCGCAGTTCT | ACTTCCGTAC | 700 |
|   | GACGGACGTG | ACCGGCGTGG | TGACCTCC   | CGAGGGCACC | GAGATGGTCA | 750 |
| 5 | TGCCGGGTGA | CAACACCGAG | ATGAAGGTGG | AGCTCATCCA | GCCCGTCGCC | 800 |
|   | ATGGA      |            |            |            |            | 805 |

## 10 2) INFORMATION FOR SEQ ID NO: 1670

## (i) SEQUENCE CHARACTERISTICS:

|    |                          |
|----|--------------------------|
|    | (A) LENGTH: 935 bases    |
|    | (B) TYPE: Nucleic acid   |
| 15 | (C) STRANDEDNESS: Double |
|    | (D) TOPOLOGY: Linear     |

(ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

|     |   |
|-----|---|
| (A) | ORGANISM: <i>Trichophyton tonsurans</i> |
| (B) | STRAIN: ATCC 56185                      |

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
| 25 | GCTTCTGACG | GTCAAATGTA | ATTGAATGCC | CGCCCAGACA  | GATGAAAGGA | 50  |
|    | TTTGACGTTT | CTAACATCAG | TCTAGGCCTC | AGACCAGAGA  | ACATTTGCTC | 100 |
|    | CTTGCCCGCC | AGGTCGGTGT | CCAGAAGCTG | GTCGTTTTTCG | TTAACAAGGT | 150 |
|    | CGATGCCGTT | GAGGACCCAG | AGATGTTGGA | GCTTGTCGAA  | CTTGAAATGC | 200 |
| 30 | GTGAACTCCT | CAGCCACTAC | GGTTTCGAGG | GTGAGGAGAC  | CCCCATCATT | 250 |
|    | TTTGGCTCTG | CTCTCTGTGC | CCTCGAGTCC | CGTCGACCTG  | AGCTTGGTGT | 300 |
|    | CGAGAAGATT | GACGAGCTAT | TGAACGCCGT | CGACACCTGG  | ATCCCCACCC | 350 |
|    | CAGAGCGCGC | CACTGATAAG | CCTTTCCTCA | TGTCCATTGA  | GGAAGTGTTT | 400 |
|    | TCTATCTCTG | GTCGTGGTAC | CGTCGTCTCC | GGTCGTGTTG  | AGCGTGGTAT | 450 |
| 35 | CCTCAAGAAG | GATTCGGACG | TCGAAATTGT | TGGTGGCTCT  | ACCACCCCTA | 500 |
|    | TCAAGACCAA | GGTCACCGAT | ATCGAAACCT | TCAAGAAGTC  | CTGCGATGAA | 550 |
|    | TCTCGAGCTG | GTGACAACTC | TGGTCTCCTT | CTCCGAGGTA  | TCAAGCGTGA | 600 |
|    | GGACTTGAAG | CGTGGAATGG | TTGTTGCTGC | CCCCGGATCC  | ACCAAGGCTC | 650 |
|    | ACACCGACTT | CATGGTCTCC | CTCTACGTCC | TGACTGAGGC  | TGAGGGTGGT | 700 |
| 40 | CGTTCCAACG | GCTTCACCCA | CAAGTACCGC | CCCCAAATGT  | TCATCCGTAC | 750 |
|    | TGCTGGTATG | TAACCCAAGT | TTCCGCTATT | TACTAAGTAG  | ATCATTGCTA | 800 |
|    | ACTTGATTTT | CCTTCCGTAG | ACGAAGCCGC | ATCTTTCAGC  | TGGCCTGGAG | 850 |
|    | AAGACCAAGA | CAAGAAGGCT | ATGCCTGGTG | ACAACGTCGA  | GATGATTTGC | 900 |
|    | AAGACCCTCC | ACCCCATTCG | TGCCGAGGCT | GGCCA       |            | 935 |
| 45 |            |            |            |             |            |     |

## 2) INFORMATION FOR SEQ ID NO: 1671

## 50 (i) SEQUENCE CHARACTERISTICS:

|     |                      |
|-----|----------------------|
| (A) | LENGTH: 772 bases    |
| (B) | TYPE: Nucleic acid   |
| (C) | STRANDEDNESS: Double |

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter aerogenes*

(B) STRAIN: ATCC 13048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671

```

10 ACGATGCCCT TGAGGTACAG AATGGTAATG AGAGCCTGGT GCTGGAAGTT      50
   CAGCAGCAGC TCGGCGGTGG CGTAGTCCGT GCTATCGCCA TGGGTTCTTC      100
   CGACGGTCTG CGTCGTGGTC TGGAAGTTAA AGACCTTGAG CACCCGATCG      150
   AAGTCCCGGT AGGTAAAGCG ACTCTGGGCC GTATCATGAA CGTCCTGGGT      200
15 CAGCCGATCG ACATGAAAGG CGACATCGGC GAAGAAGAAC GTTGGGCTAT      250
   CCACCGCGCG GCGCCTTCCT ATGAAGAGCT GTCCAGCTCT CAGGAACTGC      300
   TGGAAACCGG CATCAAAGTT ATCGACTTGA TGTGTCCGTT CGCTAAGGGC      350
   GGTAAAGTTG GTCTGTTCGG TGGTGCGGGT GTAGGTAAAA CCGTAAACAT      400
   GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT TACTCCGTGT      450
20 TTGCGGGCGT TGGTGAGCGT ACTCGTGAGG GTAACGACTT CTATCACGAA      500
   ATGACCGACT CCAACGTTCT GGATAAAGTA TCCCTGGTTT ACGGCCAGAT      550
   GAACGAGCCG CCGGGAAACC GTCTGCGCGT TGCCTGACC GGCCTGACCA      600
   TGGCTGAGAA ATTCCGTGAC GAAGGTCGTG ACGTTCTGCT GTTCGTCGAT      650
   AACATCTATC GTTACACCCT GGCCGGTACT GAAGTATCTG CACTGCTGGG      700
25 CCGTATGCCT TCAGCGGTAG GTTATCAGCC GACTCTGGCG GAAGAGATGG      750
   GCGTTCTGCA GGAACGTATC AC                                     772

```

30 2) INFORMATION FOR SEQ ID NO: 1672

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1401 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bordetella pertussis*

(B) STRAIN: Tohama 1

(C) ACCESSION NUMBER: Genome project

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1672

```

   ATGAGCAACG GAACCATCGT TCAGTGCATC GGCGCCGTGG TGGATATTCA      50
   GTTCCCCCGC GATAACATGC CCAAGATCTA CGAAGCGCTC ACCCTGGTGC      100
   ACGAGGGTTC CTCGTTCGCC GAGAAGGGCT TGACGCTGGA AGTGCAACAA      150
50 CAGCTGGGCG ACGGCGTGGT GCGTACCATC GCGCTGGGTT CCAGCGACGG      200
   GCTGCGCCGC GGCATGCAAG TGGCCGGCAC CGGCGCACC GATCTCGGTGC      250
   CCGTGGGCCA CGGCACCCTG GGCCGCATCA TGGACGTGCT GGGCCGTCCC      300
   ATCGACGAAG CCGGTCCCAT CGCCTCCGAC GAGAAGCGCG CCATCCACCA      350

```

|    |            |            |            |             |             |      |
|----|------------|------------|------------|-------------|-------------|------|
|    | GCCCGCGCCC | CGTTTCGACG | AGCTGTGCGC | GTCGGTCGAG  | CTGCTGGAAA  | 400  |
|    | CCGGCATCAA | GGTTATCGAC | CTGGTGTGCC | CGTTCGCCAA  | GGGCGGCAAG  | 450  |
|    | GTCGGCCTGT | TCGGCGGCGC | CGGCGTGGGC | AAGACCGTCA  | ACATGATGGA  | 500  |
|    | ACTGATCAAC | AACATCGCCA | AGCAGCACAG | CGGCTTGTCG  | GTGTTTCGCCG | 550  |
| 5  | GCGTGGGCGA | GCGTACCCGC | GAAGGCAACG | ACTTCTACCA  | CGAAATGGAA  | 600  |
|    | GAGTCGAACG | TTCTGGACAA | GGTGGCCATG | GTGTTTCGGCC | AGATGAACGA  | 650  |
|    | GCCCCCGGGC | AACCGCCTGC | GCGTGGCGCT | GACCGGCCTG  | ACCATGGCCG  | 700  |
|    | AGAAGTTCCG | CGACGAAGGC | CGTGACATCC | TGTTCTTCGT  | CGACAACATC  | 750  |
|    | TACCGCTACA | CCCTGGCCGG | TACCGAAGTG | TCGGCGCTGC  | TGGGCCGTAT  | 800  |
| 10 | GCCGTCGGCG | GTGGGCTACC | AGCCTACGCT | GGCCGAGGAA  | ATGGGCGTGC  | 850  |
|    | TGCAAGAGCG | CATCACCTCG | ACCAAGACCG | GTTTCGATCAC | CTCGATCCAG  | 900  |
|    | GCCGTGTACG | TGCCTGCCGA | CGACTTGACC | GACCCGTTCG  | CCGCCACGAC  | 950  |
|    | CTTCCAGCAC | TTGGACTCGA | CCGTCGTGCT | GTCGCGTGAC  | ATCGCTGCGC  | 1000 |
|    | TGGGCATCTA | TCCCGCCGTG | GACCCGCTGG | ATTCCTCCAG  | CCGCCAGCTC  | 1050 |
| 15 | GACCCGCAAG | TCGTGGGCGA | AGAGCACTAC | CAGGTGGCCC  | GTGGCGTGCA  | 1100 |
|    | GCAGACGCTG | CAGCGCTACA | AGGAACTGCG | CGACATCATC  | GCGATTCTGG  | 1150 |
|    | GCATGGACGA | ACTGTCGCCG | GAAGACAAGC | AGGCCGTGGC  | CCGCGCGCGC  | 1200 |
|    | AAGATCCAGC | GCTTCCTGTC | GCAGCCCTTC | TACGTGGCCG  | AAGTGTTTAC  | 1250 |
|    | CGGCTCGCCG | GGCAAGTACG | TGTCGCTGGC | CGAAACGATC  | CGTGGCTTCA  | 1300 |
| 20 | AGATGATCGT | CGACGGCGAG | TGCGACGCGC | TGCCCAGGCA  | GGCGTTCTAC  | 1350 |
|    | ATGGTCGGCA | CGATCGACGA | GGCCTTCGAG | AAGGCCAAGA  | AACTCCAATA  | 1400 |
|    | A          |            |            |             |             | 1401 |

25

## 2) INFORMATION FOR SEQ ID NO: 1673

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 797 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

35

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*  
 (B) STRAIN: ATCC 9345

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | CAGCTACCGA | CGGTCCAATG | GCTCAGACCC | GCGAGCACGT | TCTTCTTGCT  | 50  |
|    | CGCCAGGTTG | GCGTTCCACA | GATCATCGTT | GCTCTCAACA | AGGCTGACAT  | 100 |
|    | GGTTGACGAC | GAGGAAATCC | TCGAACTCGT | CGAAATGGAA | GTTTCGTGAGC | 150 |
| 45 | TTCTCTCTTC | CCAGGAGTAC | CCAGGTGACG | ACCTCCCAGT | CGTCAAGATC  | 200 |
|    | TCGGCACTCA | AGGCTCTCGA | AGGCGATGCC | GAATGGAGCA | AGGCAATCGA  | 250 |
|    | AGATCTCATG | GAAGCTGTCT | ATACCTACTT | CGACGATCCA | GTGCGTGACC  | 300 |
|    | TCGATAAGCC | ATTCCTCATG | CCAATCGAAG | ACGTCTTCAC | CATCACCAGT  | 350 |
|    | CGTGGCACCG | TTGTTACCGG | CCGTGCAGAG | CGCGGTATGC | TCAACTTGAA  | 400 |
| 50 | CGAAGAAGTT | GAAATCCTCG | GTATCCGTGC | ACCACAGAAG | ACAACCGTTA  | 450 |
|    | CCGGTATCGA | AATGTTCCAC | AAGTCGATGG | ATCACGCAGA | TGCAGGCGAA  | 500 |
|    | AACTGTGGTC | TTCTCCTCCG | TGGCACCAAG | CGCGAAGATG | TTGAACGTGG  | 550 |
|    | TCAGGTTGTT | GCCAAGCCAG | GCACCATCAC | CCCACACACC | AACTTCGAAG  | 600 |



|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CTCAGGTCTA | CGTGCTCGGT | AAGGAAGAAG | GTGGCCGTCA | CAACCCATTC | 650 |
| TTCTCCAAC  | ACCGTCCACA | GTTCTACTTC | CGTACCACGG | ATGTTACCGG | 700 |
| CGTGATCACC | CTTCCAGAGG | GCACCGAAAT | GGTTATGCCA | GGCGACAACA | 750 |
| CCGACATGAC | AGTTGAGCTC | ATCCAGCCAA | TCGCTATGGA | AGAGGGC    | 797 |

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## 2) INFORMATION FOR SEQ ID NO: 1674

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Butyrivibrio fibrisolvens*
- (B) STRAIN: ATCC 19171

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674

|               |             |            |            |            |     |
|---------------|-------------|------------|------------|------------|-----|
| CTGATGGTCC    | TATGCCACAG  | ACCCGTGAGC | ACATCCTATT | AGCACGTCAG | 50  |
| 25 GTAGGCGTAC | CATACATCAT  | CGTATTCCTA | AACAAGTGCG | ATATGGTTGA | 100 |
| CGACGAGGAA    | TTATTAGAGT  | TAGTTGAGAT | GGACGTACGT | GATCTATTAA | 150 |
| ATCAGTACCA    | GTTCCCAGGC  | GACGACACTC | CAATCATCCG | TGGTTCAGCA | 200 |
| CTAGGTGCAT    | TAAACGGCGA  | AGAGAAGTGG | AAAGAGGCAA | TCTATCAGTT | 250 |
| AGCAGACACT    | CTAGATTTCAT | ACATTCCAGA | GCCAAAGCGT | GATATCGATG | 300 |
| 30 ATCCATTCTT | ATTACCAATC  | GAAGATATCT | TCTCAATCTC | AGGTCGTGGT | 350 |
| ACTGTAGTAA    | CCGGCCGTGT  | AGAGCGTGGT | ATTGTACACG | TAGGTGACGA | 400 |
| AGTTGAAATC    | GTTGGTATTC  | GTCCAACCAC | CAAGACCACT | GTAAGTGGCG | 450 |
| TTGAAATGTT    | CCGTAAGTTA  | CTAGACGAAG | GTCGTGCAGG | TGATAACGTT | 500 |
| GGTGTCTTAC    | TACGTGGTAC  | CAAGCGTGAT | GAGGTTGAGC | GTGGTCAGGT | 550 |
| 35 TCTAGCTGCT | CCAGGCACAA  | TCACTCCACA | CACCAAGTTC | ACTGGTCAGG | 600 |
| TTTACGTACT    | AAGCAAGGAT  | GAAGGTGGTC | GTCACACTCC | ATTCTTCAAG | 650 |
| GGCTACCGTC    | CACAGTTCTT  | CTTCCGTACA | ACCGATATTA | CCGGTTCTAT | 700 |
| CGATCTGAAA    | GAGGGCGTAG  | AGATGGTAAT | GCCAGGTGAT | AACACCGACA | 750 |
| 40 TGACCGTAAC | CCTAATCCAC  | CCAGTAGCTA | TGGCT      |            | 785 |

40

## 2) INFORMATION FOR SEQ ID NO: 1675

## 45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*  
 (B) STRAIN: ATCC 49349

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675

5  
 TGGGGCGATC TTGGTTGTTT CTGCTGCAGA TGGTCCTATG CCACAAACTA 50  
 GAGAGCACAT TCTTCTTTCT CGTCAAGTAG GCGTTCCATA TATTGTTGTT 100  
 TTTATGAATA AAGCAGATAT GGTTGATGAT GCTGAGCTTT TAGAGTTAGT 150  
 TGAAATGGAA ATTAGAGAAAT TATTAAGCTC TTATGATTTT CCAGGCGATG 200  
 10 ATACACCTAT TATTTCTGGT TCTGCTTTAA AAGCTCTTGA AGAAGCTAAA 250  
 GCTGGACAAG ATGGTGAATG GTCAGCAAAA ATTATGGATC TTATGGCTGC 300  
 AGTTGATAGT TATATTCCAA CTCCAACCTCG TGATACTGAA AAAGACTTCT 350  
 TGATGCCAAT TGAAGACGTT TTCTCAATTT CAGGTCGTGG TACTGTTGTT 400  
 ACAGGTAGAA TTGAAAAAGG TGTTGTAAAA GTAGGTGATA CTATCGAAAT 450  
 15 CGTTGGTATT AAAGACACTC AAACAACAAC TGTAACAGGT GTTGAAATGT 500  
 TCAGAAAAGA AATGGATCAA GGCGAGGCAG GAGATAACGT AGGTGTTCTT 550  
 CTTCTGTTGA CTAATAAAGA AGAAGTTATT CGCGGTATGG TTCTTGCTAA 600  
 ACCAAAATCA ATTACTCCAC ACACTGACTT CGAAGCTGAA GTTTATATCT 650  
 TAAATAAAGA TGAAGGTGGT AGACATACTC CATTCTTTAA CAACTATAGA 700  
 20 CCACAGTTTT ATGTAAGAAC AACTGATGTT ACAGGTTTCA TTAAATTAGC 750  
 TGATGGTGTT GAAATGGTTA TGCCAGGTGA AAATGTGAGA ATTACTGTAA 800  
 GCTTGATCGC TCCAGTAGCA CTTGAAGAAG GAACT 835

25

## 2) INFORMATION FOR SEQ ID NO: 1676

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 812 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

35

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter lari*  
 (B) STRAIN: ATCC 43675

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676

TTCTGCAGCA GACGGCCCTA TGCCACAAAC TAGAGAGCAT ATCTTACTTT 50  
 CTCGTCAAGT AGGTGTACCA TATATTGTTG TTTTCATGAA CAAAGCTGAT 100  
 ATGGTTGATG ATGCAGAATT ATTAGAATTA GTTGAAATGG AAATTAGAGA 150  
 45 ATTACTAAGC TCTTATGATT TCCCAGGAGA TGATACTCCA ATTATTTTCAG 200  
 GTTCAGCATT ACAAGCTCTT GAAGAAGCAA AAGCTGGTCA AGATGGTGAA 250  
 TGGTCTAAAA AAATCTTAGA TCTTATGGCT GCAGTTGATG ATTATATTCC 300  
 AACTCCGGCT CGTGATACAG ATAAAGATTT CTTGATGCCA ATCGAAGATG 350  
 TTTTCTCAAT CTCAGGTCGT GGAAGTGTG TTAGCGGTAG AATTGAAAAA 400  
 50 GGTGTTGTAA AAGTTGGTGA TACTATAGAA ATCGTTGGTA TTAGAGACAC 450  
 TCAAACAACC ACAGTTACTG GTGTTGAAAT GTTTAGAAAA GAAATGGATC 500  
 AAGGTGAAGC TGGTGATAAT GTTGGTGTAT TACTTCGTGG AACTAAAAAA 550  
 GAAGATGTTG AACGTGGTAT GGTTCTTGCT AAACCAAAAT CAATCACTCC 600

|   |            |            |            |            |            |     |
|---|------------|------------|------------|------------|------------|-----|
|   | ACATACTGAT | TTTGAAGCAG | AAGTTTATAT | CTTAAATAAA | GATGAAGGTG | 650 |
|   | GTCGTCATAC | TCCATTCTTT | AATAATTATA | GACCGCAATT | TTATGTAAGA | 700 |
|   | ACAACTGATG | TTACAGGTGC | TATTAACTT  | GCAGAAGGCG | TTGAGATGGT | 750 |
|   | TATGCCAGGC | GATAATGATA | GAATTACTGT | AAGTCTTATT | GCTCCAGTTG | 800 |
| 5 | CACTTGAGGA | AG         |            |            |            | 812 |

## 2) INFORMATION FOR SEQ ID NO: 1677

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 15 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Campylobacter sputorum* subsp. *sputorum*  
 (B) STRAIN: ATCC 35980

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677

|    |            |             |            |            |             |     |
|----|------------|-------------|------------|------------|-------------|-----|
| 25 | GCTATTCTTG | TATGTTTCAGC | TGCAGATGGT | CCAATGCCAC | AGACTAGAGA  | 50  |
|    | GCATATTCTA | CTATCAAGAC  | AAGTTGGTGT | TCCATACATA | GTTGTTTTCT  | 100 |
|    | TAAATAAAGA | AGATATGGTT  | GATGATGCTG | AGCTTATAGA | GTTGGTTGAA  | 150 |
|    | GTTGAGGTTA | GAGATTTATT  | AAATGAATAT | GATTTCCCTG | GAGATGATAC  | 200 |
|    | TCCAATCGTA | ATAGGTTCTG  | CTCTTAAAGC | TTTAGAAGAA | GCAAAAGCTG  | 250 |
| 30 | GAACAGAGGG | TGAATGGTCT  | GCTAAAATTA | TGAAACTTAT | GGATGCTGTT  | 300 |
|    | GATAGCTATA | TCCCAACTCC  | AACAAGAGAT | ACAGATAAAG | ATTTCCCTTAT | 350 |
|    | GCCAATCGAA | GATATCTTCT  | CAATTTCTGG | TCGTGGTACA | GTTGTAACAG  | 400 |
|    | GTAGAATTGA | AAAAGGTGTA  | GTAAAAGTTG | GCGAGACTAT | TGAGATAGTT  | 450 |
|    | GGTATTAGAC | CTACTCAAAC  | AACAACAGTT | ACTGGTGTTG | AAATGTTTAG  | 500 |
| 35 | AAAAGAGCTA | GATCAAGGTG  | AAGCTGGAGA | TAATGTTGGT | ATCTTGTTAA  | 550 |
|    | GAGGTACAAA | AAAAGAAGAT  | GTTGAAAGAG | GTATGGTTTT | ATGTAAACCA  | 600 |
|    | AAATCAATCA | CTCCTCACAA  | GAAATTTGAA | GGCGAAGTTT | ATATTCTTAC  | 650 |
|    | AAAAGATGAA | GGTGGTAGAC  | ATACTCCTTT | CTTTAGTAAC | TATAGACCAC  | 700 |
|    | AATTTTATGT | TAGAACAACA  | GATGTAACAG | GTTCTATATC | TCTTCCTGAG  | 750 |
| 40 | GGAACAGAGA | TGGATATGCC  | TGGTGATAAT | GTAAAACTTA | CAGTTGAACT  | 800 |
|    | TATAAACCCA | ATTGCTCTTG  | AGCAAGGA   |            |             | 828 |

## 45 2) INFORMATION FOR SEQ ID NO: 1678

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases  
 (B) TYPE: Nucleic acid  
 50 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter upsaliensis*

(B) STRAIN: ATCC 49815

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678

5  
 10  
 15  
 20  
 25

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CGATTTTGGT | TGTTTCTGCT | GCTGATGGTC | CTATGCCACA | AACTAGAGAG | 50  |
| CACATTTTGC | TTTCTCGTCA | AGTGGGTGTT | CCTTATATCG | TAGTTTTTAT | 100 |
| GAATAAGGCT | GATATGGTTG | ATGATGCAGA | GCTTTTAGAA | TTGGTTGAAA | 150 |
| TGGAAATTAG | AGAACTTTTA | AGCTCTTATG | ATTTCCCGGG | CGATGACACT | 200 |
| CCTATCATTT | CAGGCTCTGC | TCTTCAAGCC | TTAGAAGAGG | CTAAGGCGGG | 250 |
| ACAAGATGGC | GAGTGGTCAG | CTAAGATTTT | AGAGCTTATG | AAGGCAGTTG | 300 |
| ATGAGTATAT | CCCAACTCCT | GTTCGCGATA | CTGAAAAAGA | TTTCTTGATG | 350 |
| CCTATTGAAG | ATGTTTTTTC | AATTTCTGGT | CGTGGAAGTG | TTGTAACAGG | 400 |
| TAGAATTGAA | AAAGGTGTGG | TTAAAGTCGG | CGATACTATT | GAGATAGTAG | 450 |
| GTATCAAAGA | TACTCAAAC  | ACAACAGTTA | CAGGCGTTGA | GATGTTTAGA | 500 |
| AAAGAAATGG | ATCAAGGTGA | GGCTGGCGAT | AATGTCGGTG | TGCTTTTAAG | 550 |
| AGGAACAAAA | AAAGAAGATG | TTCTTCGTGG | TATGGTTCTT | GCAAAGCCTA | 600 |
| AATCTATCAC | TCCTCATACT | GATTTTGAAG | CAGAAGTTTA | TATTCTAAAT | 650 |
| AAAGATGAGG | GCGGTCGCCA | TACTCCTTTC | TTTAACAATT | ATCGTCCGCA | 700 |
| GTTTTATGTA | AGAACGACTG | ATGTAACTGG | TTCTATTAAA | TTAGCTGATG | 750 |
| GTGTTGAGAT | GGTTATGCCG | GGTGAAAATG | TAAGAATTAC | AGTTAGCCTT | 800 |
| ATCGCTCCAG | TTGCACTTGA |            |            |            | 820 |

## 2) INFORMATION FOR SEQ ID NO: 1679

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Globicatella sanguis*

(B) STRAIN: ATCC 51173

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679

45  
 50

|            |            |            |            |             |     |
|------------|------------|------------|------------|-------------|-----|
| CTGCAGCTGA | TGGTCCAATG | CCTCAAACAC | GTGAACATAT | CTTATTATCA  | 50  |
| CGTCAAGTAG | GTGTTCTTA  | CATGGTTGTC | TTCTTAAACA | AAGTTGACAT  | 100 |
| GGTTGACGAT | GAAGAATTAT | TAGAATTAGT | TGAAATGGAA | GTTCGTGATT  | 150 |
| TATTATCTGA | ATACGAATTC | CCTGGAGACG | ACGTTCCAGT | AATCGCTGGT  | 200 |
| TCAGCTTTAA | AAGCTTTAGA | AGGCGAAGAA | CAATATGAAG | CAAAAGTATT  | 250 |
| AGAATTAATG | GAAGCTGTAG | ATACATACAT | TCCAGAACCA | GTTCGTGATA  | 300 |
| CTGAAAAACC | ATTCATGATG | CCAGTTGAAG | ATGTGTTCTC | AATCACAGGT  | 350 |
| CGTGGTACAG | TTGCTACTGG | ACGTGTTGAA | CGTGGACAAG | TTAAAGTTGG  | 400 |
| TGACGAAGTT | GAAATCGTTG | GTATTGCTGA | AGAAATTAGC | AAAACAACCTG | 450 |
| TAAGTGGTGT | TGAAATGTTC | CGTAAATTAT | TAGATTACGC | TGAAGCTGGA  | 500 |

|   |            |            |            |            |             |     |
|---|------------|------------|------------|------------|-------------|-----|
|   | GATAACATTG | GTGCGTTATT | ACGTGGTGT  | ACACGTGAAC | AAATCCAACG  | 550 |
|   | TGGTCAAGTA | TTAGCAAAAC | CAGGAACAAT | TACACCTCAT | ACTAAATTTCG | 600 |
|   | AGGCGGAAGT | TTACGTATTA | TCAAAAGAAG | AAGGTGGACG | TCATACTCCA  | 650 |
|   | TTCTTCGCTA | ACTACCGTCC | TCAATTCTAC | TTCCGTACAA | CTGACGTTAC  | 700 |
| 5 | AGGTGTTGTA | GAATTACCAG | AAGGTACAGA | AATGGTAATG | CCTGGAGATA  | 750 |
|   | ACGTATCAAT | GACAGTTGAA | TTAATTCACC | CAA        |             | 783 |

## 10 2) INFORMATION FOR SEQ ID NO: 1680

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus acidophilus*  
 (B) STRAIN: ATCC 4356

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680

|    |            |             |            |             |            |     |
|----|------------|-------------|------------|-------------|------------|-----|
| 25 | GCTATCTTAG | TTGTTGCTGC  | AACTGATGGT | CCTATGCCAC  | AAACTCGTGA | 50  |
|    | ACACATTTTG | CTTGCTCGTC  | AAGTTGGTGT | TAACATACATC | GTAGTATTCT | 100 |
|    | TGAACAAGTG | CGATTAGT    | GACGACCCAG | AATTGATCGA  | CTTGGTTGAA | 150 |
|    | ATGGAAGTTC | GTGACTTGTT  | GACTGAATAC | GATTACCCTG  | GTGATGATAT | 200 |
| 30 | TCCAGTTGTT | CGTGGTTCAG  | CATTAAAGGC | TTTACAAGGT  | GACAAGGAAG | 250 |
|    | CTCAAGACCA | AATCATGAAG  | TTGATGGACA | TTGTTGATGA  | ATACATCCCA | 300 |
|    | ACTCCAGAAC | GTCAAAGTGA  | CAAGCCATTC | TTGATGCCAG  | TTGAAGACGT | 350 |
|    | ATTCATATC  | ACTGGTCGTG  | GTACTGTTGC | TTCAGGTCGT  | ATCGACCGTG | 400 |
|    | GTACTGTAA  | GGTCGGTGAC  | GAAGTTGAAA | TCGTTGGTTT  | GGTAGATAAA | 450 |
| 35 | GTTCTTAAGT | CAGTTGTTAC  | TGGTTTGAA  | ATGTTCCACA  | AGACTTTGGA | 500 |
|    | CTTAGGTGAA | GCCGGCGATA  | ACGTTGGTGT | ATTGCTTCGT  | GGTGTGACC  | 550 |
|    | GTGATCAAGT | TGTTTCGTGGT | CAAGTATTGG | CTGCACCCGG  | CTCAATCCAA | 600 |
|    | ACTCATAAGA | AGTTTAAGGC  | ACAAGTTTAT | GTTTTGAAGA  | AGGACGAAGG | 650 |
|    | TGGTCGTAC  | ACTCCATTCT  | TCTCAGACTA | CCGTCCACAA  | TTCTACTTCC | 700 |
| 40 | ACACCACTGA | TATTACTGGT  | GAAATTGAAT | TGCCAGAAGG  | TACTGAAATG | 750 |
|    | GTTATGCCTG | GTGATAACAC  | TGAATTCAC  | GTTACTTTGA  | TCAAGCCAGC | 800 |
|    | TGCCATCGAA | AAGGGTACTA  | AGT        |             |            | 823 |

45

## 2) INFORMATION FOR SEQ ID NO: 1681

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 bases  
 (B) TYPE: Nucleic acid  
 50 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leuconostoc mesenteroides* subsp.  
*dextranicum*  
(B) STRAIN: ATCC 19255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
| 10 | GCTGCAACTG | ATGGTCCTAT | GCCACAAACA  | CGTGAACACA | TCTTGTTGGC | 50  |
|    | ACGTCAAGTT | GGTGTGACT  | ACTTGGTTGT  | CTTCTTGAAC | AAGACTGATT | 100 |
|    | TGGTTGATGA | TGAAGAATTA | GTTGAATTGG  | TTGAAATGGA | AGTTCGTGAA | 150 |
|    | TTGTTGTCAG | AATATGACTT | CCCAGGTGAC  | GATATTCCTG | TACTTAAGGG | 200 |
|    | TTCAGCTTTG | AAGGCTTTGG | AAGGTGATCC  | TGAACAAGTT | AAGGTTATCG | 250 |
| 15 | AAGAATTGAT | GGATACTGTT | GATTTCATACA | TTCCAGAACC | AGCACGTGAA | 300 |
|    | ACAGACAAGC | CATTCTTGAT | GCCTGTCGAA  | GACGTCTTCA | CAATCACTGG | 350 |
|    | TCGTGGTACA | GTTGCTTCTG | GTCGTGTTGA  | CCGTGGTGTA | TTGACTACAG | 400 |
|    | GAACTGAAAT | TGAAATCGTT | GGTTTGAAGG  | ACGAAGTTCA | AAAGACTACT | 450 |
|    | GTTACAGGTA | TCGAAATGTT | CCGTAAGACT  | TTGGAAGAAG | CTCAAGCGGG | 500 |
| 20 | TGATAACATT | GGTGCATTGT | TGCGTGGTGT  | TGATCGTAGC | AACATTGAAC | 550 |
|    | GTGGTCAAGT | TTTGCAAAG  | CCAGGTTCAA  | TTAAGACACA | CAAGAAGTTC | 600 |
|    | AAGGCTGAAG | TTTATGTCTT | GACAAAGGAA  | GAAGGTGGTC | GTCATACACC | 650 |
|    | ATTCTTCACT | AACTACCGTC | CACAATTCTA  | CTTCCACACA | ACTGATGTTA | 700 |
|    | CAGGTGTTGT | TGAATTGCCA | GCCGGTGTTG  | AAATGGTTAT | GCCTGGTGAC | 750 |
| 25 | CAAGTGACAT | TCGAAATCGA | ATTGATCTCA  | CCAGTTGCCA | TCG        | 793 |

2) INFORMATION FOR SEQ ID NO: 1682

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Prevotella buccalis*  
(B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682

|    |             |             |             |            |             |     |
|----|-------------|-------------|-------------|------------|-------------|-----|
| 45 | TATCCTTGTA  | GTTGCTGCTA  | CTGATGGTCC  | TATGCCACAG | ACACGTGAGC  | 50  |
|    | ACGTGCTTTT  | GGCTCGTCAG  | GTAAACGTTT  | CTCGTTTGGT | TGTGTTTCATG | 100 |
|    | AACAAGTGTG  | ACTTGGTAGA  | AGACGAAGAG  | ATGCTTGAAC | TCGTTGAAAT  | 150 |
|    | GGAGTTGCGC  | GAACCTTCTTG | AGCAATACGA  | ATTGCAAGAG | GATACTCCAA  | 200 |
|    | TCGTTTCGTGG | TTCTGCACTG  | GGTGCAATTGA | ATGGTGTTGA | CAAGTGGGTT  | 250 |
| 50 | GACAGCGTGA  | TGACGTTGAT  | GGACACTGTT  | GACGAGTGGA | TTCAAGAGCC  | 300 |
|    | AGAGCGTGAC  | CTTGACAAAC  | CTTTCTTGAT  | GCCAGTAGAG | GACGTGTTCT  | 350 |
|    | CTATCACAGG  | TCGTGGTACC  | GTTGTAACAG  | GACGTATTGA | GACTGGTAAG  | 400 |
|    | GTAAAGGTTG  | GCGACGAGAT  | TCAGTTGCTC  | GGTCTTGGTG | AGGACAAGAA  | 450 |

|   |            |            |            |            |            |     |
|---|------------|------------|------------|------------|------------|-----|
|   | GTCTGTTGTA | ACAGGCGTTG | AAATGTTCCG | TAAGATTCTT | TCTGAAGGTG | 500 |
|   | AAGCAGGTGA | TAACGTAGGA | CTTTTGCTCC | GCGGTATCGA | TAAGGATGAA | 550 |
|   | GTAAAGCGTG | GTATGGTTGT | TGTACACCCA | GGTGCCATCA | CTCCTCACGA | 600 |
|   | TCACTTCAAG | GCTTCCATCT | ATGTATTGAA | GAAGGAAGAG | GGTGGACGTC | 650 |
| 5 | ATACTCCATT | CGGAAACAAG | TATCGTCCTC | AGTTCTATCT | CCGTACAATG | 700 |
|   | GACTGTACAG | GTGAGATCAC | TTTGCCAGAA | GCGGTAGAGA | TGGTGATGCC | 750 |
|   | TGGTGACAAC | GTAGAGATTG | AGGTTACCTT | GATTTACAAG | GTTGCC     | 796 |

10

## 2) INFORMATION FOR SEQ ID NO: 1683

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 800 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ruminococcus bromii*
- (B) STRAIN: ATCC 27255

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GGTTGCTGCT | ACTGACGGCC | CGATGCCTCA | GACTCGTGAG | CACGTTCTGC | 50  |
|    | TCGCTCGTCA | GGTGGGTGTG | CCCGCCATCG | TCGTCGCCCT | CAACAAGTGC | 100 |
|    | GACATGGTTG | ACGATGAGGA | GCTCATTGAG | CTTGTCGAGA | TGGAGGTCGG | 150 |
| 30 | CGAGCTGCTG | ACCTCGCAGG | AGTTCGACGG | CGACAAGTGC | CCTGTCGTTT | 200 |
|    | GCATCTCCGC | CTTCCAGGCC | CTCCAGGGTG | ACGAGAAGTG | GACCCAGTCG | 250 |
|    | ATCCTCGACC | TCATGGACGC | CGTGGACGAG | TACATCCCGC | AGCCTGAGCG | 300 |
|    | CGATCTCGAC | AAGCCCTTCC | TTATGCCGAT | CGAGGACGTC | TTCACCATCA | 350 |
|    | CCGGCCCGTG | CACCGTTGTC | ACCGGTCGTG | TCGAGCGTGG | TGTCGTCAAG | 400 |
| 35 | ACTGGCGAAG | AGGTCGAGAT | CGTCGGTATC | CACGAGAAGA | CCCAGAAGAC | 450 |
|    | CACCGTTACC | GGTGTCGAGA | TGTTCCGTAA | GATCCTCGAC | GAGGGCCGCG | 500 |
|    | CTGGTGAGAA | CGTCGGCGTT | CTGCTCCGTG | GCACCAAGAA | GGAGGACGTC | 550 |
|    | GTTCGCGGCA | TGGTCCTCTC | CAAGCCTGGT | TCCACCACCC | CCCACACCGA | 600 |
|    | CTTCGAGGGC | CAGGTCTACG | TCCTCAAGAA | GGATGAGGGT | GGCCGCCACA | 650 |
| 40 | AGCCGTTCTT | CTCCCATTAC | AGCCCCCAGT | TCTACTTCCG | TACCACGGAC | 700 |
|    | GTGACTGGCA | CTGTTGAGCT | CCCCGAGGGC | ACCGAGATGG | TCATGCCTGG | 750 |
|    | CGACAACACC | GACATGACTG | TGCACCTGAT | TCACCCGGTT | GCCATGGAGG | 800 |

45

## 2) INFORMATION FOR SEQ ID NO: 1684

## (i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 545 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*  
 5 (B) STRAIN: ATCC 32075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684

|    |            |             |             |            |            |     |
|----|------------|-------------|-------------|------------|------------|-----|
|    | TGTCTTTATT | CAGGAACTGA  | TTGTATGTTT  | CTTCTCGTTT | ATATATAACA | 50  |
| 10 | TACCTTCTAT | ATTTTCATGTG | TTTCTAACGA  | ACTCATAGAA | CAACATTGCC | 100 |
|    | AAGGCTCACG | GTGGTTACTC  | CGTGTTTACC  | GGTGTCGGTG | AGCGTACCCG | 150 |
|    | TGAAGGAAAC | GATCTGTACC  | ACGAAATGCA  | GGAAACCCGC | GTCATCCAGC | 200 |
|    | TGGACGGCGA | GTCCAAAGTC  | GCCCTCGTCT  | TCGGCCAGAT | GAACGAGCCC | 250 |
|    | CCCGGAGCCC | GTGCCCCTGT  | TGCCCTGACC  | GGTCTGACCA | TCGCTGAATA | 300 |
| 15 | CTTCCGTGAC | GAAGAAGGCC  | AAGATGGTAC  | GTTCCCCCAT | TCCATATATG | 350 |
|    | TTTCTTGTGC | GCTTTGCCAA  | CTAAACACCA  | CCTAGTGCTC | CTCTTCATCG | 400 |
|    | ACAATATCTT | CCGCTTCACC  | CAAGCCGGTT  | CCGAAGTGTC | CGCCCTGCTA | 450 |
|    | GGCCGCATCC | CCTCCGCCGT  | CGGCTATCAA  | CCCACCCTCG | CCGTCGACAT | 500 |
| 20 | GGGTGGTATG | CAGGAGCGCA  | TCACAACCTAC | AACAAAAGGC | TCCAT      | 545 |

## 2) INFORMATION FOR SEQ ID NO: 1685

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegica*  
 35 (B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | GATATCGCTT | TATGGAAATT | CGAAACTCCA  | AAATTCCACG | TTACYGTTAT | 50  |
| 40 | CGATGCTCCA | GGTCACAGAG | ATTTTCATCAA | GAATATGATT | ACYGGTACCT | 100 |
|    | CCCAAGCTGA | TTGTGCTATT | TTAATCATTG  | CTGGTGGTGT | TGGTGAATTC | 150 |
|    | GAAGCTGGTA | TCTCCAAAGA | TGGTCAAACC  | AGAGAACACG | CTTTGTTAGC | 200 |
|    | TTTCACCTTA | GGTGTYAAAC | AATTGATTGT  | TGCCGTTAAC | AAAATGGACT | 250 |
|    | CTGTCAAATG | GGATCAATCC | CGTTTCGAAG  | AAATCGTCAA | GGAAGCTTCC | 300 |
| 45 | GGTTTCATCA | AGAAAGTTGG | TTACAACCCA  | AAGACTGTTC | CATTCGTTCC | 350 |
|    | AATCTCTGGT | TGGAATGGTG | ACAACATGAT  | TGAAGTYTCW | GCTAACGCYC | 400 |
|    | CATGGTACAA | AGGTTGGGAA | AAGGAAACCA  | AAGCYGGTGT | CGTTAAAGGT | 450 |
|    | AAAACCTTAT | TAGAAGCCAT | TGATGCTATT  | GAACCACCTT | CAAGACCAAC | 500 |
|    | TGAAAAACCA | TTGAGATTGC | CATTGCAAGA  | TGTCTACAAG | ATTGGTGGTA | 550 |
| 50 | TCGGAACCGT | ACCAGTCGGT | ARAGTTGAAA  | CCGGTGTCAT | TAAACCAGGT | 600 |
|    | ATGATTGTTA | CTTTCGCCCC | AGCCGGTGTT  | ACTACTGAAG | TCAAATCTGT | 650 |
|    | TGAAATGCAT | CACGAACAAT | TAGAAGCTGG  | TTACCCAGGT | GACAATGTTG | 700 |
|    | GTTTCAACGT | CAAGAATGTT | TCAGTTAAAG  | AAATCAGAAG | AGGTAAHGTT | 750 |



|   |          |    |        |      |        |      |
|---|----------|----|--------|------|--------|------|
|   | GCTGGTGA | CT | CA     | AC   | GC     | 800  |
|   | TCAAGTTA | TT | GT     | CT   | TA     | 850  |
|   | CAGTTTTG | GA | TT     | GT   | CA     | 900  |
|   | TTGGAAA  | GA | TT     | GA   | CA     | 950  |
| 5 | ATTCATCA | AA | TCTGGT | GACG | CTGCTA | 1000 |
|   | CATTRTGT | GT | TGAAGC | TTTC |        | 1020 |

## 10 2) INFORMATION FOR SEQ ID NO: 1686

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 929 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*  
 (B) STRAIN: WSA-176

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 25 | TGCTGCTTCC | GATGGTCAAA | TGTACGATTG | ATATTCCTTC | CAGCCAGTCA | 50  |
|    | GGATAACAGC | TGATACCAGT | TGCAAATAGG | CCCCAGACTC | GTGAGCACTT | 100 |
|    | GTTGCTTGCC | CGTCAGGTTG | GTGTCCAGAA | GATCGTTGTC | TTCGTCAACA | 150 |
|    | AGGTTGACGC | TGTCGATGAC | CCTGAGATGT | TGGAGCTTGT | TGAGCTCGAG | 200 |
| 30 | ATGCGTGAGC | TCCTCAACAC | TTACGGTTTC | GAGGGAGAGG | AGACCCCTAT | 250 |
|    | CATCTTCGGT | TCCGCCCTGT | GCGCTCTCGA | AGGCCGCCGC | GAGGACATTG | 300 |
|    | GTACTCAGCG | TATTGACTCC | CTCCTCGAGG | CCGTTGACAC | TTGGATCCCT | 350 |
|    | ACCCCCCAGC | GTGACTTGGA | CAAGCCCTTC | CTGATGTCCA | TTGAGGAAGT | 400 |
|    | TTTCTCCATT | GGTGGTCGTG | GTACCGTCGC | CTCTGGTCGT | GTCGAGCGTG | 450 |
| 35 | GTCTCCTCAA | GAAGGATACC | GAAGTTGAAA | TTCACGGTGC | TGATGGTATT | 500 |
|    | CTGAAGACCA | AGGTCACCGA | CATTGAGACC | TTCAAGAAGA | GCTGCGATGA | 550 |
|    | GTCTCGTGCT | GGTGACAAC  | CCGGTCTTCT | CCTCCGTGGT | ATCCGTCGTG | 600 |
|    | AGGATGTTTC | TCGTGGTATG | GTCATCGCTG | CCCCTGGCTC | CATCAAGGCC | 650 |
|    | TCCAAGAAGT | TCATGGTCTC | CATGTACGTC | TTGACTGAGG | CTGAAGGTGG | 700 |
| 40 | CCGCAAGAAC | GGCTTCGGTG | CCAATAACCG | CCCCCAGGCT | TTCATCCGCA | 750 |
|    | CTGCTGGTAA | GTTTCGAACT | ATTTGATTCA | TTGATCACGT | CCCTAACTGT | 800 |
|    | TACTTTAGAC | GAGGCTTGCG | ACCTTCATTT | CCCTGATGAG | GCCGACAAGG | 850 |
|    | ACCGCCACGT | CATGCCCGGT | GACAACGTCG | AAATGGTCCT | CAACCTCAAC | 900 |
| 45 | AACCCCGTTG | CTGCTGAGGC | TGGACAGCG  |            |            | 929 |

## 2) INFORMATION FOR SEQ ID NO: 1687

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus terreus*

(B) STRAIN: WSA-174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687

```

10  TGCCGCTTCC GATGGTCAGA TGTACGCTCA AGCCCCAGTT TCCATATAAA      50
    CATAAACGAT CTATCATCAG CACAACGCTG ACTTCTTCGC TTCCAGGCCC      100
    CAGACCCGTG AGCACTTGCT GTTGGCCCGT CAGGTCGGTG TCCAGAAGAT      150
    CGTGGTCTTC GTCAACAAGG TCGATGCCGT TGATGACCCG GAGATGTTGG      200
15  AGCTCGTTGA GCTGGAAATG CGCGAGCTCC TGACCAGCTA CGGATTCGAG      250
    GGTGAAGAGA CCCCCATCAT CTTCGGTTCT GCTCTCTGCG CTCTTGAGGG      300
    CCGCCGTCCT GAGATTGGTA CTGAGAAGAT TGACGAGCTG ATGCACGCCG      350
    TCGACACCTG GATCCCCACC CCCCAGCGTG ACCTCGACAA GCCCTTCCTG      400
    ATGTCCGTCG AGGAAGTCTT CTCCATTGCT GGTCGTGGTA CCGTCGCTTC      450
20  CGGCCGTGTC GAGCGTGGTA TTCTGAAGAA GGATAGCGAA GTCGAGATCA      500
    TCGGTGGTGC TTTCGACGCC ACGAAGACCA AGGTCACTGA CATCGAGACC      550
    TTCAAGAAGT CTTGCGACGA GTCTCGCGCT GGTGACAACT CTGGTCTCCT      600
    CCTCCGTGGT ATCCGTCGTG AGGATGTTCG GCGTGGTATG GTCATTGCTG      650
    CTCCTGGCAG CACCAAGGCC CACGACAAGT TCCTTGTCTC TATGTACGTC      700
25  CTCACTGAGG CTGAGGGTGG CCGTCGTACC GGATTCGGTA CCAACTACCG      750
    CCCCCAGGTC TTCATCCGTA CTGCCGGTAA GTGTTCCTGG AAGAGGCTTT      800
    GAGCCTATAT AGGATCTCGG ATAATTTACT AATCCACCAT ATAGATGAGG      850
    CCGCTGACCT CAGCTTCCCC GACAACGATG ACTCCCGCCG TGTCATGCCC      900
    GGTGACAACG TTGAGATGGT CCTGAAGACC CACCGCCCCG TGGCTGCTGA      950
30  G                                                                951

```

## 2) INFORMATION FOR SEQ ID NO: 1688

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Candida norvegica*

(B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688

```

50  CGTTGCCGCT ACCGATGGTC AAATGCCTCA AACTAGAGAA CATTGCTAT      50
    TGGCTAGACA GGTGTTGTT CAACACATTG TCGTGTGTTGT TAACAAGGTT      100
    GACACTATTG ATGATCCAGA AATGTTGGAA TTGGTTGAAA TGGAAATGAG      150
    AGAGTTGATT GCCACTTATG GTTTCGATGG TGATAACACC CCAGTTATCA      200

```

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | TGGGTTCTGC | TCTATGTGCT | TTGGAAGGTC | GTGAACCTGA | AATCGGTGCT  | 250 |
|    | CAATCAATCG | ACAGATTGTT | GGAAGCCGTT | GATGAATACA | TTCCAACCTCC | 300 |
|    | AACTAGAGAT | TTGGAAAAAC | CATTCTTGAT | GGGTGTTGAA | GATGTCTTCT  | 350 |
|    | CCATTTCTGG | TAGAGGTACC | GTCTGTACCG | GTCGTGTTGA | AAGAGGTAAC  | 400 |
| 5  | TTGAAGAAAG | GTGATGAAAT | CGAAATTGTC | GGCTACAACA | AGACTCCAAT  | 450 |
|    | CAAAACCACC | GTCACCGGTA | TTGAGATGTT | CAAAAAGGAA | TTAGACCAAG  | 500 |
|    | CTATGGCTGG | TGATAACTGT | GGTATCTTAT | TACGTGGTGT | TAAGAGAGAT  | 550 |
|    | GATATCAAGA | GAGGTATGGT | TATCTCTAAA | GTCAACACCG | TTTCCGCACA  | 600 |
|    | CACCAAATTC | TTGGCCTCTT | TATACGTCTT | GAATAAGAA  | GAAGGTGGTC  | 650 |
| 10 | GTCATTCAGG | TTTTGCTGAA | AACTACAGAC | CTCAATTGTT | CATCAGAACC  | 700 |
|    | GGTGATGTCA | CTGTTACTTT | AACCTTCCCA | GAAGATGCTG | ATCACTCTCA  | 750 |
|    | GCAAGTCTTA | CCAGGTGACA | ACGTTGAAAT | GGAATGTACC | TTGGTTCATC  | 800 |
|    | CAACTGCTCT | TGAAACCGGT | CAA        |            |             | 823 |

15

## 2) INFORMATION FOR SEQ ID NO: 1689

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 803 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*  
 (B) STRAIN: ATCC 201076

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689

|    |            |            |            |             |             |     |
|----|------------|------------|------------|-------------|-------------|-----|
|    | GCTGCTACTG | ACGGTCAAAT | GCCTCAAAC  | AGGGAACATA  | TGTTGTTGGC  | 50  |
|    | GAGACAAGTT | GGTATCCAAA | ACTTGTTGTT | TTTTGTAAAC  | AAAGTTGATA  | 100 |
| 35 | CCATTGATGA | CCCAGAAATG | TTGGAATTGG | TTGAAATGGA  | AATGAGGGAA  | 150 |
|    | TTATTGAGCT | CTTATGGGTT | TGATGGTGAA | AACACTCCAG  | TTATCATGGG  | 200 |
|    | ATCAGCCTTG | TGTGCTTTAG | AAGGTAAACA | ACCAGAAATC  | GGTGTTC AAG | 250 |
|    | CCATTCAAAA | ATTATTGGAT | GCTGTTGATG | AATATATTCC  | AACTCCAGAA  | 300 |
|    | AGAGATGCTG | ACCAACCATT | TTTGATGCCA | GTGGAAGATG  | TGTTTTCTAT  | 350 |
| 40 | TTCAGGTAGA | GGAACCGTTG | TCACCGGAAG | AGTTGAAAGA  | GGTATGTTGA  | 400 |
|    | AGAAAGGTGA | AGAAGTAKAA | GTCATTGGTG | AAAACCTCATT | TAAGGCTACT  | 450 |
|    | TCCACGGGTA | TTGAGATGTT | CAAAAAGGAA | TTGGATGCCG  | CTATGGCCGG  | 500 |
|    | TGACAACTGT | GGTATTTTGT | TGAGAGGTGT | CAAGAGAGAC  | GAAGTCAAGA  | 550 |
|    | GGGGTATGGT | TTTGGCCAAA | CCAGGTACCA | CCACCCACCA  | CCAAAAGTTT  | 600 |
| 45 | TTGGCTTCCA | TTTATATCTT | GACTGCTGAA | GAAGGTGGAC  | G TAGTACCCC | 650 |
|    | TTTCAGTGAA | GGATACAAAC | CACAATGTTT | CTTTAGAACT  | AGTGATGTTA  | 700 |
|    | CCACGACATT | TACTTTCCCA | GAAGGTGAAG | GTGTTGACCA  | CTCACAAATG  | 750 |
|    | GTTATGCCAG | GAGRCAATGT | TGAAATGGTG | GGAACCTTAA  | TCAAGAAAGC  | 800 |
|    | TCC        |            |            |             |             | 803 |

50

## 2) INFORMATION FOR SEQ ID NO: 1690

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690

CAGGTCCTGT TGCGACTGAA GAA

23

15

## 2) INFORMATION FOR SEQ ID NO: 1691

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691

CACAGATAAA CCTGAGTGTG CTTTC

25

30

## 2) INFORMATION FOR SEQ ID NO: 1692

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692

GGTGAGAACT GTGGTATCTT ACTT

24

45

## 2) INFORMATION FOR SEQ ID NO: 1693

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693

CATTTCAACG CCTTCTTTCA ACTG

24

10

2) INFORMATION FOR SEQ ID NO: 1694

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694

AAGGCAAGGA TGACAACGGC

20

25

2) INFORMATION FOR SEQ ID NO: 1695

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695

ACGATTTC CA CTTCTTCCTG G

21

40

2) INFORMATION FOR SEQ ID NO: 1696

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696

ATGTTCTGT AGTTGCTGGA

20

5

## 2) INFORMATION FOR SEQ ID NO: 1697

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697

TTTCTTCAGC AATACCAACA AC

22

20

## 2) INFORMATION FOR SEQ ID NO: 1698

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698

35 GGAATCAACA GATGGTTTAC AAA

23

## 2) INFORMATION FOR SEQ ID NO: 1699

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699

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GCATCTTCTG GGAAAGGTGT

20

## 2) INFORMATION FOR SEQ ID NO: 1700

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700

AAGATGCGGA AAGAAGCGAA

20

## 2) INFORMATION FOR SEQ ID NO: 1701

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701

ATTATGGATC AGTTCTTGGA TCA

23

## 2) INFORMATION FOR SEQ ID NO: 1702

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*  
 (B) STRAIN: Challis V288  
 (C) ACCESSION NUMBER: L20574

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TTCATAGACG | CTGAGCACGC | TTTGGATCCA | TCTTACGCGG | CTGCTCTAGG | 50  |
| TGTAAATATT | GATGAGCTGT | TGCTATCTCA | ACCAGATTCT | GGTGAGCAAG | 100 |
| GTTTAGAAAT | TGCAGGAAAA | TTGATTGACT | CTGGGGCAGT | TGATTTAGTT | 150 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GTCATCGACT | CTGTTGCAGC | TCTTGTACCA | CGTGCGGAAA | TCGATGGAGA | 200 |
| TATCGGTGAT | AGC        |            |            |            | 213 |

5

## 2) INFORMATION FOR SEQ ID NO: 1703

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 692 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
- (B) STRAIN: strain GS-5
- (C) ACCESSION NUMBER: M61897

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703

|    |            |             |             |            |            |     |
|----|------------|-------------|-------------|------------|------------|-----|
|    | GGGCCGGAAT | CTTCTGGTAA  | GACAACTGTC  | GCTCTTCATG | CTGCTGCTCA | 50  |
|    | GGCGCAAAAA | GATGGCGGTA  | TTGCCGCTTT  | CATTGATGCA | GAACATGCCC | 100 |
| 25 | TTGATCCAGC | CTATGCTGCT  | GCTCTTGCG   | TTAATATTGA | TGAGCTTTTG | 150 |
|    | CTTTCACAAC | CAGATTCAGG  | AGAACAGGGT  | CTTGAAATTG | CAGGGAAATT | 200 |
|    | GATTGATTCT | GGCGCTGTTG  | ATTTAGTTGT  | TGTTGACTCA | GTGGCAGCTT | 250 |
|    | TAGTACCACG | TGCGGAGATT  | GACGGAGATA  | TTGGTAATAG | TCATGTTGGC | 300 |
|    | TTACAAGCAC | GCATGATGAG  | TCAAGCGATG  | CGTAAATTAT | CAGCTTCAAT | 350 |
| 30 | CAATAAAACA | AAAACCATTG  | CTATTTTTTAT | TAATCAATTG | CGGGAAAAAG | 400 |
|    | TTGGTATTAT | GTTTGGTAAAT | CCAGAAACAA  | CCCCTGGCGG | GCGTGCCTTG | 450 |
|    | AAGTTTTTAT | CTTCTGTGCG  | TCTTGATGTC  | CGCGGCAATA | CTCAAATTAA | 500 |
|    | AGGAACCGGG | GAACAAAAAG  | ACAGCAATAT  | TGGTAAAGAG | ACCAAAATTA | 550 |
|    | AAGTTGTAA  | AAATAAAGTT  | GCTCCACCAT  | TTAAGGAAGC | TTTTGTAGAA | 600 |
| 35 | ATTATATATG | GTGAAGGCAT  | TTCTCGTACA  | GGTGAATTAG | TTAAGATTGC | 650 |
|    | CAGTGATTTG | GGAATTATCC  | AAAAAGCTGG  | AGCTTGGTAC | TC         | 692 |

## 40 2) INFORMATION FOR SEQ ID NO: 1704

## (i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 1204 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (C) ACCESSION NUMBER: Z17307



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704

|    |            |             |            |            |            |      |
|----|------------|-------------|------------|------------|------------|------|
|    | ATGGCGAAAA | AACCAAAAAA  | ATTAGAAGAA | ATTTCAAAAA | AATTTGGGGC | 50   |
|    | AGAACGTGAA | AAGGCCTTGA  | ATGACGCTCT | TAAATTGATT | GAGAAAGACT | 100  |
| 5  | TTGGTAAAGG | ATCAATCATG  | CGTTTGGGTG | AACGTGCGGA | GCAAAAGGTG | 150  |
|    | CAAGTGATGA | GCTCAGGTTT  | TTTAGCTCTT | GACATTGCCC | TTGGCTCAGG | 200  |
|    | TGGTTATCCT | AAGGGACGTA  | TCATCGAAAT | CTATGGCCCA | GAGTCATCTG | 250  |
|    | GTAAGACAAC | GGTTGCCCTT  | CATGCAGTTG | CACAAGCGCA | AAAAGAAGGT | 300  |
|    | GGGATTGCTG | CCTTTATCGA  | TGCGGAACAT | GCCCTTGATC | CAGCTTATGC | 350  |
| 10 | TGCGGCCCTT | GGTGTCAATA  | TTGACGAATT | GCTCTTGTCT | CAACCAGACT | 400  |
|    | CAGGAGAGCA | AGGTCTTGAG  | ATTGCGGGAA | AATTGATTGA | CTCAGGTGCA | 450  |
|    | GTTGATCTTG | TCGTAGTCGA  | CTCAGTTGCT | GCCCTTGTTT | CTCGTGCGGA | 500  |
|    | AATTGATGGA | GATATCGGAG  | ATAGCCATGT | TGGTTTGCAG | GCTCGTATGA | 550  |
|    | TGAGCCAGGC | CATGCGTAAA  | CTTGGCGCCT | CTATCAATAA | AACCAAAACA | 600  |
| 15 | ATTGCCATTT | TTATCAACCA  | ATTGCGTGAA | AAAGTTGGAG | TGATGTTTGG | 650  |
|    | AAATCCAGAA | ACAACACCGG  | GCGGACGTGC | TTTGAAATTC | TATGCTTCAG | 700  |
|    | TCCGCTTGGA | TGTTTCGTGGT | AATACACAAA | TTAAGGGAAC | TGGTGATCAA | 750  |
|    | AAAGAAACCA | ATGTCGGTAA  | AGAACTAAG  | ATTAAGGTTG | TAAAAAATAA | 800  |
|    | GGTAGCTCCA | CCGTTTAAGG  | AAGCCGTAGT | TGAAATTATG | TACGGAGAAG | 850  |
| 20 | GAATTTCTAA | GACTGGTGAG  | CTTTTGAAGA | TTGCAAGCGA | TTTGGATATT | 900  |
|    | ATCAAAAAAG | CAGGGGCTTG  | GTATTCTTAC | AAAGATGAAA | AAATTGGGCA | 950  |
|    | AGGTTCTGAG | AATGCTAAGA  | AATACTTGGC | AGAGCACCCA | GAAATCTTTG | 1000 |
|    | ATGAAATTGA | TAAGCAAGTC  | CGTTCTAAAT | TTGGCTTGAT | TGATGGAGAA | 1050 |
|    | GAAGTTTCAG | AACAAGATAC  | TGAAAACAAA | AAAGATGAGC | CAAAGAAAGA | 1100 |
| 25 | AGAAGCAGTG | AATGAAGAAG  | TTCCGCTTGA | CTTAGGCGAT | GAACCTGAAA | 1150 |
|    | TCGAAATTGA | AGAATAAGCT  | GTAAAGCAG  | TGGAGAAATC | CGCTACTTTT | 1200 |
|    | TCGA       |             |            |            |            | 1204 |

30.

## 2) INFORMATION FOR SEQ ID NO: 1705

## (i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 981 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

40

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
- (B) STRAIN: NZ131
- (C) ACCESSION NUMBER: U21934

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGCGTTCAG | GAAGTCTAGC | TCTTGATATT | GCTTGGATAG | CTGGTGGTTA | 50  |
|    | TCCTAAAGGA | CGTATCATCG | AAATCTATGG | TCCAGAGTCT | TCCGGTAAAA | 100 |
| 50 | CGACTGTGGC | TTTACATGCT | GTAGCACAAG | CTCAAAAAGA | AGGTGGAATC | 150 |
|    | GCAGCCTTTA | TCGATGCCGA | GCATGCGCTT | GATCCAGCTT | ATGCTGCTGC | 200 |
|    | GCTTGGGGTT | AATATTGATG | AACTTCTCTT | GTCTCAACCA | GATTCTGGAG | 250 |
|    | AACAAGGACT | TGAAATTGCA | GGTAAATTGA | TTGATTCTGG | TGCGGTTGAC | 300 |

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | CTGGTTGTTG | TCGATTCAGT | AGCAGCTTTA | GTGCCACGTG | CTGAAATTGA  | 350 |
|    | TGGTGATATT | GGCGATAGCC | ATGTCGGATT | GCAAGCACGT | ATGATGAGTC  | 400 |
|    | AGGCCATGCG | TAAATTATCA | GCTTCTATTA | ATAAAACAAA | AACTATCGCA  | 450 |
|    | ATCTTTATCA | ACCAATTGCG | TGAAAAAGTT | GGTGTGATGT | TTGGAAATCC  | 500 |
| 5  | TGAAACAACA | CCAGGTGGTC | GAGCTTTGAA | ATTCTATGCT | TCTGTTTCGGC | 550 |
|    | TGGATGTGCG | TGGAAACAAC | CAAATTAAAG | GAAGTGGTGA | CCAAAAGATA  | 600 |
|    | GCCAGCATTG | GTAAGGAGAC | CAAATCAAG  | GTTGTTAAAA | ACAAGGTCGC  | 650 |
|    | TCCGCCATTT | AAGGTAGCAG | AAGTTGAAAT | CATGTATGGG | GAAGGTATTT  | 700 |
|    | CTCGTACAGG | GGAGCTTGTC | AAAATTGCTT | CTGATTTGGA | CATTATCCAA  | 750 |
| 10 | AAAGCAGGTG | CTTGTTCTC  | TTATAATGGT | GAGAAGATTG | GCCAAGGTTT  | 800 |
|    | TGAAAATGCT | AAGCGTTATT | TGGCCGATCA | TCCACAATTG | TTTGATGAAA  | 850 |
|    | TCGACCGTAA | AGTACGTGTT | AAATTTGGTT | TGCTTGAAGA | AAGCGAAGAA  | 900 |
|    | GAATCTGCTA | TGGCAGTAGC | ATCAGAAGAA | ACCGATGATC | TTGCTTTAGA  | 950 |
|    | TTTAGATAAT | GGTATTGAAA | TTGAAGATTA | A          |             | 981 |
| 15 |            |            |            |            |             |     |

## 2) INFORMATION FOR SEQ ID NO: 1706

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus salivarius* subsp. *thermophilus*
  - (C) ACCESSION NUMBER: M94062
- 30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
| 35 | GCGTATGCAC | GAGCTCTAGG | TGTTAATATC | GATGAGCTTC | TTTTGTTCGCA | 50  |
|    | GCCTGATTCT | GGTGAGCAAG | GTCTCGAAAT | TGCAGGTAAG | CTGATTGACT  | 100 |
|    | CTGGTGCAGT | GGATTTAGTT | GTTGTTGACT | CAGTTGCGGC | CTTCGTACCA  | 150 |
|    | CGTGACAGAA | TTGATGGAGA | TAGTGGTGAC | AGTCATGTAG | GACTTCAAGC  | 200 |
|    | GCGTATGATG | AGTCAAGCCA | TGCGTAAACT | TTCTGCATCT | ATTAATAAAA  | 250 |
| 40 | CAAAAACGAT | TGCTATCTTT | ATTAACCAGT | TGCGTGAAAA | AGTTGGTATC  | 300 |
|    | ATGTTTGGTA | AC         |            |            |             | 312 |

## 45 2) INFORMATION FOR SEQ ID NO: 1707

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 831 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 50
- (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: J02967

5.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707

|    |             |            |            |             |             |     |
|----|-------------|------------|------------|-------------|-------------|-----|
|    | ATGAAAAACA  | CAATACATAT | CAACTTCGCT | ATTTTTTTTAA | TAATTGCAAA  | 50  |
|    | TATTATCTAC  | AGCAGCGCCA | GTGCATCAAC | AGATATCTCT  | ACTGTTGCAT  | 100 |
| 10 | CTCCATTATT  | TGAAGGAAC  | GAAGGTTGTT | TTTTACTTTA  | CGATGCATCC  | 150 |
|    | ACAAACGCTG  | AAATTGCTCA | ATTCAATAAA | GCAAAGTGTG  | CAACGCAAAT  | 200 |
|    | GGCACCAGAT  | TCAACTTTCA | AGATCGCATT | ATCACTTATG  | GCATTTGATG  | 250 |
|    | CGGAAATAAT  | AGATCAGAAA | ACCATATTCA | AATGGGATAA  | AACCCCCAAA  | 300 |
|    | GGAATGGAGA  | TCTGGAACAG | CAATCATACA | CCAAAGACGT  | GGATGCAATT  | 350 |
| 15 | TTCTGTTGTT  | TGGGTTTCGC | AAGAAATAAC | CCAAAAAATT  | AGATTAAATA  | 400 |
|    | AAATCAAGAA  | TTATCTCAAA | GATTTTGATT | ATGGAAATCA  | AGACTTCTCT  | 450 |
|    | GGAGATAAAG  | AAAGAAACAA | CGGATTAACA | GAAGCATGGC  | TCGAAAAGTAG | 500 |
|    | CTTAAAAAATT | TCACCAGAAG | AACAAATTCA | ATTCCTGCGT  | AAAATTATTA  | 550 |
|    | ATCACAATCT  | CCCAGTTAAA | AACTCAGCCA | TAGAAAACAC  | CATAGAGAAC  | 600 |
| 20 | ATGTATCTAC  | AAGATCTGGA | TAATAGTACA | AAACTGTATG  | GGAAAAGTGG  | 650 |
|    | TGCAGGATTC  | ACAGCAAATA | GAACCTTACA | AAACGGATGG  | TTTGAAGGGT  | 700 |
|    | TTATTATAAG  | CAAATCAGGA | CATAAATATG | TTTTTGTGTC  | CGCACTTACA  | 750 |
|    | GGAAACTTGG  | GGTCGAATTT | AACATCAAGC | ATAAAAGCCA  | AGAAAAATGC  | 800 |
|    | GATCACCATT  | CTAAACACAC | TAAATTTATA | A           |             | 831 |

25.

## 2) INFORMATION FOR SEQ ID NO: 1708

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

40

(B) STRAIN: HH22

(C) ACCESSION NUMBER: M60253

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 45 | TTGAAAAAGT | TAATATTTTT | AATTGTAATT | GCTTTAGTTT | TAAGTGCATG | 50  |
|    | TAATTCAAAC | AGTTCACATG | CCAAAGAGTT | AAATGATTTA | GAAAAAAAT  | 100 |
|    | ATAATGCTCA | TATTGGTGTT | TATGCTTTAG | ATACTAAAAG | TGGTAAGGAA | 150 |
|    | GTAAATTTTA | ATTCAGATAA | GAGATTTGCC | TATGCTTCAA | CTTCAAAAGC | 200 |
|    | GATAAATAGT | GCTATTTTGT | TAGAACAAGT | ACCTTATAAT | AAGTTAAATA | 250 |
| 50 | AAAAAGTACA | TATTAACAAA | GATGATATAG | TTGCTTATTC | TCCTATTTTA | 300 |
|    | GAAAAATATG | TAGGAAAAGA | TATCACTTTA | AAAGCACTTA | TTGAGGCTTC | 350 |
|    | AATGACATAT | AGTGATAATA | CAGCAAACAA | TAAAATTATA | AAAGAAATCG | 400 |
|    | GTGGAATCAA | AAAAGTTAAA | CAACGTCTAA | AAGAAGTAGG | AGATAAAGTA | 450 |

|   |            |             |            |            |            |     |
|---|------------|-------------|------------|------------|------------|-----|
|   | ACAAATCCAG | TTAGATATGA  | GATAGAATTA | AATTACTATT | CACCAAAGAG | 500 |
|   | CAAAAAAGAT | ACTTCAACAC  | CTGCTGCTTT | CGGTAAGACT | TTAAATAAAC | 550 |
|   | TTATCGCAA  | TGGAATAATTA | AGCAAAGAAA | ACAAAAAATT | CTTACTTGAT | 600 |
|   | TTAATGTAA  | ATAATAAAAG  | CGGAGATACT | TTAATTAAAG | ACGGTGTTCC | 650 |
| 5 | AAAAGACTAT | AAGGTTGCTG  | ATAAAAGTGG | TCAAGCAATA | ACATATGCTT | 700 |
|   | CTAGAAATGA | TGTTGCTTTT  | GTTTATCCTA | AGGGCCAATC | TGAACCTATT | 750 |
|   | GTTTTAGTCA | TTTTTACGAA  | TAAAGACAAT | AAAAGTGATA | AGCCAAATGA | 800 |
|   | TAAGTTGATA | AGTGAAACCG  | CCAAGAGTGT | AATGAAGGAA | TTTTAA     | 846 |

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## 2) INFORMATION FOR SEQ ID NO: 1709

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 555 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*  
 (C) ACCESSION NUMBER: M29695

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGTCCGCGA | GCACCCCCCC | CATAACTCTT | CGCCTCATGA | CCGAGCGCGA | 50  |
|    | CCTGCCGATG | CTCCATGACT | GGCTCAACCG | GCCGCACATC | GTTGAGTGGT | 100 |
| 30 | GGGGTGGCGA | CGAAGAGCGA | CCGACTCTTG | ATGAAGTGCT | GGAACACTAC | 150 |
|    | CTGCCCAGAG | CGATGGCGGA | AGAGTCCGTA | ACACCGTACA | TCGCAATGCT | 200 |
|    | GGGCGAGGAA | CCGATCGGCT | ATGCTCAGTC | GTACGTCGCG | CTCGGAAGCG | 250 |
|    | GTGATGGCTG | GTGGGAAGAT | GAAACTGATC | CAGGAGTGCG | AGGAATAGAC | 300 |
|    | CAGTCTCTGG | CTGACCCGAC | ACAGTTGAAC | AAAGGCCTAG | GAACAAGGCT | 350 |
| 35 | TGTCCGCGCT | CTCGTTGAAC | TACTGTTCTC | GGACCCCACC | GTGACGAAGA | 400 |
|    | TTCAGACCGA | CCCGACTCCG | AACAACCATC | GAGCCATACG | CTGCTATGAG | 450 |
|    | AAGGCAGGAT | TCGTGCGGGA | GAAGATCATC | ACCACGCCTG | ACGGGCCGGC | 500 |
|    | GGTTTACATG | GTTCAAACAC | GACAAGCCTT | CGAGAGAAAG | CGCGGTGTTG | 550 |
|    | CCTAA      |            |            |            |            | 555 |

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## 2) INFORMATION FOR SEQ ID NO: 1710

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 732 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*  
 (C) ACCESSION NUMBER: K02987

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 5  | ATGAACCAGA | AAAACCCTAA | AGACACGCAA | AATTTTATTA | CTTCTAAAAA | 50  |
|    | GCATGTAAAA | GAAATATTGA | ATCACACGAA | TATCAGTAAA | CAAGACAACG | 100 |
|    | TAATAGAAAT | CGGATCAGGA | AAAGGACATT | TTACCAAAGA | GCTAGTCAAA | 150 |
|    | ATGAGTCGAT | CAGTTACTGC | TATAGAAATT | GATGGAGGCT | TATGTCAAGT | 200 |
| 10 | GACTAAAGAA | GCGGTAAACC | CCTCTGAGAA | TATAAAAGTG | ATTCAAACGG | 250 |
|    | ATATTCTAAA | ATTTTCCTTC | CCAAAACATA | TAAACTATAA | GATATATGGT | 300 |
|    | AATATTCCTT | ATAACATCAG | TACGGATATT | GTCAAAGAG  | TTACCTTTGA | 350 |
|    | AAGTCAGGCT | AAATATAGCT | ATCTTATCGT | TGAGAAGGGA | TTTGCGAAAA | 400 |
|    | GATTGCAAAA | TCTGCAACGA | GCTTTGGGTT | TACTATTAAT | GGTGGAGATG | 450 |
| 15 | GATATAAAAA | TGCTCAAAAA | AGTACCACCA | CTATATTTTC | ATCCTAAGCC | 500 |
|    | AAGTGTAGAC | TCTGTATTGA | TTGTTCTTGA | ACGACATCAA | CCATTGATTT | 550 |
|    | CAAAGAAGGA | CTACAAAAAG | TATCGATCTT | TTGTTTATAA | GTGGGTAAAC | 600 |
|    | CGTGAATATC | GTGTTCTTTT | CACTAAAAAC | CAATTCCGAC | AGGCTTTGAA | 650 |
|    | GCATGCAAAT | GTCACTAATA | TTAATAAACT | ATCGAAGGAA | CAATTTCTTT | 700 |
| 20 | CTATTTTCAA | TAGTTACAAA | TTGTTTCACT | AA         |            | 732 |

## 2) INFORMATION FOR SEQ ID NO: 1711

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 738 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: *Escherichia coli*  
 (B) STRAIN: BM2570  
 (C) ACCESSION NUMBER: M19270

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
| 40 | ATGAACAAAA | ATATAAAATA | TTCTCAAAAC | TTTTTAACGA  | GTGAAAAAGT | 50  |
|    | ACTCAACCAA | ATAATAAAAC | AATTGAATTT | AAAAGAAACC  | GATACCGTTT | 100 |
|    | ACGAAATTGG | AACAGGTAAA | GGGCATTTAA | CGACGAAACT  | GGCTAAAATA | 150 |
|    | AGTAAACAGG | TAACGTCTAT | TGAATTAGAC | AGTCATCTAT  | TCAACTTATC | 200 |
| 45 | GTCAGAAAAA | TTAAAATCGA | ATACTCGTGT | CACTTTAATT  | CACCAAGATA | 250 |
|    | TTCTACAGTT | TCAATTCCCT | AACAAACAGA | GGTATAAAAT  | TGTTGGGAAT | 300 |
|    | ATTCCTTACC | ATTTAAGCAC | ACAAATTATT | AAAAAAGTGG  | TTTTTGAAAG | 350 |
|    | CCATGCGTCT | GACATCTATC | TGATTGTTGA | AGAAGGATTC  | TACAAGCGTA | 400 |
|    | CCTTGGATAT | TCACCGAACA | CTAGGGTTGC | TCTTGCACAC  | TCAAGTCTCG | 450 |
| 50 | ATTCAGCAAT | TGCTTAAGCT | GCCAGCGGAA | TGCTTTTCATC | CTAAACCAAG | 500 |
|    | AGTAAACAGT | GTCTTAATAA | AACTTACCCG | CCATACCACA  | GATGTTCCAG | 550 |
|    | ATAAATATTG | GAAGCTATAT | ACGTACTTTG | TTTCAAAATG  | GGTCAATCGA | 600 |
|    | GAATATCGTC | AACTGTTTAC | TAAAAATCAG | TTTCATCAAG  | CAATGAAACA | 650 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CGCCAAAGTA | AACAATTTAA | GTACCGTTAC | TTATGAGCAA | GTATTGTCTA | 700 |
| TTTTTAATAG | TTATCTATTA | TTTAACGGGA | GGAAATAA   |            | 738 |

5

## 2) INFORMATION FOR SEQ ID NO: 1712

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 735 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: RN451
- (C) ACCESSION NUMBER: M17990

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| ATGAACGAGA    | AAAATATAAA | ACACAGTCAA | AACTTTATTA | CTTCAAAACA | 50  |
| TAATATAGAT    | AAAATAATGA | CAAATATAAG | ATTAAATGAA | CATGATAATA | 100 |
| 25 TCTTTGAAAT | CGGCTCAGGA | AAAGGGCATT | TTACCCTTGA | ATTAGTACAG | 150 |
| AGGTGTAATT    | TCGTAAGTGC | CATTGAAATA | GACCATAAAT | TATGCAAAAC | 200 |
| TACAGAAAAT    | AAACTTGTTG | ATCACGATAA | TTTCCAAGTT | TTAAACAAGG | 250 |
| ATATATTGCA    | GTTTAAATTT | CCTAAAAACC | AATCCTATAA | AATATTTGGT | 300 |
| AATATACCTT    | ATAACATAAG | TACGGATATA | ATACGCAAAA | TTGTTTTTGA | 350 |
| 30 TAGTATAGCT | GATGAGATTT | ATTTAATCGT | GGAATACGGG | TTTGCTAAAA | 400 |
| GATTATTAAA    | TACAAAACGC | TCATTGGCAT | TATTTTTAAT | GGCAGAAGTT | 450 |
| GATATTTCTA    | TATTAAGTAT | GGTTCCAAGA | GAATATTTTC | ATCCTAAACC | 500 |
| TAGAGTGAAT    | AGCTCACTTA | TCAGATTAAA | TAGAAAAAAA | TCAAGAATAT | 550 |
| CACACAAAGA    | TAAACAGAAG | TATAATTATT | TCGTTATGAA | ATGGGTTAAC | 600 |
| 35 AAAGAATACA | AGAAAATATT | TACAAAAAAT | CAATTTAACA | ATTCCTTAAA | 650 |
| ACATGCAGGA    | ATTGACGATT | TAAACAATAT | TAGCTTTGAA | CAATTCTTAT | 700 |
| CTCTTTTCAA    | TAGCTATAAA | TTATTTAATA | AGTAA      |            | 735 |

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## 2) INFORMATION FOR SEQ ID NO: 1713

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1029 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: V583

(C) ACCESSION NUMBER: U00456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713

|    |            |            |             |            |            |      |
|----|------------|------------|-------------|------------|------------|------|
| 5  | ATGAATAAAA | TAAAAGTCGC | AATTATCTTC  | GGCGGTTGCT | CGGAGGAACA | 50   |
|    | TGATGTGTCG | GTAAAATCCG | CAATAGAAAT  | TGCTGCGAAC | ATTAATACTG | 100  |
|    | AAAAATTCGA | TCCGCACTAC | ATCGGAATTA  | CAAAAACGG  | CGTATGGAAG | 150  |
|    | CTATGCAAGA | AGCCATGTAC | GGAATGGGAA  | GCCGATAGTC | TCCCCGCCAT | 200  |
|    | ATTCTCCCCG | GATAGGAAAA | CGCATGGTCT  | GCTTGTCATG | AAAGAAAGAG | 250  |
| 10 | AATACGAAAC | TCGGCGTATT | GACGTGGCTT  | TCCCGGTTTT | GCATGGCAAA | 300  |
|    | TGCGGGGAGG | ATGGTGCGAT | ACAGGGTCTG  | TTTGAATTGT | CTGGTATCCC | 350  |
|    | CTATGTAGGC | TGCGATATTC | AAAGCTCCGC  | AGCTTGCATG | GACAAATCAC | 400  |
|    | TGGCCTACAT | TCTTACAAAA | AATGCGGGCA  | TCGCCGTCCC | CGAATTTCAA | 450  |
|    | ATGATTGAAA | AAGGTGACAA | ACCGGAGGCG  | AGGACGCTTA | CCTACCCTGT | 500  |
| 15 | CTTTGTGAAG | CCGGCACGGT | CAGGTTTCGTC | CTTTGGCGTA | ACCAAAGTAA | 550  |
|    | ACAGTACGGA | AGAATAAAC  | GCTGCGATAG  | AAGCAGCAGG | ACAATATGAT | 600  |
|    | GGAAAAATCT | TAATTGAGCA | AGCGATTTCG  | GGCTGTGAGG | TCGGCTGCGC | 650  |
|    | GGTCATGGGA | AACGAGGATG | ATTTGATTGT  | CGGCGAAGTG | GATCAAATCC | 700  |
|    | GGTTGAGCCA | CGGTATCTTC | CGCATCCATC  | AGGAAAACGA | GCCGGAAAAA | 750  |
| 20 | GGCTCAGAGA | ATGCGATGAT | TATCGTTCCA  | GCAGACATTC | CGGTCGAGGA | 800  |
|    | ACGAAATCGG | GTGCAAGAAA | CGGCAAAGAA  | AGTATATCGG | GTGCTTGGAT | 850  |
|    | GCAGAGGGCT | TGCTCGTGTT | GATCTTTTTT  | TGCAGGAGGA | TGGCGGCATC | 900  |
|    | GTTCTAAACG | AGGTCAATAC | CCTGCCCCGT  | TTTACATCGT | ACAGCCGCTA | 950  |
|    | TCCACGCATG | GCGGCTGCCG | CAGGAATCAC  | GCTTCCCGCA | CTAATTGACA | 1000 |
| 25 | GCCTGATTAC | ATTGGCGATA | GAGAGGTGA   |            |            | 1029 |

2) INFORMATION FOR SEQ ID NO: 1714

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 45 | GCACAGGTTC | AGTTGGGCTT | GATCTTGCTT | TAGGTATAGG | CGGTGTTCCA | 50  |
|    | AAAGGAAGAA | TTATAGAAAT | TTATGGRCTT | GAAAGTTCAG | GTAAAACCAC | 100 |
|    | TCTAACTCTA | CACATTATCG | CAGAATGCCA | AAAAGCAGGT | GGRGTTTGTG | 150 |
|    | CTTTTATCGA | TGCAGAACAT | GCRCTTGATG | TRAAATATGC | TAAAAATTTG | 200 |
|    | GGTGTAATA  | CAGATGATTT | GTATGTTTCT | CAGCCTGATT | TTGGAGARCA | 250 |
| 50 | AGCCTTAGAA | ATTGTAGAAA | CTATAGCAAG | AAGTGGCGCA | GTAGATCTTA | 300 |
|    | TCGTAGTAGA | TAGCGTTGCA | GCGCTTACCC | CAAAAGCAGA | AATTGAAGGC | 350 |
|    | GATATGGGTG | ATCAACATGT | AGGACTTCAA | GCAAGACTTA | TGTCTCAAGC | 400 |
|    | TCTAAGAAAA | CTTACAGGTA | TAGTTCATAA | AATGAATACC | ACAGTAATTT | 450 |

|   |            |            |            |            |             |     |
|---|------------|------------|------------|------------|-------------|-----|
|   | TYATCAACCA | AATTCGTATG | AAAATCGGTG | CTATGGGTTA | TGGTACTCCT  | 500 |
|   | GAAACCACAA | CAGGTGGAAA | TGCATTAAAA | TTTTATGCTT | CTGTGCGTTT  | 550 |
|   | AGATGTTAGA | AAAGTAGCAA | CCTTAAACA  | AAACGAAGAA | CCTATAGGAA  | 600 |
|   | ACCGCGTTAA | AGTAAAAGTA | GTTAAAAATA | AAGTTGCTCC | TCCATTTCAGA | 650 |
| 5 | CAAGCTGAAT | TTGATGTGAT | GTTTGGAGAG | GGTTTAAGCC | GTGAAGGTGA  | 700 |
|   | ATTGATCGAT | TATGGTGTAA | AACTTGATAT | CGTAGATAAA | AGTGGTGCGT  | 750 |
|   | GGTTTTCTTA | TAAAGATAAA | AAACTTGGAC | AAGGTAGAGA | AAATTCAAAA  | 800 |
|   | GCTTTCCTAA | AAGAAAAC   |            |            |             | 818 |

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## 2) INFORMATION FOR SEQ ID NO: 1715

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 809 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

- 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*  
 (B) STRAIN: ATCC 49175  
 25 (C) ACCESSION NUMBER: AF124224

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715

|    |             |             |            |             |             |     |
|----|-------------|-------------|------------|-------------|-------------|-----|
|    | TGGTGCTATC  | TTAGTAGTAT  | CTGCAGCTGA | TGGTCCAATG  | CCTCAAACAC  | 50  |
| 30 | GTGAACACAT  | CTTATTATCA  | CGTCAAGTAG | GTGTTCCCTTA | CATCGTTGTA  | 100 |
|    | TTCTTAAACA  | AAGTTGACAT  | GGTTGACGAT | GAAGAATTAT  | TAGAATTAGT  | 150 |
|    | AGAAATGGAA  | GTTTCGTGACT | TATTATCAGA | ATACGATTTC  | CCAGGCGATG  | 200 |
|    | ACACTCCAGT  | TGTTGCAGGT  | TCTGCTTTAC | GCGCTTTAGA  | AGGCGACGCT  | 250 |
|    | TCATACRAAG  | AAAAAATCTT  | AGAATTAATG | GCTGCTGTTG  | ACGAATACAT  | 300 |
| 35 | TCCAACCTCCA | GAACGYGACG  | TTGACAAACC | ATTCATGATG  | CCAGTTGAAG  | 350 |
|    | ACGTGTTCTC  | AATCACAGGT  | CGTGGTACTG | TTGCTACAGG  | TCGTGTTGAA  | 400 |
|    | CGTGGACAAG  | TTCGTGTTGG  | TGACGAAGTT | GAAATCGTTG  | GTATTTTCAGA | 450 |
|    | AGAAACTTCA  | AAAACAACCTG | TAAGTGGTGT | TGAAATGTTC  | CGTAAATTGT  | 500 |
|    | TAGACTACGC  | TGAAGCAGGG  | GATAACATTG | GTACATTATT  | ACGTGGTGTT  | 550 |
| 40 | ACACGTGACA  | ACATCGAACG  | TGGACAAAGT | CTTGCTAAAC  | CAGGAACAAT  | 600 |
|    | CACTCCACAT  | ACTAAATTCA  | AAGCTGAAGT | TTACGTATTA  | ACTAAAGAAG  | 650 |
|    | AAGGTGGACG  | TCATACTCCA  | TTCTTCTCTA | ACTACCGTCC  | TCAATTCTAC  | 700 |
|    | TTCCGTACAA  | CAGACATCAC  | TGGTGTGTTG | GTGTTACCAG  | AAGGCGTTGA  | 750 |
|    | AATGGTAATG  | CCTGGTGATA  | ACGTAACAT  | GGAAGTTGAA  | TTAATTCACC  | 800 |
| 45 | CAGTAGCGA   |             |            |             |             | 809 |

## 2) INFORMATION FOR SEQ ID NO: 1716

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid



- (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia defectiva*  
(B) STRAIN: ATCC 49176  
(C) ACCESSION NUMBER: AF124225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716

|    |            |             |            |             |            |     |
|----|------------|-------------|------------|-------------|------------|-----|
|    | CGGCGCGATC | CTCGTTGTAT  | CTGCTGCTGA | CGGCCCAATG  | CCACAAACTC | 50  |
|    | GTGAACACAT | CCTCTTGTCT  | CGTCAAGTTG | GTGTTCCCTTA | CATCGTAGTA | 100 |
| 15 | TTCTTGAACA | AAGTTGACAT  | GGTTGACGAC | GAAGAATTGC  | TCGAATTAGT | 150 |
|    | TGAAATGGAA | GTTTCGTGACC | TCTTGTCTGA | ATACGACTTC  | CCAGGCGACG | 200 |
|    | ACACTCCAGT | TATCGCTGGT  | TCAGCTTTGA | AAGCTTTAGA  | AGGCGACGCT | 250 |
|    | AACTACGAAG | CTAAAGTTTT  | AGAATTGATG | GAACAAGTTG  | ATGCTTACAT | 300 |
|    | TCCAGAACCA | GAACGTGACA  | CTGACAAGCC | ATTCATGATG  | CCAGTCGAAG | 350 |
| 20 | ACGTATTCTC | TATCACTGGT  | CGTGGTACTG | TTGCAACTGG  | TCGTGTTGAA | 400 |
|    | CGTGGTCAAG | TTCGCGTTGG  | TGACGAAGTT | GAAATCGTTG  | GTATCGAAGA | 450 |
|    | AGAAACTTCT | AAGACTACCG  | TTACCGGTGT | TGAAATGTTC  | CGTAAGTTAT | 500 |
|    | TGGATTACGC | TGAAGCTGGG  | GACAACGTTG | GTACCTTGTT  | ACGTGGTGTA | 550 |
|    | ACTCGTGACC | AAATCCAACG  | TGGTCAAGTA | TTATCTAAAC  | CAGGTTCAAT | 600 |
| 25 | CACTCCGYAC | ACTAAGTTCG  | AAGCTGAAGT | GTACGTATTG  | TCTAAAGAAG | 650 |
|    | AAGGTGGTCG | TCACACTCCA  | TTCTTCTCTA | ACTACCGTCC  | ACAATTCTAC | 700 |
|    | TTCCGTACAA | CTGACGTAAC  | TGGTGTGTTT | ACTTTACCAG  | AAGGTACTGA | 750 |
|    | AATGGTTATG | CCAGGCGACA  | ACGTACAAAT | GGTTGTTGAA  | TTGATCCACC | 800 |
| 30 | CAATCGCGAT | CGAAGAA     |            |             |            | 817 |

## 2) INFORMATION FOR SEQ ID NO: 1717

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium accolens*  
(B) STRAIN: ATCC 49725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CGGCGCTATC | CTGGTTGTTG | CTGCAACCGA | TGGCCCGATG | CCGCAGACCC | 50  |
| 50 | GCGAGCACGT | TCTGCTTGCT | CGCCAGGTTG | GCGTTCCTTA | CATCCTCGTT | 100 |
|    | GCACTGAACA | AGTGCGACAT | GGTTGATGAT | GAGGAAATCA | TCGAGCTCGT | 150 |
|    | GGAGATGGAG | ATCTCCGAGC | TGCTCGCAGA | GCAGGACTAC | GATGAGGAAG | 200 |
|    | CTCCTATCGT | TCACATCTCC | GCTCTGAAGG | CACTCGAGGG | TGACGAGAAG | 250 |

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | TGGGTACAGT | CCATCGTTGA | CCTGATGGAT | GCCTGCGACA | ACTCCATCCC | 300 |
|    | TGATCCGGAG | CGCGCTACCG | ATCAGCCGTT | CTTGATGCCT | ATCGAGGACA | 350 |
|    | TCTTCACCAT | TACCGGCCCG | GGTACCGTTG | TTACCGGCCG | TGTTGAGCGT | 400 |
|    | GGTCGTCTGA | ACGTCAACGA | GGACGTTGAG | ATCATCGGTA | TCCAGGAGAA | 450 |
| 5  | GTCCCAGAAC | ACCACCGTTA | CCGGTATCGA | GATGTTCCGC | AAGATGATGG | 500 |
|    | ACTACACCGA | GGCTGGCGAC | AACTGTGGTC | TGCTTCTGCG | TGGTACCAAG | 550 |
|    | CGTGAGGACG | TTGAGCGTGG | CCAGGTTGTT | ATCAAGCCGG | GCGCTTACAC | 600 |
|    | CCCTCACACC | AAGTTCGAGG | GTTCCGTCTA | CGTCCTGAAG | AAGGAAGAGG | 650 |
|    | GCGGCCGCCA | CACCCCGYTC | ATGAACAAC  | ACCGTCCTCA | GTTCTACTTC | 700 |
| 10 | CGCACCACCG | ACGTTACCGG | TGTTGTGAAC | CTGCCTGAGG | GCACCGAGAT | 750 |
|    | GGTTATGCCT | GGCGACAACG | TTGAGATGTC | TGTTGAGCTC | ATCCAGCCTG | 800 |
|    | TTGCTATGGA | CGAG       |            |            |            | 814 |

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## 2) INFORMATION FOR SEQ ID NO: 1718

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 814 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium genitalium*
- (B) STRAIN: ATCC 33031

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CGGCGCCATC | CTGGTTGTTG | CTGCAACCGA | TGGCCCGATG | CCGCAGACCC | 50  |
|    | GTGAGCACGT | TCTGCTGGCT | CGCCAGGTTG | GCGTTCCGTA | CATCCTAGTT | 100 |
|    | GCACTGAACA | AGTGCGACAT | GGTTGATGAT | GAGGAGCTGC | TGGAGCTCGT | 150 |
| 35 | CGAGATGGAG | GTCCGCGAGC | TGCTGGCTGA | GCAGGACTTC | GACGAGGAAG | 200 |
|    | CACCTGTTGT | TCACATCTCC | GCACTGAAGG | CCCTGGAGGG | CGACGAGAAG | 250 |
|    | TGGGCTAAGC | AGATCCTGGA | GCTCATGGAG | GCTTGCGACA | ACTCCATCCC | 300 |
|    | GGATCCGGAG | CGCGAGACCG | ACAAGCCGTT | CCTGATGCCG | GTTGRGGACA | 350 |
|    | TCTTCACCAT | TACCGGCCCG | GGTACCGTTG | TTACCGGCCG | TGTTGAGCGT | 400 |
| 40 | GGCGTCCTGA | ACCTGAACGA | CGAGGTCGAG | ATCCTGGGCA | TCCGCGAGAA | 450 |
|    | GTCCACCAAG | ACCACCGTTA | CCTCCATCGA | GATGTTCAAC | AAGCTGCTGG | 500 |
|    | ACACCGCAGA | GGCTGGCGAC | AACGCCGCAC | TGCTGCTGCG | TGGCCTGAAG | 550 |
|    | CGCGAAGATG | TTGAGCGTGG | TCAGATCGTT | GCTAAGCCGG | GCGAGTACAC | 600 |
|    | CCCGCACACC | GAGTTCGAGG | GCTCCGTCTA | CGTTCTGTCC | AAGGACGAGG | 650 |
| 45 | GTGGCCGCCA | CACCCCGTTC | TTCGACAAC  | ACCGTCCGCA | GTTCTATTTT | 700 |
|    | CGCACCACCG | ACGTTACCGG | TGTTGTGAAG | CTGCCGGAGG | GCACCGAGAT | 750 |
|    | GGTTATGCCG | GGCGACAACG | TTGACATGTC | CGTCACCCTG | ATCCAGCCGG | 800 |
|    | TTGCTATGGA | CGAG       |            |            |            | 814 |

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## 2) INFORMATION FOR SEQ ID NO: 1719

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 814 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Corynebacterium jeikeium*
- (B) STRAIN: ATCC 43216

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 15 | CGGCGCCATC | CTGGTTGTTG | CCGCAACCGA | TGGCCCGATG | CCGCAGACCC | 50  |
|    | GCGAGCACGT | TCTGCTGGCY | CGCCAGGTTG | GCGTTCGTA  | CATCCTGGTT | 100 |
|    | GCACTGAACA | AGTGTGACAT | GGTTGACGAT | GAGGAGCTGC | TGGAGCTCGT | 150 |
|    | CGAGATGGAG | GTCCGCGAGC | TGCTGGCTGA | GCAGGACTTC | GACGAGGAAG | 200 |
|    | CTCCGGTTGT | TCACATCTCC | GCACTGAAGG | CCCTGGAGGG | CGACGAGAAG | 250 |
| 20 | TGGGCTAACC | AGATTCTCGA | GCTGATGCAG | GCTTGCGACG | AGTCTATCCC | 300 |
|    | GGATCCGGAG | CGCGAGACCG | ACAAGCCGTT | CCTGATGCCG | GTTGWGGACA | 350 |
|    | TCTTCACCAT | TACCGGTCGC | GGTACCGTTG | TTACCGGCCG | TGTTGAGCGT | 400 |
|    | GGCATCCTGA | ACCTGAACGA | CGAGGTTGAG | ATCCTGGGTA | TCCGCGAGAA | 450 |
|    | GTCCCAGAAG | ACCACCGTTA | CCTCCATCGA | GATGTTCAAC | AAGCTGCTGG | 500 |
| 25 | ACACCGCAGA | GGCTGGCRAC | AACGCTGCAC | TGCTGCTGCG | TGGTCTGAAG | 550 |
|    | CGCGAGGACG | TTGAGCGTGG | CCAGATCATC | GCTAAGCCGG | GCGAGTACAC | 600 |
|    | CCCGCACACC | GAGTTCGAGG | GCTCCGTCTA | CGTTCTGTCC | AAGGACGAGG | 650 |
|    | GCGGCCGCCA | CACCCCGTTC | TTCGACAAC  | ACCGTCCGCA | GTTCTACTTC | 700 |
|    | CGCACCACCG | ACGTTACCGG | TGTTGTGAAG | CTGCCTGAGG | GCACCGAGAT | 750 |
| 30 | GGTTATGCCG | GGCGACAACG | TYGACATGTC | CGTCACCCTG | ATCCAGCCGG | 800 |
|    | TTGCTATGGA | CGAG       |            |            |            | 814 |

## 35 2) INFORMATION FOR SEQ ID NO: 1720

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 748 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
- (B) STRAIN: ATCC 10700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720

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|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CGGCGCTATC | TTGGTTGTTG | CAGCTACCGA | CGGCCCAATG | CCACAGACTC | 50  |
| GCGAGCACGT | TCTGCTGGCT | CGCCAGGTTG | GCGTTCCTTA | CATCCTGGTT | 100 |
| GCACTAAACA | AGTGCGACAT | GGTTGACGAC | GAGGAAATCC | TCGAGCTCGT | 150 |

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | CGAGATGGAG | ATCCGCGAAT | TGCTGGCTGA  | CCAGGAATTC | GACGAAGAAG | 200 |
|    | CTCCAATCGT | TCACATCTCC | GCAGTCGGCG  | CCTTGGAAGG | CGAAGAGAGG | 250 |
|    | TGGGTTAACG | CCATCGTTGA | ACTGATGGAT  | GCTTGTGACG | AGTCGATCCC | 300 |
|    | TGATCCAGAC | CGTGCTACCG | ACAAGCCATT  | CCTGATGCCT | ATCGAGGACA | 350 |
| 5  | TCTTCACCAT | TACCGGTCGT | GGCACC GTTG | TTACGGGTCG | TGTTGAGCGT | 400 |
|    | GGTTCCTGA  | AGGTCAACGA | AGAAGTCGAG  | ATCATCGGCA | TCAAGGAAAA | 450 |
|    | GTCCCAGAAG | ACCACCATCA | CCGGTATCGA  | AATGTTCCGC | AAGATGCTGG | 500 |
|    | ACTACACCGA | GGCCGGCGAC | AACGCTGGTC  | TGCTGCTTCG | CGGTACCAAG | 550 |
|    | CGTGAAGACG | TTGAGCGTGG | ACAGGTATATC | GTTGCTCCAG | GTGCTTACAG | 600 |
| 10 | CACCCACAAG | AAGTTCGAAG | GTTCCGTCTA  | CGTTCTTTCC | AAGGACGAGG | 650 |
|    | GCGGCCGCCA | CACCCCGTTC | TTCGACAACT  | ACCGTCCTCA | GTTCTACTTC | 700 |
|    | CGCACCACCG | ACGTTACCGG | TGTTGTTACC  | CTGCCTGAGG | GCACCGAG   | 748 |

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## 2) INFORMATION FOR SEQ ID NO: 1721

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 813 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium striatum*
- (B) STRAIN: ATCC 6940

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | GGCGCTATCT | TGGTTGTTGC | TGCAACCGAT  | GGCCCGRTGC | CGCAGACCCG | 50  |
|    | CGAGCACGTT | CTTCTGGCTC | GCCAGGTTGG  | CGTTCCTTAC | ATCCTCGTTG | 100 |
|    | CACTGAACAA | GTGCGACATG | GTTGACGACG  | AGGAAATTAT | CGAGCTCGTC | 150 |
| 35 | GAGATGGAGA | TCCGCGAACT | GCTCGCAGAG  | CAGGACTACG | ATGAGGAAGC | 200 |
|    | TCCGATCGTT | CACATCTCTG | CTCTGAAGGC  | TCTTGAGGGC | GRCGAGAAGT | 250 |
|    | GGGTACAGGC | TATCGTTGAC | CTGATGCAGG  | CTTGCGATGA | CTCCATCCCG | 300 |
|    | GATCCGGAGC | GCGAGCTGGA | CAAGCCGTTC  | CTGATGCCAA | TCGAGGACAT | 350 |
|    | CTTCACCATC | ACCGGCCGCG | GTACCGTTGT  | TACTGGCCGT | GTTGAGCGTG | 400 |
| 40 | GCTCCCTGAA | CGTCAACGAG | GACGTTGAGA  | TCATCGGTAT | CCAGGACARG | 450 |
|    | TCCATCTCCA | CCACCGTTAC | CGGTATCGAG  | ATGYTCCGCA | AGATGATGGA | 500 |
|    | CTACACCGAG | GCTGGCGACA | ACTGTGGTCT  | GCTTCTGCGT | GGTACCAAGC | 550 |
|    | GTGAAGAGGT | TGAGCGCGGC | CAGGTTGTTA  | TTAAGCCGGG | CGCTTACACC | 600 |
|    | CCTCACACCC | AGTTCGAGGG | TTCCGTCTAC  | GTCCTGAAGA | AGGAAGAGGG | 650 |
| 45 | CGGCCGCCAC | ACCCCGTTCA | TGGACAACCTA | CCGTCCGCAG | TTCTACTTCC | 700 |
|    | GCACCACCGA | CGTTACCGGC | GTCATCAAGC  | TGCCTGAGGG | CACCGAGATG | 750 |
|    | GTTATGCCTG | GCGACAACGT | CGAGATGTCY  | GTCGAGCTGA | TCCAGCCGGT | 800 |
|    | CGCTATGGAC | GAG        |             |            |            | 813 |

50

## 2) INFORMATION FOR SEQ ID NO: 1722

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*  
 (B) STRAIN: ATCC 14025  
 (C) ACCESSION NUMBER: AF124220

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722

|            |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-----|
| CGGAGCTATC | TTAGTAGTAT  | CTGCTGCTGA  | TGGCCCTATG  | CCTCAAACCTC | 50  |
| GTGAACACAT | CTTGTTATCT  | CGTAACGTTG  | GTGTTCCCTTA | CATCGTTGTA  | 100 |
| TTCTTAAACA | AAATGGATAT  | GGTTGACGAT  | GAAGAATTAC  | TTGAATTAGT  | 150 |
| TGAAATGGAA | GTTCTGACT   | TATTAACCTGA | ATACGACTTC  | CCAGGCGACG  | 200 |
| ACACTCCAGT | TATCGCAGGT  | TCAGCGTTGA  | AAGCTTTAGA  | AGGCGACGCT  | 250 |
| TCATACGAAG | AAAAAATCTT  | AGAATTAATG  | GCTGCTGTTG  | ACGAATATAT  | 300 |
| CCCAACACCA | GTTCTGATA   | CTGACAAACC  | ATTCATGATG  | CCAGTCGAAG  | 350 |
| ACGTATTCTC | AATCACTGGT  | CGTGGTACTG  | TTGCAACTGG  | TCGTGTTGAA  | 400 |
| CGTGGACAAG | TTCGCGTTGG  | TGACGAAGTT  | GAAATCGTAG  | GTATCGCTGA  | 450 |
| CGAAACTGCT | AAAACAACCTG | TTACAGGTGT  | TGAAATGTTC  | CGTAAATTGT  | 500 |
| TAGACTACGC | TGAAGCAGGT  | GACAACATCG  | GTGCTTTGTT  | ACGTGGTGTT  | 550 |
| GCACGTGAAG | ATATCCAACG  | TGGACAAGTA  | TTGGCTAAAC  | CAGCTTCAAT  | 600 |
| CACTCCACAT | ACAAAATTCT  | CTGCAGAAGT  | TTATGTTCTA  | ACTAAAGAAG  | 650 |
| AAGGTGGACG | TCATACTCCA  | TTCTTCACTA  | ACTACCGTCC  | TCAGTTCTAC  | 700 |
| TTCCGTACAA | CTGACGTAAC  | TGGTGTAGTT  | GATCTACCAG  | AAGGTACTGA  | 750 |
| AATGGTWATG | CCTGGGGATA  | ACGTAACCTAT | GGAAGTTGAA  | TTGATYCACC  | 800 |
| CAATYGCGGT | AGAAGAC     |             |             |             | 817 |

## 2) INFORMATION FOR SEQ ID NO: 1723

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*  
 (B) STRAIN: ATCC 14018

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TGGCGCAATC | CTCGTGGTTG | CTGCTACCGA | CGGTCCAATG | GCTCAGACCC | 50  |
| GTGAACACGT | CTTGCTTGCT | AAGCAGGTGC | GCGTTCCAAA | AATTCTTGTT | 100 |

|    |            |             |            |            |            |     |
|----|------------|-------------|------------|------------|------------|-----|
|    | GCTTTGAACA | AGTGCGATAT  | GGTTGACGAC | GAAGAGCTTA | TCGATCTCGT | 150 |
|    | TGAAGAAGAG | GTCCGTGACC  | TCCTCGAAGA | AAACGGCTTC | GATCGCGATT | 200 |
|    | GCCCAGTCYT | CCGTACTTCC  | GCTTACGGCG | CTTTGCATGA | TGACGCTCCA | 250 |
|    | GACCACGACA | AGTGGGTAGA  | GACCGTCAAG | GAAGTCATGA | AGGCTGTTGA | 300 |
| 5  | CGAGTACATC | CCAACCCCAA  | CTCACGATCT | TGACAAGCCA | TTCTTGATGC | 350 |
|    | CAATCGAAGA | TGTGTTTACC  | ATCTCCGGTC | GTGGTYCCGT | TGTCACCGGT | 400 |
|    | CGTGTTGAGC | GTGGTAAGCT  | CCCAATCAAC | ACCCCAGTTG | AGATCGTTGG | 450 |
|    | TTTGCGCGAT | ACCCAGACCA  | CCACCGTCAC | CTCTATCGAG | ACCTTCCACA | 500 |
|    | AGCAGATGGA | TGAGGCAGAG  | GCTGGCGATA | ACACTGGTCT | TCTTCTCCGC | 550 |
| 10 | GGTATCAACC | GTACCGACGT  | TGAGCGTGGT | CAGGTTGTGG | CTGCTCCAGG | 600 |
|    | TTCTGTGACT | CCACACACCA  | AGTTCGAAGG | CGAAGTTTAC | GTCTTGACCA | 650 |
|    | AGGACGAAGG | TGGCCGTCAC  | TCGCCATTCT | TCTCCAACTA | CCGTCCACAG | 700 |
|    | TTCTACTTCC | GTACCACCGA  | TGTTACTGGC | GTTATCACCT | TGCCAGACGG | 750 |
|    | CATCGAAATG | GTTTCAGCCAG | GCGATCACGC | AACCTTCACT | GTTGAGTTGA | 800 |
| 15 | TCCAGGCTAT | CGCAATGGAA  | GAG        |            |            | 823 |

## 2) INFORMATION FOR SEQ ID NO: 1724

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Listeria innocua*
- (B) STRAIN: ATCC 33090

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724

|    |             |            |            |            |             |     |
|----|-------------|------------|------------|------------|-------------|-----|
| 35 | CGGAGCTATC  | TTAGTAGTAT | CTGCTGCTGA | TGGCCCAATG | CCACAAACTC  | 50  |
|    | GTGAACATAT  | CTTACTTTCA | CGTCAAGTTG | GTGTTCCATA | CATCGTTGTA  | 100 |
|    | TTCATGAACA  | AATGTGACAT | GGTTGACGAT | GAAGAATTAC | TAGAATTAGT  | 150 |
|    | TGAAATGGAA  | ATTCGTGATC | TATTAAGTGA | ATATGAATTC | CCTGGCGATG  | 200 |
|    | ACATTCCCTGT | AATCAAAGGT | TCAGCTCTTA | AAGCACTTCA | AGGTGAAGCT  | 250 |
| 40 | GACTGGGAAG  | CTAAAATTGA | CGAGTTAATG | GAAGCTGTAG | ATTCTTACAT  | 300 |
|    | TCCAACTCCA  | GAACGTGATA | CTGACAAACC | ATTCATGATG | CCAGTTGAGG  | 350 |
|    | ATGTATTCTC  | AATCACTGGT | CGTGGAACAG | TTGCAACTGG | ACGTGTTGAA  | 400 |
|    | CGTGGACAAG  | TTAAAGTTGG | TGACGAAGTA | GAAGTTATCG | GTATTGAAGA  | 450 |
|    | AGAAAGCAAA  | AAAGTAGTAG | TAAGTGGAGT | AGAAATGTTC | CGTAAATTAC  | 500 |
| 45 | TAGACTACGC  | TGAAGCTGGC | GACAACATTG | GCGCACTTCT | ACGTGGTGTT  | 550 |
|    | GCTCGTGAAG  | ATATCCAACG | TGGTCAAGTA | TTAGCTAAAC | CAGGTTTCGAT | 600 |
|    | TACTCCACAC  | ACTAACTTCA | AAGCTGAAAC | TTATGTTTTA | ACTAAAGAAG  | 650 |
|    | AAGGTGGACG  | TCACACTCCA | TTCTTCAACA | ACTACCGCCC | ACAATTCTAT  | 700 |
|    | TTCCGTACTA  | CTGACGTAAC | TGGTATTGTT | ACACTTCCAG | AAGGTACTGA  | 750 |
| 50 | AATGGTAATG  | CCTGGTGATA | ACATTGAGCT | TGCAGTTGAA | CTAATTGCAC  | 800 |
|    | CAATCGCTAT  | CGAAGAC    |            |            |             | 817 |

## 2) INFORMATION FOR SEQ ID NO: 1725

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*  
 (B) STRAIN: ATCC 19119

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CGGAGCTATC | TTAGTAGTAT | CTGCTGCTGA | TGGTCCAATG | CCACAAACTC | 50  |
|    | GTGAACATAT | TCTTACTTTC | ACGTCAAGTT | GGTGTTCAT  | ACATCGTTGT | 100 |
|    | ATTCATGAAC | AAATGTGACA | TGGTTGACGA | TGAAGAATTA | CTTGAATTAG | 150 |
| 20 | TTGAAATGGA | AATTCGTGAT | CTATTAAGT  | AATATGAATT | CCCTGGCGAC | 200 |
|    | GACATTCCTG | TAATCAAAGG | TTCAGCTCTT | AAAGCACTTC | AAGGTGAAGC | 250 |
|    | TGATTGGGAA | GCTAAAATTG | ACGAGTTAAT | GGAAGCTGTA | GATTCTTACA | 300 |
|    | TTCCAAGTCC | AGAACGTGAT | ACTGACAAAC | CATTCATGAT | GCCAGTTGAG | 350 |
|    | GATGTATTCT | CAATCACTGG | TCGTGGAACA | GTTGCAACTG | GACGTGTTGA | 400 |
| 25 | ACGTGGACAA | GTTAAAGTTG | GTGACGAAGT | AGAAGTTATC | GGTATTGAAG | 450 |
|    | AAGAAAGCAA | AAAAGTAGTA | GTAAGTGGAG | TAGAAATGTT | CCGTAAATTA | 500 |
|    | CTAGACTACG | CTGAAGCTGG | CGACAACATT | GGCGCACTTC | TACGTGGTGT | 550 |
|    | TGCTCGTGAA | GATATCCAAC | GTGGTCAAGT | ATTAGCTAAA | CCAGGTTCGA | 600 |
|    | TTACTCCACA | TACTAACTTC | AAAGCTGAAA | CTTATGTTTT | AACTAAAGAA | 650 |
| 30 | GAAGGTGGAC | GTCATACTCC | ATTCTTCAAC | AACTACCGCC | CACAATTCTA | 700 |
|    | TTTCCGTACT | ACTGACGTAA | CTGGTATTGT | TACACTTCCA | GAAGGTACTG | 750 |
|    | AAATGGTAAT | GCCTGGTGAT | AACATTGAGC | TTGCAGTTGA | ACTAATTGCA | 800 |
|    | CCAATCGCTA | TCGAAGAC   |            |            |            | 818 |

## 2) INFORMATION FOR SEQ ID NO: 1726

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*  
 (B) STRAIN: LSPQ 5093202

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726

|  |            |            |            |            |            |    |
|--|------------|------------|------------|------------|------------|----|
|  | CGGAGCTATC | TTAGTAGTAT | CTGCTGCTGA | TGGCCCAATG | CCACAAACTC | 50 |
|--|------------|------------|------------|------------|------------|----|

|    |             |            |            |            |             |     |
|----|-------------|------------|------------|------------|-------------|-----|
|    | GTGAACATAT  | CTTACTTTCA | CGTCAAGTTG | GTGTTCCATA | CATCGTTGTA  | 100 |
|    | TTCATGAACA  | AATGTGACAT | GGTTGACGAT | GAAGAATTAC | TAGAATTAGT  | 150 |
|    | TGAAATGGAA  | ATTCGTGATC | TATTAAGTGA | ATATGAATTC | CCTGGCGATG  | 200 |
|    | ACATTCCTGT  | AATCAAAGGT | TCAGCTCTTA | AAGCACTTCA | AGGTGAAGCT  | 250 |
| 5  | GACTGGGAAG  | CTAAAATTGA | CGAGTTAATG | GAAGCTGTAG | ATTCTTACAT  | 300 |
|    | TCCAACCTCCW | GAACGTGATA | CTGACAAACC | ATTCATGATG | CCAGTTGAGG  | 350 |
|    | ATGTATTCTC  | AATCACTGGT | CGTGGAACAG | TTGCAACTGG | ACGTGTTGAA  | 400 |
|    | CGTGGACAAG  | TTAAAGTTGG | TGACGAAGTA | GAAGTTATCG | GTATCGAAGA  | 450 |
|    | AGAAAGCAAA  | AAAGTAGTAG | TAAGTGGAGT | AGAAATGTTC | CGTAAATTAC  | 500 |
| 10 | TAGACTACGC  | TGAAGCTGGC | GACAACATTG | GCGCACTTCT | ACGTGGTGT   | 550 |
|    | GCTCGTGAAG  | ATATCCAACR | TGGTCAAGTA | TTAGCTAAAC | CAGGTTTCGAT | 600 |
|    | TACTCCACAC  | ACTAACTTCA | AAGCTGAAAC | TTATGTTTTA | ACTAAAGAAG  | 650 |
|    | AAGGTGGACG  | TCACACTCCA | TTCTTCAACA | ACTACCGCCC | ACAATTCTAT  | 700 |
|    | TTCCGTACTA  | CTGACGTAAC | TGGTATTGTT | ACACTTCCAG | AAGGTACTGA  | 750 |
| 15 | AATGGTAAYG  | CCTGGTGATA | ACATTGAGCT | TGCAGTTGAA | CTAATTGCAC  | 800 |
|    | CAATCGCTAT  | CGAAGAC    |            |            |             | 817 |

## 20 2) INFORMATION FOR SEQ ID NO: 1727

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria seeligeri*  
 (B) STRAIN: ATCC 35967

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727

|    |             |            |            |            |             |     |
|----|-------------|------------|------------|------------|-------------|-----|
| 35 | CGGAGCTATC  | TTAGTAGTAT | CTGCTGCTGA | TGGCCCAATG | CCACAAACTC  | 50  |
|    | GTGAACATAT  | CTTACTTTCA | CGTCAAGTTG | GTGTTCCATA | CATCGTTGTA  | 100 |
|    | TTCATGAACA  | AATGTGACAT | GGTTGACGAT | GAAGAATTAC | TTGAATTAGT  | 150 |
|    | TGAAATGGAA  | ATTCGTGATC | TATTAAGTGA | ATATGAATTC | CCTGGTGATG  | 200 |
| 40 | ACATTCCTGT  | AATCAAAGGT | TCAGCTCTTA | AAGCACTTCA | AGGTGAAGCT  | 250 |
|    | GACTGGGAAG  | CTAAAATTGA | CGAGTTAATG | GAAGCTGTAG | ATTCTTACAT  | 300 |
|    | TCCAACCTCCA | GAACGTGATA | CTGACAAACC | ATTCATGATG | CCAGTTGAGG  | 350 |
|    | ATGTATTCTC  | AATCACTGGT | CGTGGAACAG | TTGCAACTGG | ACGTGTTGAA  | 400 |
|    | CGTGGACAAG  | TTAAAGTTGG | TGACGAAGTA | GAAGTTATCG | GTATTGAAGA  | 450 |
| 45 | AGAAAGCAAA  | AAAGTAATAG | TAAGTGGAGT | AGAAATGTTC | CGTAAATTAC  | 500 |
|    | TAGACTACGC  | TGAAGCTGGC | GACAACATTG | GCGCACTTCT | ACGTGGTGT   | 550 |
|    | GCTCGTGAAG  | ATATCCAACG | TGGTCAAGTA | TTAGCTAAAC | CAGGTTTCGAT | 600 |
|    | TACTCCACAT  | ACTAACTTCA | AAGCTGAAAC | TTATGTTTTA | ACTAAAGAAG  | 650 |
|    | AAGGTGGACG  | TCACACTCCA | TTCTTCAACA | ACTACCGCCC | ACAATTCTAT  | 700 |
| 50 | TTCCGTACTA  | CTGACGTAAC | TGGTATTGTT | ACACTTCCAG | AAGGTACTGA  | 750 |
|    | AATGGTAATG  | CCTGGTGATA | ACATTGAGCT | TGCAGTTGAA | CTAATTGCAC  | 800 |
|    | CAATCGCTAT  | CGAAGAC    |            |            |             | 817 |



## 2) INFORMATION FOR SEQ ID NO: 1728

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*  
 (B) STRAIN: ATCC 25923

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728

|             |             |             |            |             |     |
|-------------|-------------|-------------|------------|-------------|-----|
| CGGTGGTATC  | TTAGTAGTAT  | CTGCTGCTGA  | CGGTCCAATG | CCACAAACTC  | 50  |
| GTGAACACAT  | TCTTTTATCA  | CGTAACGTTG  | GTGTACCAGC | ATTAGTAGTA  | 100 |
| TTCTTAAACA  | AAGTTGACAT  | GGTTGACGAT  | GAAGAATTAT | TAGAATTAGT  | 150 |
| AGAAATGGAA  | GTTCGTGACT  | TATTAAGCGA  | ATATGACTTC | CCAGGTGACG  | 200 |
| ATGTACCTGT  | AATCGCTGGT  | TCAGCATTAR  | AAGCTTTAGA | AGGCGATGCT  | 250 |
| CAATACGAAG  | AAAAAATCTT  | AGAATTARTG  | GAAGCTGTAG | ATACTTACAT  | 300 |
| TCCAAC TCCA | GAACGTGATT  | CTGACAAACC  | ATTCATGATG | CCAGTTGAGG  | 350 |
| ACGTATTCTC  | AATCACTGGT  | CGTGGTACTG  | TTGCTACAGG | CCGTGTTGAA  | 400 |
| CGTGGTCAAA  | TCAAAGTTGG  | TGAAGAAGTT  | GAAATCATCG | GTTTACATGA  | 450 |
| CACATCTAAA  | ACAAC TGTTA | CAGGTGTTGA  | AATGTTCCGT | AAATTATTAG  | 500 |
| ACTACGCTGA  | AGCTGGTGAC  | AACATTGGTG  | CATTATTACG | TGGTGTGCT   | 550 |
| CGTGAAGACG  | TACAACGTGG  | TCAAGTATTA  | GCTGCTCCTG | GTTCAATTAC  | 600 |
| ACCACATACT  | GAATTCAAAG  | CAGAAGTATA  | CGTATTATCA | AAAGACGAAG  | 650 |
| GTGGACGTCA  | CACTCCATTC  | TTCTCAAAC T | ATCGTCCACA | ATTCTATTT C | 700 |
| CGTACTACTG  | ACGTAAC TGG | TGTTGTTTAC  | TTACCAGAAG | GTACTGAAAT  | 750 |
| GGTAATGCCT  | GGTGATAACG  | TTGAAATGAC  | AGTAGAATTA | ATCGCTCCAA  | 800 |
| TCGCGATTGA  | AGAC        |             |            |             | 814 |

## 2) INFORMATION FOR SEQ ID NO: 1729

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*  
 (B) STRAIN: ATCC 15305

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729

|            |            |            |            |            |    |
|------------|------------|------------|------------|------------|----|
| CGGAGCTATC | TTAGTAGTAT | CTGCTGCTGA | TGGCCCAATG | CCACAAACTC | 50 |
|------------|------------|------------|------------|------------|----|

|    |            |             |             |            |            |     |
|----|------------|-------------|-------------|------------|------------|-----|
|    | GTGAACACAT | TCTTTTATCA  | CGTRACGTTG  | GTGYTCCAGC | ATTAGTTGTA | 100 |
|    | TTCTTAAACA | AAGTTGACAT  | GGTTGACGAY  | GAAGAATTAT | TAGAATTRGT | 150 |
|    | AGAAATGGAA | GTTTCGTGRCT | TATTAAGCGA  | ATATGACTTC | CCAGGTGACG | 200 |
|    | ATGTACCTGT | AATCTCTGGT  | TCTGCATTAA  | AAGCTTTAGA | AGGCGACGCT | 250 |
| 5  | GACTATGAGC | AAAAAATCTT  | AGACTTAATG  | CAAGCTGTTG | ATGACTYCAT | 300 |
|    | TCCAACACCA | GAACGTGATT  | CTGACAAACC  | ATTCATGATG | CCAGTTGAGG | 350 |
|    | ACGTATTCTC | AATCACTGGT  | CGTGGTACTG  | TTGCTACAGG | CCGTGTTGAA | 400 |
|    | CGTGGTCAAA | TCAAAGTCGG  | TGAAGAAATC  | GARATCATCG | GTATGCAAGA | 450 |
|    | AGAATCAAGC | AAAACAAC TG | TTACTGGTGT  | AGAAATGTTC | CGTAAATTAT | 500 |
| 10 | TAGACTACGC | TGAAGCTGGT  | GACAACATTG  | GTGCATTATT | ACGTGGTGT  | 550 |
|    | TCACGTGATG | ATGTACAACG  | TGGTCAAGTT  | TTAGCTGCTC | CTGGTACTAT | 600 |
|    | CACACCACAT | ACAAAATTCA  | AAGCGGATGT  | TTACGTTTTA | TCTAAAGATG | 650 |
|    | AAGGTGGTCG | TCATACGCCA  | TTCTTCACTA  | ACTACCGCCC | ACAATTCTAT | 700 |
|    | TTCCGTAATA | CTGACGTAAC  | TGGTGTGTGTT | AACTTACCAG | AAGGTACTGA | 750 |
| 15 | AATGGTTATG | CCTGGCGATA  | ACGTTGAAAT  | GGATGTTGAA | TTAATTTCTC | 800 |
|    | CAATCGCTAT | TGAAGAC     |             |            |            | 817 |

## 20 2) INFORMATION FOR SEQ ID NO: 1730

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus simulans*  
 (B) STRAIN: ATCC 27848

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730

|    |            |             |            |            |            |     |
|----|------------|-------------|------------|------------|------------|-----|
| 35 | CGGCGGTATC | TTAGTAGTAT  | CTGCTGCAGA | TGGTCCAATG | CCACAAACTC | 50  |
|    | GTGAACACAT | CTTATTATCA  | CGTAACGTTG | GTGTACCAGC | TTTAGTTGTA | 100 |
|    | TTCTTAAACA | AAGCTGACAT  | GGTTGACGAC | GAAGAATTAT | TAGAATTAGT | 150 |
|    | TGAAATGGAA | GTTTCGTGACT | TATTATCTGA | ATACGACTTC | CCTGGTGACG | 200 |
| 40 | ATGTACCAGT | TATCGTTGGT  | TCTGCATTAA | AAGCTTTAGA | AGGCGACCCA | 250 |
|    | GAATACGAAC | AAAAAATCTT  | AGACTTAATG | CAAGCTGTAG | ATGACTACAT | 300 |
|    | CCCAACTCCA | GAACGTGACT  | CTGATAAACC | ATTCATGATG | CCAGTTGAGG | 350 |
|    | ACGTATTCTC | AATCACTGGT  | CGTGGTACTG | TAGCAACAGG | CCGTGTTGAA | 400 |
|    | CGTGGTCAAA | TCAAAGTCGG  | TGAAGAAGTT | GAAATCATCG | GTATCACTGA | 450 |
| 45 | AGAAAGCAAG | AAAACAACAG  | TTACAGGTGT | AGAAATGTTC | CGTAAATTAT | 500 |
|    | TAGACTACGC | TGAAGCTGGT  | GACAACATCG | GTGCTTTATT | ACGTGGTGT  | 550 |
|    | GCACGTGAAG | ACGTACAACG  | TGGACAAGTA | TTAGCAGCTC | CTGGCTCTAT | 600 |
|    | TACTCCACAC | ACAAAATTCA  | AAGCTGATGT | TTACGTTTTA | TCTAAAGAAG | 650 |
|    | AAGGTGGACG | TCATACTCCA  | TTCTTCACTA | ACTACCGCCC | ACAATTCTAC | 700 |
| 50 | TTCCGTAATA | CTGACGTAAC  | TGGCGTTGTT | CACTTACCAG | AAGGTACTGA | 750 |
|    | AATGGTTATG | CCTGGCGATA  | ACGTAGAAAT | GACTGTTGAA | TTGATCGCTC | 800 |
|    | CAATCGCGAT | TGAAGAC     |            |            |            | 817 |

## 2) INFORMATION FOR SEQ ID NO: 1731

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*  
 (B) STRAIN: ATCC 27591  
 (C) ACCESSION NUMBER:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CGGAGCTATC | CTTGTAGTTG | CTTCAACTGA | TGGACCAATG | CCACAAACTC | 50  |
| GTGAGCACAT | CCTTCTTTCA | CGTCAAGTTG | GTGTAAACA  | CCTTATCGTA | 100 |
| TTCATGAACA | AAGTTGACCT | TGTTGATGAT | GAAGAATTGC | TTGAATTGGT | 150 |
| TGAAATGGAA | ATTCGTGACC | TTCTTTCAGA | ATACGACTTC | CCAGGTGATG | 200 |
| ACCTTCCAGT | TATCCAAGGT | TCAGCTCTTA | AAGCACTTGA | AGGCGACGAA | 250 |
| AAATACGAAG | ACATCATCAT | GGAATTGATG | AGCACTGTTG | ATGAGTACAT | 300 |
| TCCAGAACCA | GAACGTGATA | CTGACAAACC | TTTACTTCTT | CCAGTTGAAG | 350 |
| ATGTATTCTC | AATCACTGGA | CGTGGTACAG | TTGCTTCAGG | ACGTATCGAC | 400 |
| CGTGGTACTG | TTCGTGTCAA | CGACGAAGTT | GAAATCGTTG | GTATTAAAGA | 450 |
| AGATATCCAA | AAAGCAGTTG | TTACTGGTGT | TGAAATGTTC | CGTAAACAAC | 500 |
| TTGACGAAGG | TCTTGCAAGG | GACAACGTTG | GTGTTCTTCT | TCGTGGTGTT | 550 |
| CAACGTGATG | AAATCGAACG | TGGTCAAGTT | CTTGCTAAAC | CAGGTTCAAT | 600 |
| CAACCCACAC | ACTAAATTTA | AAGGTGAAGT | TTACATCCTT | TCTAAAGAAG | 650 |
| AAGGTGGACG | TCATACTCCA | TTCTTCAACA | ACTACCGTCC | ACAATTCTAC | 700 |
| TTCCGTACAA | CTGACGTAAC | AGGTTCAATC | GAACCTCCAG | CAGGAACAGA | 750 |
| AATGGTTATG | CCTGGTGATA | ACGTTACTAT | CGAAGTTGAA | TTGATTACC  | 800 |
| CAATCGCCGT | AGAACAA    |            |            |            | 817 |

## 2) INFORMATION FOR SEQ ID NO: 1732

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: ATCC 27336

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CGGAGCTATC | CTTGTAGTAG | CTTCAACTGA | CGGACCAATG | CCACAAACTC | 50  |
|    | GTGAGCACAT | CCTTCTTTCA | CGTCAGGTTG | GTGTTAAACA | CCTTATCGTC | 100 |
|    | TTCATGAACA | AAGTTGACTT | GGTTGACGAC | GAAGAATTGC | TTGAATTGGT | 150 |
|    | TGAAATGGAA | ATCCGTGACC | TATTGTCAGA | ATACGACTTC | CCAGGTGACG | 200 |
| 5  | ATCTTCCAGT | TATCCAAGGT | TCAGCACTTA | AAGCTCTTGA | AGGTGACTCT | 250 |
|    | AAATACGAAG | ACATCGTTAT | GGAATTGATG | AACACAGTTG | ATGAGTATAT | 300 |
|    | CCCAGAACCA | GAACGTGACA | CTGACAAACC | ATTGCTTCTT | CCAGTCGAGG | 350 |
|    | ACGTATTCTC | AATCACTGGA | CGTGGTACAG | TTGCTTCAGG | ACGTATCGAC | 400 |
|    | CGTGGTATCG | TTAAAGTCAA | CGACGAAATC | GAAATCGTTG | GTATCAAAGA | 450 |
| 10 | AGAAACTCRA | AAAGCAGTTG | TTACTGGTGT | TGAAATGTTC | CGTAAACAAC | 500 |
|    | TTGACGAAGG | TCTTGCTGGA | GATAACGTAG | GTGTCCTTCT | TCGTGGTGTT | 550 |
|    | CAACGTGATG | AAATCGAACG | TGGACAAAGT | ATCGCTAAAC | CAGGTTCAAT | 600 |
|    | CAACCCACAC | ACTAAATTCA | AAGGTGAAGT | CTACATCCTT | ACTAAAGAAG | 650 |
|    | AAGGTGGACG | TCACACTCCA | TTCTTCAACA | ACTACCGTCC | ACAATTCTAC | 700 |
| 15 | TTCCGTACTA | CTGACGTTAC | AGGTTCAATC | GAACTTCCAG | CAGGTACTGA | 750 |
|    | AATGGTAATG | CCTGGTGATA | ACGTGACAAT | CGACGTTGAG | TTGATTCACC | 800 |
|    | CAATCGCCGT | AGAACAA    |            |            |            | 817 |

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## 2) INFORMATION FOR SEQ ID NO: 1733

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 817 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*  
(B) STRAIN: ATCC 7073

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CGGTGCGATC | CTTGTAGTAG | CATCTACTGA | CGGACCAATG | CCACAAACTC | 50  |
|    | GTGAGCACAT | CCTTCTTTCA | CGTCAGGTTG | GTGTTAAACA | CCTTATCGTC | 100 |
|    | TTCATGAACA | AAGTTGACTT | GGTTGACGAT | GAAGAATTGC | TTGAATTGGT | 150 |
| 40 | TGAAATGGAA | ATCCGTGACC | TTCTTTCAGA | ATACGATTTT | CCAGGTGATG | 200 |
|    | ACATTCCAGT | TATCCAAGGT | TCAGCTCTTA | AAGCTCTTGA | AGGTGATTCT | 250 |
|    | AAATACGAAG | ACATCATCAT | GGACTTGATG | AACACTGTTG | ACGAATACAT | 300 |
|    | CCCAGAACCA | GAACGTGACA | CTGACAAACC | ATTGTTGCTT | CCAGTCGAAG | 350 |
|    | ACGTATTCTC | AATCACTGGT | CGTGGTACTG | TTGCTTCAGG | ACGTATCGAC | 400 |
| 45 | CGTGGTGTTG | TTCGTGTCAA | TGACGAAGTT | GAAATCGTTG | GTCTTAAAGA | 450 |
|    | AGACATCCAA | AAAGCAGTTG | TTACTGGTGT | TGAAATGTTC | CGTAAACAAC | 500 |
|    | TTGACGRAGG | TATTGCCGGA | GATAACGTCG | GTGTTCTTCT | TCGTGGTATC | 550 |
|    | CAACGTGATG | AAATCGAACG | TGGTCAAGTA | TTGGCTGCAC | CTGGTTCAAT | 600 |
|    | CAACCCACAC | ACTAAATTCA | AAGGTGAAGT | TTACATCCTT | TCTAAAGAAG | 650 |
| 50 | AAGGTGGACG | TCACACTCCA | TTCTTCAACA | ACTACCGTCC | ACAGTTCTAC | 700 |
|    | TTCCGTACAA | CTGACGTAAC | AGGTTCAATC | GAACTTCCTG | CAGGTACTGA | 750 |
|    | AATGGTTATG | CCTGGTGATA | ACGTGACTAT | CGACGTTGAG | TTGATCCACC | 800 |
|    | CAATCGCCGT | TGAACAA    |            |            |            | 817 |

## 2) INFORMATION FOR SEQ ID NO: 1734

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Agrobacterium tumefaciens*  
 (C) ACCESSION NUMBER: x99673

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734

|            |            |             |            |            |     |
|------------|------------|-------------|------------|------------|-----|
| AACATGATCA | CCGGTGCTGC | CGAGATGGAC  | GGCGCGATCC | TGGTTTGCTC | 50  |
| GGCTGCCGAC | GGCCCGATGC | CACAGACCCG  | CGAGCACATC | CTGCTTGCCC | 100 |
| GTCAGGTGGG | CGTTCCGGCC | ATCGTCGTGT  | TCCTCAACAA | GGTCGACCAG | 150 |
| GTTGACGACG | CCGAGCTTCT | CGAGCTCGTC  | GAGCTTGAAG | TTCGCGAACT | 200 |
| TCTGTCGTCC | TACGACTTCC | CGGGCGACGA  | TATCCCGATC | ATCAAGGGTT | 250 |
| CGGCACTTGC | TGCTCTTGAA | GATTCTGACA  | AGAAGATCGG | TGAAGACGCG | 300 |
| ATCCGCGAGC | TGATGGCTGC | TGTCGACGCC  | TACATCCCGA | CGCCTGAGCG | 350 |
| TCCGATCGAC | CAGCCGTTCC | TGATGCCGAT  | CGAAGACGTG | TTCTCGATCT | 400 |
| CGGGTCGTGG | TACGGTTGTG | ACGGGTCGCG  | TTGAGCGCGG | TATCGTCAAG | 450 |
| GTTGGTGAAG | AAGTCGAAAT | CGTCGGCATC  | CGTCCGACCT | CGAAGACGAC | 500 |
| TGTTACCGGC | GTTGAAATGT | TCCGCAAGCT  | GCTCGACCAG | GGCCAGGCCG | 550 |
| GCGACAACAT | CGGTGCACTC | GTTTCGCGCG  | TTACCCGTGA | CGGCGTCGAG | 600 |
| CGTGGTCAGA | TCCTGTGCAA | GCCGGGTTTCG | GTCAAGCCGC | ACAAGAAGTT | 650 |
| CATGGCAGAA | GCCTACATCC | TGACGAAGGA  | AGAAGGCGGC | CGTCATACGC | 700 |
| CGTTCTTCAC | GAATAACCGT | CCGCAGTTCT  | ACTTCCGTAC | GACTGACGTT | 750 |
| ACCGGTATCG | TTTCGCTTCC | TGAAGGCACG  | GAAATGGTTA | TGCCTGGCGA | 800 |
| CAACGTCACT | GTTGAAGTCG | AGCTGATCGT  | TCCGATCGCG | ATGGAAGAAA | 850 |
| AGCTGCGCTT | CGCTATCCGC | GAAGGCGGCC  | GTACCGTCGG | CGCCGGC    | 897 |

## 2) INFORMATION FOR SEQ ID NO: 1735

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus subtilis*  
 (B) STRAIN: 168  
 (C) ACCESSION NUMBER: Z99104

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735

|    |            |             |            |            |            |     |
|----|------------|-------------|------------|------------|------------|-----|
|    | ATGATCACTG | GTGCTGCGCA  | AATGGACGGA | GCTATCCTTG | TAGTATCTGC | 50  |
|    | TGCTGATGGC | CCAATGCCAC  | AAACTCGTGA | GCACATCCTT | CTTTCTAAAA | 100 |
|    | ACGTTGGTGT | ACCATACATC  | GTTGTATTCT | TAAACAAATG | CGACATGGTA | 150 |
| 5  | GACGACGAAG | AGCTTCTTGA  | ACTAGTTGAA | ATGGAAGTTC | GCGATCTTCT | 200 |
|    | TAGCGAATAC | GACTTCCCTG  | GTGATGATGT | ACCAGTTGTT | AAAGGTTCTG | 250 |
|    | CTCTTAAAGC | TCTTGAAGGA  | GACGCTGAGT | GGGAAGCTAA | AATCTTCGAA | 300 |
|    | CTTATGGATG | CGGTTGATGA  | GTACATCCCA | ACTCCAGAAC | GCGACACTGA | 350 |
|    | AAAACCATTC | ATGATGCCAG  | TTGAGGACGT | ATTCTCAATC | ACTGGTCGTG | 400 |
| 10 | GTACAGTTGC | TACTGGCCGT  | GTAGAACGCG | GACAAGTTAA | AGTCGGTGAC | 450 |
|    | GAAGTTGAAA | TCATCGGTCT  | TCAAGAAGAG | AACAAGAAAA | CAACTGTTC  | 500 |
|    | AGGTGTTGAA | ATGTTCCGTA  | AGCTTCTTGA | TTACGCTGAA | GCTGGTGACA | 550 |
|    | ACATTGGTGC | CCTTCTTCGC  | GGTGTATCTC | GTGAAGAAAT | CCAACGTGGT | 600 |
|    | CAAGTACTTG | CTAAACCAGG  | TACAATCACT | CCACACAGCA | AATTCAAAGC | 650 |
| 15 | TGAAGTTTAC | GTTCTTTCTA  | AAGAAGAGGG | TGGACGTCAT | ACTCCATTCT | 700 |
|    | TCTCTAACTA | CCGTCCCTCAG | TTCTACTTCC | GTACAACTGA | CGTAACTGGT | 750 |
|    | ATCATCCATC | TTCCAGAAGG  | CGTAGAAATG | GTTATGCCTG | GAGATAACAC | 800 |
|    | TGAAATGAAC | GTTGAACTTA  | TTTCTACAAT | CGCTATCGAA | GAAGGAACCT | 850 |
|    | GTTTCTCTAT | TCGTGAAGGC  | GGACGTACTG | TTGGT      |            | 885 |
| 20 |            |             |            |            |            |     |

## 2) INFORMATION FOR SEQ ID NO: 1736

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*  
 (B) STRAIN: DSM 2151  
 (C) ACCESSION NUMBER: P33165

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 40 | ATGGTTACTG | GTGCTGCTCA | GATGGACGGT | GCTATCATTG | TAGTTGCTGC | 50  |
|    | TACTGATGGT | CCGATGCCTC | AGACTCGTGA | GCACATCCTT | TTGGCTCGTC | 100 |
|    | AGGTAAACGT | TCCGAAGCTG | GTTGTATTCA | TGAACAAGTG | CGATATGGTT | 150 |
|    | GAAGATGCTG | AGATGTTGGA | ACTTGTGTA  | ATGGAAATGA | GAGAATTGCT | 200 |
|    | TTCATTCTAT | GATTTCGACG | GTGACAATAC | TCCGATCATT | CAGGGTTCTG | 250 |
| 45 | CTCTTGGTGC | ATTGAACGGC | GTAGAAAAAT | GGGAAGACAA | AGTAATGGAA | 300 |
|    | CTGATGGAAG | CTGTTGATAC | TTGGATTCCA | CTGCCTCCGC | GCGATGTTGA | 350 |
|    | TAAACCTTTC | TTGATGCCGG | TAGAAGACGT | GTTCTCTATC | ACAGGTCGTG | 400 |
|    | GTAAGTAGC  | TACAGGTCGT | ATCGAAACTG | GTGTTATCCA | TGTAGGTGAT | 450 |
|    | GAAATCGAAA | TCCTCGGTTT | GGGTGAAGAT | AAGAAATCAG | TTGTAACAGG | 500 |
| 50 | TGTTGAAATG | TTCCGCAAAC | TTCTGGATCA | GGGTGAAGCT | GGTGACAACG | 550 |
|    | TAGGTCTGTT | GCTTCGTGGT | GTTGACAAGA | ACGAAATCAA | ACGTGGTATG | 600 |
|    | GTTCTTTGTA | AACCGGGTCA | GATTAAACCT | CACTCTAAAT | TCAAAGCAGA | 650 |
|    | GGTTTATATC | CTGAAGAAAG | AAGAAGGTGG | TCGTCACACT | CCATTCCATA | 700 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ACAAATATCG | TCCTCAGTTC | TACCTGCGTA | CTATGGACTG | TACAGGTGAA | 750 |
| ATCACTCTTC | CGGAAGGAAC | TGAAATGGTA | ATGCCGGGTG | ATAACGTAAC | 800 |
| TATCACTGTA | GAGTTGATCT | ATCCGGTTGC | ACTGAACATC | GGTCTTCGTT | 850 |
| TCGCTATCCG | CGAAGGTGGA | CGTACAGTAG | GT         |            | 882 |

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## 2) INFORMATION FOR SEQ ID NO: 1737

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*  
 (B) STRAIN: U78183  
 (C) ACCESSION NUMBER: U78183

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737

|    |             |            |            |            |             |     |
|----|-------------|------------|------------|------------|-------------|-----|
| 25 | AATATGATTA  | CAGGAGCAGC | TCAAATGGAT | GCAGCGATAC | TTTTAGTTGC  | 50  |
|    | TGCTGATAGT  | GGTGCTGAGC | CTCAAACAAA | AGAGCATTTG | CTTCTTGCTC  | 100 |
|    | AAAGAATGGG  | AATAAAGAAA | ATAATAGTTT | TTTTAAATAA | ATTGGACTTA  | 150 |
|    | GCAGATCCTG  | AACTTGTTGA | GCTTGTTGAA | GTTGAAGTTT | TAGAACTTGT  | 200 |
|    | TGAAAAATAT  | GGCTTTTCAG | CTGATACTCC | AATAATCAAA | GGTTCAGCTT  | 250 |
| 30 | TTGGGGCTAT  | GTCAAATCCA | GAAGATCCTG | AATCTACAAA | ATGCGTTAAA  | 300 |
|    | GAAGTTCTTG  | AATCTATGGA | TAATTATTTT | GATCTTCCAG | AAAGAGATAT  | 350 |
|    | TGACAAGCCA  | TTTTTGCTTG | CTGTTGAAGA | TGTATTTTCT | ATTTCAAGGAA | 400 |
|    | GAGGCACTGT  | TGCTACTGGG | CGTATTGAAA | GAGGTATTAT | TAAAGTTGGT  | 450 |
|    | CAAGAAGTTG  | AAATAGTTGG | AATTAAAGAA | ACCAGAAAAA | CTACTGTTAC  | 500 |
| 35 | TGGTGTGAA   | ATGTTCCAGA | AAATTCCTGA | GCAAGGTCAA | GCAGGGGATA  | 550 |
|    | ATGTTGGTCT  | TCTTTTGAGA | GGCGTTGATA | AAAAAGACAT | TGAGAGGGGG  | 600 |
|    | CAAGTTTTGT  | CAGCTCCAGG | TACAATTACT | CCACACAAGA | AATTTAAAGC  | 650 |
|    | TTCAATTTAT  | TGTTTGACTA | AAGAAGAAGG | CGGTAGGCAC | AAGCCATTTT  | 700 |
|    | TCCCAGGGTA  | TAGACCACAG | TTCTTTTTTA | GAACAACCGA | TGTTACTGGA  | 750 |
| 40 | GTTGTTGCTT  | TAGAGGGCAA | AGAAATGGTT | ATGCCTGGTG | ATAATGTTGA  | 800 |
|    | TATTATTGTT  | GAGCTGATCT | CTTCAATAGC | TATGGATAAG | AATGTAGAAT  | 850 |
|    | TTGCTGTTCTG | AGAAGGTGGA | AGAACCGTTG | CTTCAGGA   |             | 888 |

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## 2) INFORMATION FOR SEQ ID NO: 1738

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevibacterium linens*  
 5 (B) STRAIN: DSM 20425  
 (C) ACCESSION NUMBER: X76863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 10 | AACATGATCA | CCGGTGCCGC | TCAGATGGAC | GGTGCGATCC | TCGTCGTCGC | 50  |
|    | CGCTACCGAC | GGACCGATGC | CCCAGACCCG | TGAGCACGTG | CTGCTCGCGC | 100 |
|    | GTCAGGTCGG | CGTTCCCTAC | ATCGTCGTGG | CTCTGAACAA | GTCCGACATG | 150 |
|    | GTCGATGACG | AGGAGCTCCT | CGAGCTCGTC | GAATTCGAGG | TCCGCGACCT | 200 |
|    | GCTCTCGAGC | CAGGACTTCG | ACGGAGACAA | CGCTCCGGTC | ATTCCGGTGT | 250 |
| 15 | CCGCTCTCAA | GGCGCTGGAA | GGCGACGAGA | AGTGGGTCAA | GAGCGTTCAG | 300 |
|    | GATCTCATGG | CTGCCGTCGA | TGACAACGTT | CCGGAGCCGG | AGCGCGATGT | 350 |
|    | CGACAAGCCG | TTCCTCATGC | CCGTGCGAGG | CGTCTTCACG | ATCACCGGTC | 400 |
|    | GTGGAACCGT | CGTCACCGGT | CGTGTCGAGC | GCGGCGTGCT | CCTGCCTAAC | 450 |
|    | GACGAAATCG | AAATCGTCGG | CATCAAGGAG | AAGTCGTCCA | AGACGACTGT | 500 |
| 20 | CACCGCTATC | GAGATGTTCC | GCAAGACCCT | GCCGGATGCC | CGTGCAGGTG | 550 |
|    | AGAACGTCGG | TCTGCTCCTC | CGCGGCACCA | AGCGCGAGGA | TGTTGAGCGC | 600 |
|    | GGTCAGGTCA | TCGTGAAGCC | GGGTTCGATC | ACCCCGCACA | CCAAGTTCGA | 650 |
|    | GGCTCAGGTC | TACATCCTGA | GCAAGGACGA | GGGCGGACGT | CACAACCCGT | 700 |
|    | TCTACTCGAA | CTACCGTCCG | CAGTTCTACT | TCCGGACCAC | GGACGTCACC | 750 |
| 25 | GGTGTGATCA | CGCTGCCCCG | GGGCACCGAG | ATGGTCATGC | CCGGCGACAA | 800 |
|    | CACCGATATG | TCGGTCGAGC | TCATCCAGCC | GATCGCTATG | GAGGACCGCC | 850 |
|    | TCCGCTTCGC | AATCCGCGAA | GGTGGCCGCA | CCGTGCGCGC | CGGT       | 894 |

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2) INFORMATION FOR SEQ ID NO: 1739

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases  
 35 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*  
 (B) STRAIN: F/IC-Cal-13  
 (C) ACCESSION NUMBER: L22216

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGATCACGG | GCGCAGCGCA | GATGGACGGC | GCGATCCTGG | TTTGCTCGGC | 50  |
|    | AGCAGACGGC | CCGATGCCGC | AAACGCGTGA | GCACATCCTG | CTGGCGCGTC | 100 |
| 50 | AGGTTGGTGT | TCCGTACATC | ATCGTGTTCC | TGAACAAGTG | CGACAGTGTG | 150 |
|    | GACGACGCTG | AACTGCTCGA | GCTGGTCGAG | ATGGAAGTTC | GCGAACTCCT | 200 |
|    | GTCGAAGTAC | GACTTCCCGG | GCGACGACAC | GCCGATCGTG | AAGGGTTCGG | 250 |
|    | CCAAGCTGGC | GCTGGAAGGC | GACACGGGCG | AGCTGGGCGA | AGTGGCGATC | 300 |



|    |             |            |             |            |            |     |
|----|-------------|------------|-------------|------------|------------|-----|
|    | ATGAGCCTGG  | CAGACGCGCT | GGACACGTAC  | ATCCCGACGC | CGGAGCGTGC | 350 |
|    | AGTTGACGGC  | GCGTTCCTGA | TGCCGGTGGA  | AGACGTGTTC | TCGATCTCGG | 400 |
|    | GCCGTGGTAC  | GGTGGTGACG | GGTCGTGTCTG | AGCGCGGCAT | CGTGAAGGTC | 450 |
|    | GGCGAAGAAA  | TCGAAATCGT | CGGTATCAAG  | CCGACGGTGA | AGACGACCTG | 500 |
| 5  | CACGGGCGTT  | GAAATGTTCC | GCAAGCTGCT  | GGACCAAGGT | CAGGCAGGCG | 550 |
|    | ACAACGTCGG  | TATCCTGCTG | CGCGGCACGA  | AGCGTGAAGA | CGTGGAGCGT | 600 |
|    | GGCCAGGTTC  | TGGCGAAGCC | GGGTTCGATC  | ACGCCGCACA | CGCACTTCAC | 650 |
|    | GGCTGAAGTG  | TACGTGCTGA | GCAAGGACGA  | AGGCGGCCGT | CACACGCCGT | 700 |
|    | TCTTCAACAA  | CTACCGTCCG | CAGTTCTACT  | TCCGTACGAC | GGACGTGACG | 750 |
| 10 | GGCTCGATCG  | AGCTGCCGAA | GGACAAGGAA  | ATGGTGATGC | CGGGCGACAA | 800 |
|    | CGTGTCTGATC | ACGGTGAAGC | TGATTGCTCC  | GATCGCGATG | GAAGAAGGTC | 850 |
|    | TGCGCTTCGC  | AATCCGTGAA | GGCGGCCGTA  | CGGTCGGC   |            | 888 |

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## 2) INFORMATION FOR SEQ ID NO: 1740

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fibrobacter succinogenes*  
 (B) STRAIN: S85  
 (C) ACCESSION NUMBER: X76866

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | AACATGGTGA | CTGGTGCTGC | TCAGATGGAC | GGCGCTATCC | TCGTTGTTGC | 50  |
|    | CGCTACTGAC | GGTCCGATGC | CGCAGACTCG | CGAACACATC | CTTCTCGCTC | 100 |
| 35 | ACCAGGTTGG | CGTGCCGAAG | ATCGTCGTGT | TCATGAACAA | GTGCGACATG | 150 |
|    | GTTGACGATG | CTGAAATTCT | CGACCTCGTC | GAAATGGAAG | TTCGCGAACT | 200 |
|    | CCTCTCCAAG | TATGACTTCG | ACGGTGACAA | CACCCCGATC | ATCCGTGGTT | 250 |
|    | CCGCTCTCAA | GGCCCTCGAA | GGCGATCCGG | AATACCAGGA | CAAGGTCATG | 300 |
|    | GAATCATGA  | ACGCTTGCGA | CGAATACATC | CCGCTCCCGC | AGCGCGATAC | 350 |
| 40 | CGACAAGCCG | TTCCTCATGC | CGATCGAAGA | CGTGTTACG  | ATTACTGGCC | 400 |
|    | GCGGCACTGT | CGCTACTGGC | CGTATCGAAC | GCGGTGTCGT | TCGCTTGAAC | 450 |
|    | GACAAGGTTG | AACGTATCGG | TCTCGGTGAA | ACCACCGAAT | ACGTCATCAC | 500 |
|    | CGGTGTTGAA | ATGTTCCGTA | AGCTCCTCGA | CGACGCTCAG | GCAGGTGACA | 550 |
|    | ACGTTGGTCT | CCTCCTCCGT | GGTGCTGAAA | AGAAGGACAT | CGTCCGTGGC | 600 |
| 45 | ATGGTTCTCG | CAGCTCCGAA | GTCTGTCACT | CCGCACACCG | AATTTAAGGC | 650 |
|    | TGAAATCTAC | GTTCTCACGA | AGGACGAAGG | TGGCCGTCAC | ACGCCGTTCA | 700 |
|    | TGAATGGCTA | CCGTCCGCAG | TTCTACTTCC | GCACCACCGA | CGTTACTGGT | 750 |
|    | ACGATCCAGC | TCCCGGAAGG | TGTCGAAATG | GTTACTCCGG | GTGACACGGT | 800 |
|    | CACGATCCAC | GTGAACCTCA | TCGCTCCGAT | CGCTATGGAA | AAGCAGCTCC | 850 |
| 50 | GCTTCGCTAT | CCGTGAAGGT | GGACGTACTG | TTGGTGCTGG | C          | 891 |

## 2) INFORMATION FOR SEQ ID NO: 1741

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Flavobacterium ferrugineum*  
 (B) STRAIN: DSM 13524  
 (C) ACCESSION NUMBER: X76867

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | AACATGATCA | CCGGTGCTGC | CCAGATGGAC | GGTGCTATCT | TAGTTGTGGC | 50  |
|    | TGCATCAGAC | GGTCCTATGC | CTCAAACAAA | AGAACACATC | CTGCTTGCTG | 100 |
| 20 | CCCAGGTAGG | TGTACCTAAA | ATGGTTGTGT | TTCTGAATAA | AGTTGACCTC | 150 |
|    | GTTGACGACG | AAGAGCTCCT | GGAGCTGGTT | GAGATCGAGG | TTCGCGAAGA | 200 |
|    | ACTGACTAAA | CGCGGTTTCG | ACGGCGACAA | CACTCCAATC | ATCAAAGGTT | 250 |
|    | CCGCTACAGG | CGCCCTCGCT | GGTGAAGAAA | AGTGGGTAA  | AGAAATTGAA | 300 |
|    | AACCTGATGG | ACGCTGTTGA | CAGCTACATC | CCACTGCCTC | CTCGTCCGGT | 350 |
| 25 | TGATCTGCCG | TTCCTGATGA | GCGTAGAGGA | CGTATTCTCT | ATCACTGGTC | 400 |
|    | GTGGTACTGT | TGCTACCGGT | CGTATCGAGC | GTGGCCGTAT | CAAAGTTGGT | 450 |
|    | GAGCCTGTTG | AGATCGTAGG | TCTGCAGGAG | TCTCCCCTGA | ACTCTACCGT | 500 |
|    | TACAGGTGTT | GAGATGTTCC | GCAAACCTCT | CGACGAAGGT | GAAGCTGGTG | 550 |
|    | ATAACGCCGG | TCTCCTCCTC | CGTGGTGTTG | AAAAAACACA | GATCCGTCGC | 600 |
| 30 | GGTATGGTAA | TCGTAAACC  | CGGTTCCATC | ACTCCGCACA | CGGACTTCAA | 650 |
|    | AGGCGAAGTT | TACGTACTGA | GCAAAGACGA | AGGTGGCCGT | CACACTCCAT | 700 |
|    | TCTTCAACAA | ATACCGTCCT | CAATTCTACT | TCCGTACAAC | TGACGTTACA | 750 |
|    | GGTGAAGTAG | AACTGAACGC | AGGAACAGAA | ATGGTTATGC | CTGGTGATAA | 800 |
|    | CACCAACCTG | ACCGTTAAAC | TGATCCAACC | GATCGCTATG | GAAAAAGGTC | 850 |
| 35 | TGAAATTTCG | GATCCGCGAA | GGTGGCCGTA | CCGTAGGTGC | AGGA       | 894 |

## 2) INFORMATION FOR SEQ ID NO: 1742

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*  
 (B) STRAIN: 26695  
 (C) ACCESSION NUMBER: AE000626

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | AACATGATCA | CCGGTGCGGC | GCAAATGGAC  | GGAGCGATTT | TGGTTGTTTC | 50  |
|    | TGCAGCTGAT | GGCCCTATGC | CTCAAAC TAG | GGAGCATATC | TTATTGTCTC | 100 |
| 5  | GTCAAGTAGG | CGTGCCTCAC | ATCGTTGTTT  | TCTTAAACAA | ACAAGACATG | 150 |
|    | GTAGATGACC | AAGAATTGTT | AGAACTTGTA  | GAAATGGAAG | TGCGCGAATT | 200 |
|    | GTTGAGCGCG | TATGAATTTT | CTGGCGATGA  | CACTCCTATC | GTAGCGGGTT | 250 |
|    | CAGCTTTAAG | AGCTTTAGAA | GAAGCAAAGG  | CTGGTAATGT | GGGTGAATGG | 300 |
|    | GGTGAAAAAG | TGCTTAAACT | TATGGCTGAA  | GTGGATGCCT | ATATCCCTAC | 350 |
| 10 | TCCAGAAAGA | GACACTGAAA | AAACTTTCTT  | GATGCCGGTT | GAAGATGTGT | 400 |
|    | TCTCTATTGC | GGGTAGAGGG | ACTGTGGTTA  | CAGGTAGGAT | TGAAAGAGGC | 450 |
|    | GTGGTGAAAG | TAGGCGATGA | AGTGGAAATC  | GTTGGTATCA | GACCTACACA | 500 |
|    | AAAAACGACT | GTAACCGGTG | TAGAAATGTT  | TAGGAAAGAG | TTGGAAAAAG | 550 |
|    | GTGAAGCCGG | CGATAATGTG | GGCGTGCTTT  | TGAGAGGAAC | TAAAAAAGAA | 600 |
| 15 | GAAGTGGAAC | GCGGTATGGT | TCTATGCAAA  | CCAGGTTCTA | TCACTCCGCA | 650 |
|    | CAAGAAATTT | GAGGGAGAAA | TTTATGTCCT  | TTCTAAAGAA | GAAGGCGGGA | 700 |
|    | GACACACTCC | ATTCTTCACC | AATTACCGCC  | CGCAATTCTA | TGTGCGCACA | 750 |
|    | ACTGATGTGA | CTGGCTCTAT | CACCCTTCCT  | GAAGGCGTAG | AAATGGTTAT | 800 |
|    | GCCTGGCGAT | AATGTGAAAA | TCACTGTAGA  | GTTGATTAGC | CCTGTTGCGT | 850 |
| 20 | TAGAGTTGGG | AACTAAATTT | GCGATTCTGT  | AAGGCGGTAG | GACCGTTGGT | 900 |
|    | GCTGGT     |            |             |            |            | 906 |

## 25 2) INFORMATION FOR SEQ ID NO: 1743

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases  
 (B) TYPE: Nucleic acid  
 30 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*  
 (B) STRAIN: IFO 3333  
 (C) ACCESSION NUMBER: M17788

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | AACATGATCA | CCGGCGCCGC | TCAGATGGAC | GGCGCGATCC | TCGTGGTCGC | 50  |
|    | CGCTACCGAC | GGCCCGATGG | CCCAGACCCG | TGAGCACGTG | CTCCTGGCCC | 100 |
|    | GCCAGGTCGG | CGTGCCGGCC | CTGCTCGTGG | CCCTGAACAA | GTCGGACATG | 150 |
| 45 | GTGGAGGACG | AGGAGCTCCT | CGAGCGTGTC | GAGATGGAGG | TCCGGCAGCT | 200 |
|    | GCTGTCCTCC | AGGAGCTTCG | ACGTCGACGA | GGCCCCGGTC | ATCCGCACCT | 250 |
|    | CCGCTCTGAA | GGCCCTCGAG | GGCGACCCCC | AGTGGGTCAA | GTCCGTCGAG | 300 |
|    | GACCTCATGG | ATGCCGTGGA | CGAGTACATC | CCGGACCCGG | TGCGCGACAA | 350 |
|    | GGACAAGCCG | TTCCTGATGC | CGATCGAGGA | CGTCTTCACG | ATCACCGGCC | 400 |
| 50 | GTGGCACCGT | GGTGACCGGT | CGCGCCGAGC | GCGGCACCCT | GAAGATCAAC | 450 |
|    | TCCGAGGTCG | AGATCGTCGG | CATCCGCGAC | GTGCAGAAGA | CCACTGTCAC | 500 |
|    | CGGCATCGAG | ATGTTCCACA | AGCAGCTCGA | CGAGGCCTGG | GCCGGCGAGA | 550 |
|    | ACTGCGGTCT | GCTCGTGCGC | GGTCTGAAGC | GCGACGACGT | CGAGCGCGGC | 600 |

|   |            |             |            |             |            |     |
|---|------------|-------------|------------|-------------|------------|-----|
|   | CAGGTGCTGG | TGGAGCCGGG  | CTCCATCACC | CCGCACACCA  | ACTTCGAGGC | 650 |
|   | GAACGTCTAC | ATCCTGTCCA  | AGGACGAGGG | TGGGCGTCAC  | ACCCCGTTCT | 700 |
|   | ACTCGAACTA | CCGCGCGCAG  | TTCTACTTCC | GCACCACCGA  | CGTCACCGGC | 750 |
|   | GTCATCACGC | TGCCCCGAGGG | CACCGAGATG | GTCATGCCCCG | GCGACACCAC | 800 |
| 5 | CGAGATGTCG | GTCGAGCTCA  | TCCAGCCGAT | CGCCATGGAG  | GAGGGCCTCG | 850 |
|   | GCTTCGCCAT | CCGCGAGGGT  | GGCCGCACCG | TGGGCTCCGG  | C          | 891 |

## 10 2) INFORMATION FOR SEQ ID NO: 1744

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*  
 (B) STRAIN: Erdmann.  
 (C) ACCESSION NUMBER: X63539

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
|    | AACATGATCA  | CCGGCGCCGC | GCAGATGGAC | GGTGCGATCC | TGGTGGTCGC | 50  |
|    | CGCCACCGAC  | GGCCCGATGC | CCCAGACCCG | CGAGCACGTT | CTGCTGGCGC | 100 |
|    | GTCAAGTGGG  | TGTGCCCTAC | ATCCTGGTAG | CGCTGAACAA | GGCCGACGCA | 150 |
| 30 | GTGGACGACG  | AGGAGCTGCT | CGAACTCGTC | GAGATGGAGG | TCCGCGAGCT | 200 |
|    | GCTGGCTGCC  | CAGGAATTCG | ACGAGGACGC | CCCGGTTGTG | CGGGTCTCGG | 250 |
|    | CGCTCAAGGC  | GCTCGAGGGT | GACGCGAAGT | GGGTTGCCTC | TGTCGAGGAA | 300 |
|    | CTGATGAACG  | CGGTCGACGA | GTCGATTCCG | GACCCGGTCC | GCGAGACCGA | 350 |
|    | CAAGCCGTTT  | CTGATGCCGG | TCGAGGACGT | CTTACCATT  | ACCGGCCGCG | 400 |
| 35 | GAACCGTGGT  | CACCGGACGT | GTGGAGCGCG | GCGTGATCAA | CGTGAACGAG | 450 |
|    | GAAGTTGAGA  | TCGTCGGCAT | TCGCCCATCG | ACCACCAAGA | CCACCGTCAC | 500 |
|    | CGGTGTGGAG  | ATGTTCCGCA | AGCTGCTCGA | CCAGGGCCAG | GCGGGCGACA | 550 |
|    | ACGTTGGTTT  | GCTGCTGCGG | GGCGTCAAGC | GCGAGGACGT | CGAGCGTGGC | 600 |
|    | CAGGTTGTCA  | CCAAGCCCGG | CACCACCACG | CCGCACACCG | AGTTCGAAGG | 650 |
| 40 | CCAGGTCTAC  | ATCCTGTCCA | AGGACGAGGG | CGGCCGGCAC | ACGCCGTTCT | 700 |
|    | TCAACAACCTA | CCGTCCGCAG | TTCTACTTCC | GCACCACCGA | CGTGACCGGT | 750 |
|    | GTGGTGACAC  | TGCCGGAGGG | CACCGAGATG | GTGATGCCCG | GTGACAACAC | 800 |
|    | CAACATCTCG  | GTGAAGTTGA | TCCAGCCCGT | CGCCATGGAC | GAAGGTCTGC | 850 |
| 45 | GTTTCGCGAT  | CCGCGAGGGT | GGCCGCACCG | TGGGCGCCGG | C          | 891 |

## 2) INFORMATION FOR SEQ ID NO: 1745

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma genitalium*

(B) STRAIN: G37

(C) ACCESSION NUMBER: U39732

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | AATATGATCA | CAGGTGCTGC | ACAAATGGAT | GGAGCTATTC | TAGTTGTTTC | 50  |
|    | AGCAACTGAT | AGTGTGATGC | CCCAAACCCG | CGAGCACATC | TTACTTGCCC | 100 |
|    | GCCAAGTAGG | GGTTCCTAAA | ATGGTAGTTT | TTCTAAACAA | GTGTGATATT | 150 |
| 15 | GCTAGTGATG | AAGAGGTACA | AGAACTTGTT | GCTGAAGAAG | TACGTGATCT | 200 |
|    | GTTAACTTCC | TATGGTTTTG | ATGGTAAGAA | CACTCCTATT | ATTTATGGCT | 250 |
|    | CAGCTTTAAA | AGCATTGGAA | GGTGATCCAA | AGTGGGAGGC | TAAGATCCAT | 300 |
|    | GATTTGATTA | AAGCAGTTGA | TGAATGGATT | CCAACTCCTA | CACGTGAAGT | 350 |
|    | AGATAAACCT | TTCTTATTAG | CAATTGAAGA | TACGATGACC | ATTACTGGTA | 400 |
| 20 | GAGGTACAGT | TGTTACAGGA | AGAGTTGAAA | GAGGTGAACT | CAAAGTAGGT | 450 |
|    | CAAGAAGTTG | AAATTGTTGG | TTTAAACCA  | ATTAGAAAAG | CAGTTGTTAC | 500 |
|    | TGGAATTGAA | ATGTTCAAAA | AGGAACTTGA | TTCAGCAATG | GCTGGTGACA | 550 |
|    | ATGCTGGGGT | ATTATTACGT | GGTGTGAAC  | GTAAAGAAGT | TGAAAGAGGT | 600 |
|    | CAAGTTTTAG | CAAACCAGG  | CTCTATTAAA | CCGCACAAGA | AATTTAAAGC | 650 |
| 25 | TGAGATCTAT | GCTTTAAAGA | AAGAAGAAGG | TGGTAGACAC | ACTGGTTTTT | 700 |
|    | TAAACGGTTA | CCGTCCTCAA | TTCTATTTC  | GTACCACTGA | TGTAAGTGGT | 750 |
|    | TCTATTGCTT | TAGCTGAAAA | TACTGAAATG | GTTCTACCTG | GTGATAATGC | 800 |
|    | TTCTATTACT | GTTGAGTTAA | TTGCTCCTAT | CGCTTGTGAA | AAAGGTAGTA | 850 |
| 30 | AGTTCTCAAT | TCGTGAAGGT | GGTAGAACTG | TAGGGGCAGG | C          | 891 |

2) INFORMATION FOR SEQ ID NO: 1746

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

45 (B) STRAIN: MS11

(C) ACCESSION NUMBER: L36380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 50 | AACATGATTA | CCGGCGCCGC | ACAAATGGAC | GGTGCAATCC | TGGTATGTTC | 50  |
|    | TGCTGCCGAC | GGCCCTATGC | CGCAAACCCG | CGAACACATC | CTGCTGGCCC | 100 |
|    | GTCAAGTAGG | CGTACCTTAC | ATCATCGTGT | TCATGAACAA | ATGCGACATG | 150 |
|    | GTCGACGATG | CCGAGCTGTT | CCAACTGGTT | GAAATGGAAA | TCCGCGACCT | 200 |

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | GCTGTCCAGC | TACGACTTCC | CCGGCGACGA | CTGCCCCGATC | GTACAAGGTT | 250 |
|    | CCGCACTGAA | AGCCTTGGA  | GGCGATGCCG | CTTACGAAGA  | AAAAATCTTC | 300 |
|    | GAAGTGGCTA | CCGCATTGGA | CAGATACATC | CCGACTCCCG  | AGCGTGCCGT | 350 |
|    | GGACAAACCA | TTCCTGCTGC | CTATCGAAGA | CGTGTTCTCC  | ATTTCCGGCC | 400 |
| 5  | GCGGTACCGT | AGTCACCGGC | CGTGTAGAGC | GAGGTATCAT  | CCACGTTGGT | 450 |
|    | GACGAGATTG | AAATCGTCGG | TCTGAAAGAA | ACCCAAAAAA  | CCACCTGTAC | 500 |
|    | CGGCGTTGAA | ATGTTCCGCA | AACTGCTGGA | CGAAGGTCAG  | GCGGGCGACA | 550 |
|    | ACGTAGGCGT | ATTGCTGCGC | GGTACCAAAC | GTGAAGACGT  | AGAACGCGGT | 600 |
|    | CAGGTATTGG | CCAAACGGGG | TACTATCACT | CCTCACACCA  | AGTTCAAAGC | 650 |
| 10 | AGAAGTGTAC | GTATTGAGCA | AAGAAGAGGG | CGGCCCCCAT  | ACCCCGTTTT | 700 |
|    | TCGCCAACTA | CCGTCCCCAA | TTCTACTTCC | GTACCACTGA  | CGTAACCGGC | 750 |
|    | ACGATTACTT | TGGAAAAAGG | TGTGGAAATG | GTAATGCCGG  | GTGAGAACGT | 800 |
|    | AACCATTACT | GTAGAACTGA | TTGCGCCTAT | CGCTATGGAA  | GAAGGTCTGC | 850 |
| 15 | GCTTTGCGAT | TCGCGAAGGC | GGCCGTACCG | TGGGTGCCGG  | C          | 891 |

## 2) INFORMATION FOR SEQ ID NO: 1747

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 891 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Rickettsia prowazekii*
  - 30 (B) STRAIN: Madrid E
  - (C) ACCESSION NUMBER: Z54170

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747

|    |            |             |             |            |             |     |
|----|------------|-------------|-------------|------------|-------------|-----|
| 35 | AATATGATAA | CTGGTGCCGC  | TCAGATGGAT  | GGTGCTATAT | TAGTAGTTTC  | 50  |
|    | TGCTGCTGAT | GGTCCTATGC  | CTCAAACCTAG | AGAACATATA | TTACTGGCAA  | 100 |
|    | AACAGGTAGG | TGTACCTGCT  | ATGGTAGTAT  | TTTTGAATAA | AGTAGATATG  | 150 |
|    | GTAGATGATC | CTGACCTATT  | AGAATTAGTT  | GAGATGGAAG | TAAGAGAATT  | 200 |
|    | ATTATCAAAA | TATGGTTTCC  | CTGGTAATGA  | AATACCTATT | ATTAAAGGTT  | 250 |
| 40 | CTGCACTTCA | AGCTTTAGAA  | GGAAAACCTG  | AAGGTGAAAA | AGCTATTAAT  | 300 |
|    | GAGTTAATGA | ATGCAGTAGA  | TACGTATATA  | CCTCAGCCTA | TAGAGCTACA  | 350 |
|    | AGATAAACCT | TTTTTAATGC  | CAATAGAGGA  | TGTATTTTCT | ATTTTCAGGCA | 400 |
|    | GAGGTACCGT | TGTAACCTGGT | AGAGTGAGGT  | CAGGCATAAT | TAAGGTGGGT  | 450 |
|    | GAAGAAATTG | AAATAGTAGG  | TCTAAAAAAT  | ACGCAAAAAA | CGACTTGTAC  | 500 |
| 45 | AGGTGTAGAA | ATGTTTCAGAA | AATTACTTGA  | TGAAGGACAA | TCTGGAGATA  | 550 |
|    | ATGTCGGTAT | ATTACTACGT  | GGTACAAAAA  | GAGAAGAAGT | AGAAAGAGGA  | 600 |
|    | CAAGTACTTG | CAAACCTGG   | GAGCATAAAA  | CCGCATGATA | AATTTGAAGC  | 650 |
|    | TGAAGTGTAT | GTGCTTAGTA  | AAGAGGAAGG  | TGGACGTCAT | ACCCCATTTA  | 700 |
|    | CTAATGATTA | TCGCCCACAG  | TTCTATTTTA  | GAACAACAGA | TGTTACCGGC  | 750 |
| 50 | ACAATAAAAT | TGCCTTCTGA  | TAAGCAGATG  | GTTATGCCTG | GAGATAATGC  | 800 |
|    | TACTTTTTCA | GTAGAATTAA  | TTAAGCCGAT  | TGCTATGCAA | GAAGGGTTAA  | 850 |
|    | AATTCTCTAT | ACGTGAAGGT  | GGTAGAACAG  | TAGGAGCCGG | T           | 891 |

## 2) INFORMATION FOR SEQ ID NO: 1748

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Typhimurium  
 (B) STRAIN: LT2 trpE91  
 (C) ACCESSION NUMBER: X55116

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | AACATGATCA | CCGGTGCTGC | TCAGATGGAC | GGCGCGATCC | TGGTTGTTGC | 50  |
| 20 | TGCGACTGAC | GGCCCGATGC | CGCAGACCCG | TGAGCACATC | CTGCTGGGTC | 100 |
|    | GTCAGGTAGG | CGTTCCGTAC | ATCATCGTGT | TCCTGAACAA | ATGCGACATG | 150 |
|    | GTTGATGACG | AAGAGCTGCT | GGAAGTGGTT | GAGATGGAAG | TTCGCGAACT | 200 |
|    | GCTGTCTCAG | TACGACTTCC | CGGGCGACGA | CACTCCGATC | GTTCGTGGTT | 250 |
|    | CTGCTCTGAA | AGCGCTGGAA | GGCGACGCAG | AGTGGGAAGC | GAAAATCATC | 300 |
| 25 | GAACTGGCTG | GCTTCCTGGA | TTCTTATATT | CCGGAACCAG | AGCGTGCGAT | 350 |
|    | TGACAAGCCG | TTCCTGCTGC | CGATCGAAGA | CGTATTCTCC | ATCTCCGGTC | 400 |
|    | GTGGTACCGT | TGTTACCGGT | CGTGTAGAGC | GCGGTATCAT | CAAAGTGGGC | 450 |
|    | GAAGAAGTTG | AAATCGTTGG | TATCAAAGAG | ACTCAGAAGT | CTACCTGTAC | 500 |
|    | TGGCGTTGAA | ATGTTCCGCA | AACTGCTGGA | CGAAGGCCGT | GCCGGTGAGA | 550 |
| 30 | ACGTAGGTGT | TCTGCTGCGT | GGTATCAAAC | GTGAAGAAAT | CGAACGTGGT | 600 |
|    | CAGGTACTGG | CTAAGCCGGG | CACCATCAAG | CCGCACACCA | AGTTCGAATC | 650 |
|    | TGAAGTGTAC | ATTCTGTCCA | AAGATGAAGG | CGGCCGTCAT | ACTCCGTTCT | 700 |
|    | TCAAAGGCTA | CCGTCCGCAG | TTCTACTTCC | GTACTACTGA | CGTGACTGGT | 750 |
|    | ACCATCGAAC | TGCCGGAAGG | CGTAGAGATG | GTAATGCCGG | GCGACAACAT | 800 |
| 35 | CAAAATGGTT | GTTACCCTGA | TCCACCCGAT | CGCGATGGAC | GACGGTCTGC | 850 |
|    | GTTTCGCAAT | CCGTGAAGGC | GGCCGTACCG | TTGGCGCGGG | C          | 891 |

## 40 2) INFORMATION FOR SEQ ID NO: 1749

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*  
 (B) STRAIN: DSM 50426

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749

|    |            |             |            |            |            |     |
|----|------------|-------------|------------|------------|------------|-----|
|    | ATGATCACTG | GTGCTGCACA  | GATGGACGGC | GCGATTCTGG | TAGTCGCTTC | 50  |
|    | AACAGACGGT | CCAATGCCAC  | AGACTCGTGA | GCACATCCTG | CTTTCTCGTC | 100 |
| 5  | AGGTTGGCGT | ACCATTCATC  | ATCGTATTCA | TGAACAAATG | TGACATGGTA | 150 |
|    | GATGACGAAG | AGCTGTTAGA  | GCTAGTTGAG | ATGGAAGTGC | GTGAACTGTT | 200 |
|    | ATCAGAATAC | GATTTCCCAG  | GTGATGACTT | ACCGGTAATC | CAAGGTTTCA | 250 |
|    | CTCTGAAAGC | GCTAGAAGGC  | GAGCCAGAGT | GGGAAGCAAA | AATCCTTGAA | 300 |
|    | TTAGCAGCGG | CGCTGGATTTC | TTACATTCCA | GAACCACAAC | GTGACATCGA | 350 |
| 10 | TAAGCCGTTT | CTACTGCCAA  | TCGAAGACGT | ATTCTCAATT | TCAGGCCGTG | 400 |
|    | GTACAGTAGT | AACAGGTCGT  | GTGAGCGTG  | GTATTGTACG | CGTAGGCGAC | 450 |
|    | GAAGTTGAAA | TCGTTGGTGT  | ACGTGCGACA | ACTAAGACAA | CGTGTACTGG | 500 |
|    | TGTAGAAATG | TTCCGTAAAC  | TGCTTGACGA | AGGTCGTGCA | GGTGAGAACT | 550 |
|    | GTGGTATTTT | GTTACGTGGT  | ACTAAGCGTG | ATGACGTAGA | ACGTGGTCAA | 600 |
| 15 | GTATTAGCGA | AGCCAGGTTT  | AATCAACCCA | CACACTACTT | TTGAATCAGA | 650 |
|    | AGTTTACGTA | CTGTCAAAAG  | AAGAAGGTGG | TCGTACACAC | CCATTCTTCA | 700 |
|    | AAGGCTACCG | TCCACAGTTC  | TACTTCCGTA | CAACTGACGT | AACCGGTACT | 750 |
|    | ATCGAACTGC | CAGAAGGCGT  | AGAGATGGTA | ATGCCAGGCG | ATAACATCAA | 800 |
|    | GATGGTAGTG | ACACTGATTT  | GCCCAATCGC | GATGGACGAA | GGTTTACGCT | 850 |
| 20 | TCGCAATCCG | TGAAGGCGGT  | CGTACAGTGG | T          |            | 881 |

## 2) INFORMATION FOR SEQ ID NO: 1750

25

## (i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 897 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stigmatella aurantiaca*
- (B) STRAIN: DW4
- (C) ACCESSION NUMBER: X82820

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750

40

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | AACATGATCA | CGGGCGCGGC | GCAGATGGAC | GGAGCGATTC | TGGTGGTGTC | 50  |
|    | CGCGGCCGAC | GGCCCGATGC | CCCAGACGCG | TGAGCACATC | CTGCTGGCCA | 100 |
|    | GGCAGGTGGG | CGTGCCCTAC | ATCGTCGTCT | TCCTGAACAA | GGTGGACATG | 150 |
|    | CTGGACGATC | CGGAGCTGCG | CGAGCTGGTG | GAGATGGAGG | TGCGCGACCT | 200 |
| 45 | GCTCAAGAAG | TACGAGTTCC | CGGGCGACAG | CATCCCCATC | ATCCCTGGCA | 250 |
|    | GCGCGCTCAA | GGCGCTGGAG | GGAGACACCA | GCGACATCGG | CGAGGGAGCG | 300 |
|    | ATCCTGAAGC | TGATGGCGGC | GGTGGACGAG | TACATCCCGA | CGCCGCAGCG | 350 |
|    | TGCGACGGAC | AAGCCGTTCC | TGATGCCGGT | GGAAGACGTG | TTCTCCATCG | 400 |
|    | CAGGCCGAGG | AACGGTGGCG | ACGGGCCGAG | TGGAGCGCGG | CAAGATCAAG | 450 |
| 50 | GTGGGCGAGG | AAGTGGAGAT | CGTGGGGATC | CGTCCGACGC | AGAAGACGGT | 500 |
|    | CATCACGGGG | GTGGAGATGT | TCCGCAAGCT | GCTGGACGAG | GGCATGGCGG | 550 |
|    | GAGACAACAT | CGGAGCGCTG | CTGCGAGGCC | TGAAGCGCGA | GGACCTGGAG | 600 |
|    | CGTGGGCAGG | TGCTGGCGAA | CTGGGGGAGC | ATCAACCCGC | ACACGAAGTT | 650 |



|   |            |            |            |            |            |     |
|---|------------|------------|------------|------------|------------|-----|
|   | CAAGGCGCAG | GTGTACGTGC | TGTCGAAGGA | AGAGGGAGGG | CGGCACACGC | 700 |
|   | CGTTCTTCAA | GGGATACCGG | CCGCAGTTCT | ACTTCCGGAC | GACGGACGTG | 750 |
|   | ACCGGAACGG | TGAAGCTGCC | GGACAACGTG | GAGATGGTGA | TGCCGGGAGA | 800 |
|   | CAACATCGCC | ATCGAGGTGG | AGCTCATTAC | TCCGGTCGCC | ATGGAGAAGG | 850 |
| 5 | AGCTGCCGTT | CGCCATCCGT | GAGGGTGGCC | GCACGGTGGG | CGCCGGC    | 897 |

## 2) INFORMATION FOR SEQ ID NO: 1751

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiomonas cuprina*  
 (B) STRAIN: Hoe5  
 (C) ACCESSION NUMBER: x76871

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1751

25

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | AACATGATCA | CCGGTGCGGC | CCAGATGGAC | GGCGCCATCC | TGGTCGTGTC  | 50  |
|    | CGCCGCCGAC | GGCCCCATGC | CCCAAACCCG | CGAGCACATC | CTGCTGGCGC  | 100 |
|    | GTCAGGTGGG | CGTGCCCTAC | ATCATCGTGT | TCCTCAACAA | GTGCGACATG  | 150 |
|    | GTCGACGACG | CCGAGCTGCT | CGAACTCGTC | GAGATGGAAG | TGCGCGAGCT  | 200 |
| 30 | GCTGTCCAAG | TACGACTTCC | CCGGTGACGA | CACCCCCATC | ATCAAGGGCT  | 250 |
|    | CGGCCAAGCT | GGCCCTCGAA | GGCGACAAGG | GCGAACTGGG | CGAAGGCGCC  | 300 |
|    | ATTCTCAAGC | TGGCCGAGGC | CCTGGACACC | TACATCCCCA | CGCCCGAGCG  | 350 |
|    | GGCCGTCGAC | GGCGCGTTCC | TCATGCCCGT | GGAAGACGTG | TTCTCCATCT  | 400 |
|    | CCGGGCGCGG | CACGGTGGTC | ACCGGGCGTG | TGGAGCGCGG | CATCATCAAG  | 450 |
| 35 | GTCGGCGAGG | AAATCGAGAT | TGTCGGCCTC | AAGCCCACCC | TCAAGACCAC  | 500 |
|    | CTGCACCGGC | GTGGAAATGT | TCAGGAAGCT | GCTCGACCAG | GGCCAGGCCG  | 550 |
|    | GCGACAACGT | CGGCATCTTG | CTGCGCGGCA | CCAAGCGCGA | GGAAGTCGAG  | 600 |
|    | CGCGGCCAGG | TGCTGTGCAA | ACCCGGCTCG | ATCAAGCCCC | ACACCCACTT  | 650 |
|    | CACCGCCGAG | GTGTACGTGC | TGAGCAAGGA | CGAGGGCGGC | CGCCACACCC  | 700 |
| 40 | CCTTCTTCAA | CAACTACCGC | CCGCAGTTCT | ACTTCCGCAC | CACCGACGTC  | 750 |
|    | ACCGGCGCCA | TCGAACTGCC | CAAGGACAAG | GAAATGGTCA | TGCCCCGGCGA | 800 |
|    | TAATGTGAGC | ATCACCGTCA | AGCTCATCGC | CCCCATCGCC | ATGGAAGAAG  | 850 |
|    | GCCTGCGCTT | CGCCATCCGC | GAAGGCGGCC | GCACCGTCGG | CGCCGGC     | 897 |

45

## 2) INFORMATION FOR SEQ ID NO: 1752

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Treponema pallidum*  
 (B) STRAIN: Nichols  
 (C) ACCESSION NUMBER: AE001202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752

```

10 AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC 50
   TGC GCCTGAC GGC GTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC 100
   GTCAGGTTGG TGTTCCCTCC ATCATTGTTT TTTTGAACAA GGTTGATTTG 150
   GTTGATGATC CTGAGTTGCT AGAGCTGGTG GAAGAAGAGG TGC GTGATGC 200
15 GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC AAGGGGTCTG 250
   CGTTTAAAGC TCTGCAGGAT GGCGCTTCCC CGGAGGATGC AGCTTGTATT 300
   GAGGAACTGC TTGCGGCCAT GGATTCCCTAC TTTGAAGACC CAGTGC GTGA 350
   CGACGCAAGA CCTTCTTTC TCTCTATCGA GGATGTGTAC ACTATTTCTG 400
   GCGTG GTTAC CGTTGT CACG GGGCGCATCG AATGTGGGGT AATTAGTCTG 450
20 AATGAAGAGG TCGAGATCGT CGGGATTAAG CCCACTAAGA AAACAGTGGT 500
   TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA ATTGCAGGTG 550
   ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAAGA GGTTGAGCGC 600
   GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA 650
   GCGCAGATC TACGTGCTCT CTAAGGAAGA GGGTGGCCGT CACAGTCCTT 700
25 TTTTTC AAGG TTATCGTCCG CAGTTTTATT TTAGAACTAC TGACATTACC 750
   GGTACGATTT CTCTTCCTGA AGGGGTAGAC ATGGTGAAGC CGGGGGATAA 800
   CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG GACAAGGGTC 850
   TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT 894

```

30

2) INFORMATION FOR SEQ ID NO: 1753

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 891 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Ureaplasma urealyticum*  
 (B) STRAIN: ATCC 33697  
 (C) ACCESSION NUMBER: Z34275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753

```

50 AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC 50
   TGCATCTGAT GGGGTTATGG CTCAAAC TAA AGAACATATT TTATTAGCAC 100
   GTCAAGTTGG TGTTCCAAAA ATCGTTGTTT TCTTAAACAA ATGTGATTTT 150
   ATGACAGATC CAGATATGCA AGATCTTGTT GAAATGGAAG TTCGTGAATT 200
   ATTATCTAAA TATGGATTTG ATGGCGATAA CACACCAGTT ATTCGTGGTT 250

```

|    |             |            |            |             |             |     |
|----|-------------|------------|------------|-------------|-------------|-----|
|    | CAGGTCTTAA  | GGCTTTAGAA | GGAGATCCAG | TTTGAGAAGC  | AAAAATTGAT  | 300 |
|    | GAATTAATGG  | ACGCAGTTGA | TTCATGAATT | CCATTACCAG  | AACGTAGTAC  | 350 |
|    | TGACAAACCA  | TTCTTATTAG | CAATTGAAGA | TGTATTACACA | ATTTACAGGAC | 400 |
|    | GTGGTACAGT  | AGTAACTGGA | CGTGTTGAAC | GTGGTGTATT  | AAAAGTTAAT  | 450 |
| 5  | GATGAGGTTG  | AAATTGTTGG | TCTAAAAGAC | ACTCAAAAAA  | CTGTTGTTAC  | 500 |
|    | AGGAATTGAA  | ATGTTTAGAA | AATCATTAGA | TCAAGCTGAA  | GCTGGTGATA  | 550 |
|    | ATGCTGGTAT  | TTTATTACGT | GGTATTAAAA | AAGAAGATGT  | TGAACGTGGT  | 600 |
|    | CAAGTACTTG  | TAAAACCAGG | ATCAATTAAA | CCTCACCGTA  | CTTTTACTGC  | 650 |
|    | TAAAGTTTAT  | ATTCTTAAAA | AAGAAGAAGG | TGGACGTCAT  | ACACCTATTG  | 700 |
| 10 | TTTCAGGATA  | CCGTCCACAA | TTCTATTTTA | GAACAACAGA  | TGTAACAGGT  | 750 |
|    | GCTATTTTCAT | TACCTGCTGG | TGTTGATTTG | GTTATGCCAG  | GTGATGACGT  | 800 |
|    | TGAAATGACT  | GTAGAATTAA | TTGCTCCAGT | TGCGATTGAA  | GATGGATCTA  | 850 |
|    | AATTCTCAAT  | CCGTGAAGGT | GGTAAACTG  | TAGGTCATGG  | T           | 891 |

15

## 2) INFORMATION FOR SEQ ID NO: 1754

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 909 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Wolinella succinogenes*
- (B) STRAIN: DSM 1740
- 30 (C) ACCESSION NUMBER: X76862

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | AACATGATTA | CAGGTGCTGC | TCAAATGGAT  | GGCGCGATTC | TTGTTGTTTC | 50  |
| 35 | TGCGGCGGAT | GGCCCCATGC | CCCAAAC TAG | GGAGCACATT | CTTCTTTCTC | 100 |
|    | GACAAGTAGG | CGTTCCTTAC | ATCGTG GTTT | TCTTGAACAA | AGAAGATATG | 150 |
|    | GTTGATGACG | CTGAGCTTCT | TGAGCTTGTT  | GAAATGGAAG | TTAGAGAACT | 200 |
|    | TCTTAGCAAC | TACGACTTCC | CTGGAGATGA  | CACTCCTATC | GTTGCAGGTT | 250 |
|    | CCGCTCTTAA | AGCTCTTGAA | GAGGCTAACG  | ACCAGGAAAA | TGTTGGCGAG | 300 |
| 40 | TGGGGCGAGA | AAGTATTGAA | GCTTATGGCT  | GAGGTTGACC | GATATATTCC | 350 |
|    | TACGCCTGAG | CGAGATGTGG | ATAAGCCTTT  | CCTTATGCCT | GTTGAAGACG | 400 |
|    | TATTCTCCAT | CGCGGGTCGT | GGAACCGTTG  | TGACAGGAAG | AATTGAAAGA | 450 |
|    | GGCGTGTTA  | AAGTCGGTGA | CGAAGTAGAA  | ATCGTTGGTA | TCCGAAACAC | 500 |
|    | ACAAAAACA  | ACCGTAACTG | GCGTTGAGAT  | GTTCCGAAAA | GAGCTCGACA | 550 |
| 45 | AGGGTGAGGC | GGGTGACAAC | GTTGGTGTTT  | TTTTGAGAGG | CACCAAGAAA | 600 |
|    | GAAGATGTTG | AGAGAGGTAT | GGTTCTTTGT  | AAAATAGGTT | CTATCACTCC | 650 |
|    | TCACACTAAC | TTTGAAGGTG | AAGTTTACGT  | TCTTTCCAAA | GAGGAAGGCG | 700 |
|    | GACGACACAC | TCCATTCTTC | AATGGATACC  | GACCTCAGTT | CTATGTTAGA | 750 |
|    | ACTACAGACG | TTACCGGTTT | TATCTCTCTT  | CCTGAGGGCG | TAGAGATGGT | 800 |
| 50 | TATGCCTGGT | GACAACGTTA | AGATCAATGT  | TGAGCTTATC | GCTCCTGTAG | 850 |
|    | CCCTCGAAGA | GGGAACACGA | TTGCGGATCC  | GTGAAGGTGG | TCGAACCGTT | 900 |
|    | GGTGCGGGT  |            |             |            |            | 909 |

## 2) INFORMATION FOR SEQ ID NO: 1755

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia cepacia*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 15 | ATGATCACGG | GCGCAGCGCA | GATGGACGGC | GCGATCCTGG | TTTGCTCGGC | 50  |
|    | AGCAGACGGC | CCGATGCCGC | AAACGCGTGA | GCACATCCTG | CTGGCGCGTC | 100 |
|    | AGGTTGGTGT | TCCGTACATC | ATCGTGTTCC | TGAACAAGTG | CGACAGTGTG | 150 |
|    | GACGACGCTG | AACTGCTCGA | GCTGGTCGAG | ATGGAAGTTC | GCGAACTCCT | 200 |
| 20 | GTCGAAGTAC | GACTTCCCGG | GCGACGACAC | GCCGATCGTG | AAGGGTTCGG | 250 |
|    | CCAAGCTGGC | GCTGGAAGGC | GACACGGGCG | AGCTGGGCGA | AGTGGCGATC | 300 |
|    | ATGAGCCTGG | CAGACGCGCT | GGACACGTAC | ATCCCGACGC | CGGAGCGTGC | 350 |
|    | AGTTGACGGC | GCGTTCCTGA | TGCCGGTGGA | AGACGTGTTC | TCGATCTCGG | 400 |
|    | GCCGTGGTAC | GGTGGTGACG | GGTCGTGTCG | AGCGCGGCAT | CGTGAAGGTC | 450 |
| 25 | GGCGAAGAAA | TCGAAATCGT | CGGTATCAAG | CCGACGGTGA | AGACGACCTG | 500 |
|    | CACGGGCGTT | GAAATGTTCC | GCAAGCTGCT | GGACCAAGGT | CAGGCAGGCG | 550 |
|    | ACAACGTCGG | TATCCTGCTG | CGCGGCACGA | AGCGTGAAGA | CGTGGAGCGT | 600 |
|    | GGCCAGGTTT | TGGCGAAGCC | GGGTTCGATC | ACGCCGCACA | CGCACTTCAC | 650 |
|    | GGCTGAAGTG | TACGTGCTGA | GCAAGGACGA | AGGCGGCCGT | CACACGCCGT | 700 |
| 30 | TCTTCAACAA | CTACCGTCCG | CAGTTCTACT | TCCGTACGAC | GGACGTGACG | 750 |
|    | GGCTCGATCG | AGCTGCCGAA | GGACAAGGAA | ATGGTGATGC | CGGGCGACAA | 800 |
|    | CGTGTGATC  | ACGGTGAAGC | TGATTGCTCC | GATCGCGATG | GAAGAAGGTC | 850 |
|    | TGCGCTTCGC | AATCCGTGAA | GGCGGCCGTA | CGGTCCGC   |            | 888 |

## 2) INFORMATION FOR SEQ ID NO: 1756

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*  
 (B) STRAIN: CIP 9444

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756

|            |           |            |            |            |    |
|------------|-----------|------------|------------|------------|----|
| TGAAAGTTCA | GGTAAACAA | CAGTTTCATT | ACACGCAATT | GCAGAAGTAC | 50 |
|------------|-----------|------------|------------|------------|----|

|              |            |            |            |            |     |
|--------------|------------|------------|------------|------------|-----|
| AGCGTCAAGG   | TGGACAAGCA | GCGTTCATTG | ATGCTGAGCA | TGCAATGGAT | 100 |
| CCTGTATATG   | CACAAAAACT | AGGTGTTAAC | ATCGATGAAT | TACTATTATC | 150 |
| ACAACCTGAT   | ACAGGGGAGC | AAGGTTTAGA | AATCGCAGAA | GCACTTGTAC | 200 |
| GAAGTGGTGC   | GGTTGATATT | ATCGTAATTG | ACTCTGTAGC | AGCTCTTGTA | 250 |
| 5 CCGAAAGCTG | AAATTGAAGG | AGACATGGGT | GACTCACACG | TAGGTTTACA | 300 |
| AGCTCGTCTA   | ATGTCTCAAG | CACTTCGTAA | ACTTTCAGGT | GCAATCAATA | 350 |
| AATCAAAAAC   | AATCGCAATC | TTTATTAACC | AAATTCGT   |            | 388 |

10

## 2) INFORMATION FOR SEQ ID NO: 1757

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 388 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: ATCC 4229

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| TGAAAGTTCA    | GGTAAAACAA | CAGTTTCATT | ACACGCAATT | GCAGAAGTAC | 50  |
| AGCGTCAAGG    | TGGACAAGCA | GCGTTCATTG | ATGCTGAGCA | TGCAATGGAT | 100 |
| CCTGTATATG    | CACAAAAACT | AGGTGTTAAC | ATCGATGAAT | TACTATTATC | 150 |
| 30 ACAACCTGAT | ACAGGGGAGC | AAGGTTTAGA | AATCGCAGAA | GCACTTGTAC | 200 |
| GAAGTGGTGC    | GGTTGATATT | ATCGTAATTG | ACTCTGTAGC | AGCTCTTGTA | 250 |
| CCGAAAGCTG    | AAATTGAAGG | AGACATGGGT | GACTCACACG | TAGGTTTACA | 300 |
| AGCTCGTCTA    | ATGTCTCAAG | CACTTCGTAA | ACTTTCAGGT | GCAATCAATA | 350 |
| AATCAAAAAC    | AATCGCAATC | TTTATTAACC | AAATTCGT   |            | 388 |

35

## 2) INFORMATION FOR SEQ ID NO: 1758

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 7064
- (C) ACCESSION NUMBER:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758

```

    TGAAAGTTCA GGTAAAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC      50
    AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT      100
    CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC      150
5   ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC      200
    GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
    CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA      300
    AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA      350
    AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT      388
10

```

## 2) INFORMATION FOR SEQ ID NO: 1759

```

15   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 388 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Bacillus cereus
25   (B) STRAIN: ATCC 13472
          (C) ACCESSION NUMBER:

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759

```

30   TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
    AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT      100
    CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
    ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGTAC      200
    GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
35   CCGAAAGCAG AGATTGAAGG TGACATGGGT GACTCACACG TAGGTTTACA      300
    AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
    AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

40

## 2) INFORMATION FOR SEQ ID NO: 1760

```

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 374 bases
45   (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
          (D) TOPOLOGY: Linear

      (ii) MOLECULE TYPE: Genomic DNA
50
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Bacillus mycoides
          (B) STRAIN: ATCC 6462

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760

```

5  AAACGACAGT TTCATTACAT GCAATTGCAG AAGTACAACG TCAAGGTGGA      50
   CAAGCAGCAT TCATCGATGC GGAGCACGCA ATGGATCCTG TATATGCACA      100
   AAAATTAGGC GTTAACATAG ATGAATTACT ATTATCACAG CCTGATACAG      150
   GGGAGCAAGG ATTAGAAATC GCAGAAGCAC TTGTACGAAG TGGTGCGGTT      200
   GACATTATCG TAATTGACTC TGTAGCAGCT CTTGTACCGA AAGCAGAGAT      250
   TGAAGGAGAC ATGGGTGACT CACACGTAGG TTTACAAGCA CGTTTAATGT      300
10 CACAAGCACT TCGTAAGCTT TCAGGAGCAA TCAACAAATC AAAACAATT      350
   GCAATCTTTA TTAACCAAAT TCGT                                374

```

## 15 2) INFORMATION FOR SEQ ID NO: 1761

## (i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 381 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

## (ii) MOLECULE TYPE: Genomic DNA

## 25 (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Bacillus pseudomycoides
   (B) STRAIN: NRRL BD-10

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761

```

30 GGAAAGTTCA GGTAAAACAA CGGTTTCCTT ACATGCGATT GCAGAAAGTGC      50
   AACGTCAAGG TGGACAAGCG GCATTTATTG ATGCGGAGCA TGCGATGGAT      100
   CCTGTATATG CACAAAAGTT AGGTGTTAAT ATTGATGAGT TACTATTATC      150
   GCAGCCTGAT ACAGGAGAAC AAGGTTTAGA AATCGCAGAA GCATTAGTAC      200
35 GAAGCGGTGC GATTGATATC ATTGTAATTG ACTCTGTAGC AGCTCTTGTA      250
   CAAAAGCAG AAATCGAAGG GGAAATGGGT GACTCCCACG TTGGTTTACA      300
   AGCGCGTTTA ATGTCACAAG CACTTCGTAA GCTTCTGGT GCGATTAACA      350
   AATCAAAAAC AATTGCAATC TTCATTAACC A                                381

```

40

## 2) INFORMATION FOR SEQ ID NO: 1762

## (i) SEQUENCE CHARACTERISTICS:

```

45 (A) LENGTH: 388 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

## 50 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Bacillus thuringiensis

```

(B) STRAIN: HER 1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762

```

5  TGAAAGTTCA GGTAACACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
   AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT      100
   CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
   ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGTAC      200
   GAAGTGGTGC GGTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
10  CCGAAAGCAG AGATTGAAGG CGACATGGGT GACTCACACG TAGGTTTACA      300
   AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
   AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

15

2) INFORMATION FOR SEQ ID NO: 1763

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 388 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

     (A) ORGANISM: Bacillus thuringiensis
     (B) STRAIN: HER 1418

```

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763

```

   TGAAAGTTCA GGTAACACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
   AACGTCAAGG TGGACAAGCA GCATTCATTG ATGCGGAGCA CGCAATGGAT      100
   CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
35  ACAGCCTGAT ACAGGGGAGC AAGGATTGGA AATCGCGGAA GCACTTGTAC      200
   GAAGTGGTGC GGTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
   CCGAAAGCAG AGATTGAAGG CGATATGGGT GACTCACACG TAGGTTTACA      300
   AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
   AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

40

2) INFORMATION FOR SEQ ID NO: 1764

(i) SEQUENCE CHARACTERISTICS:

```

45  (A) LENGTH: 358 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:



(A) ORGANISM: *Klebsiella oxytoca*  
(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764

5 CTCCTATCTG GATTATGCGA TGTCGGTTCAT TGTTGGCCGT GCGCTGCCGG 50  
ATGTCCGAGA TGGCCTGAAG CCGGTACACC GTCGCGTACT ATACGCCATG 100  
AACGTATTGG GCAATGACTG GAACAAAGCC TATAAAAAAT CTGCCCGTGT 150  
CGTGGGTGAC GTCATCGGTA AATACCACCC TCATGGTGAT ACTGCCGTAT 200  
10 ACGACACCAT TGTACGTATG GCGCAGCCCT TCTCCCTGCG TTACATGCTG 250  
GTAGATGGCC AGGGTAACTT TGGTTCGGTC GACGGCGACT CCGCCGCAGC 300  
GATGCGTTAT ACGGAAATCC GTATGTCGAA GATCGCCCAT GAACTGATGG 350  
CCGACCTC 358

15

2) INFORMATION FOR SEQ ID NO: 1765

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 365 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*  
(B) STRAIN: ATCC 11296

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765

TTAAGAACTC TTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG 50  
CTGCCGGATG TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTTTA 100  
35 CGCCATGAAC GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCAG 150  
CCCGTGTCGT TGGTGACGTA ATCGGTAAAT ACCACCCGCA CGGCGACTCC 200  
GCGGTATACG ACACCATCGT GCGTATGGCG CAGCCGTTCT CGCTGCGTTA 250  
CATGCTGGTG GACGGCCAGG GTAACTTTGG TTCCATCGAC GGCGACTCCG 300  
CCGCGGCGAT GCGTTATACC GAAATTCGTC TGGCGAAAAT CGCTCATGAG 350  
40 CTGATGGCCG ATCTT 365

45

2) INFORMATION FOR SEQ ID NO: 1766

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 344 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*  
 (B) STRAIN: ATCC 33531

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766

```

AAGAGCTCGT ATCTGGATTA TGCGATGTCG GTCATTGTTG GCCGTGCGCT      50
GCCGGATGTC CGAGATGGCC TGAAACCGGT ACACCGTCGC GTACTTTACG      100
CCATGAACGT ATTGGGCAAT GACTGGAACA AAGCCTATAA AAAATCCGCC      150
10 CGTGTTCGTTG GTGACGTAAT CGGTAAATAC CACCCTCATG GTGATACCGC      200
CGTTTATGAC ACCATTGTAC GTATGGCACA GCCATTCTCC TTGCGTTATA      250
TGCTGGTCGA TGGCCAGGGT AACTTCGGTT CTGTCGATGG CGACTCCGCC      300
GCAGCGATGC GTTATACGGA AATCCGTATG TCGAAAATCG CCCA          344

```

15

## 2) INFORMATION FOR SEQ ID NO: 1767

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 345 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*  
 (B) STRAIN: ATCC 27336

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767

```

AACTCTTATC TGGATTATGC GATGTCGGTC ATTGTTGGCC GTGCGCTGCC      50
GGATGTCCGA GATGGCCTGA AGCCGGTACA CCGTCGCGTA CTTTACGCCA      100
35 TGAACGTATT GGGCAATGAC TGGAACAAAG CCTATAAAAA ATCAGCCCGT      150
GTCGTTGGTG ACGTAATCGG TAAATACCAC CCGCACGGCG ACTCCGCGGT      200
ATACGACACC ATCGTGCGTA TGGCGCAGCC GTTCTCGCTG CGTTACATGC      250
TGGTGGACGG CCAGGGTAAC TTTGGTTCCA TCGACGGCGA CTCCGCCGCG      300
CGGATGCGTT ATACCGAAAT TCGTCTGGCG AAAATCGCTC ATGAG          345

```

40

## 2) INFORMATION FOR SEQ ID NO: 1768

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 356 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*  
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768

```

5  CTTATCTGGA TTATGCGATG TCGGTCATTG TTGGCCGTGC GCTGCCGGAT      50
   GTCCGAGATG GCCTGAAGCC GGTACACCGT CGCGTACTTT ACGCCATGAA      100
   CGTATTGGGC AATGACTGGA ACAAAGCCTA TAAAAAATCA GCCCGTGTCTG      150
   TTGGTGACGT AATCGGTAAA TACCACCCGC ACGGCGACTC CGCGGTATAC      200
10  GACACCATCG TGC GTATGGC GCAGCCGTTT TCGCTGCGTT ACATGCTGGT      250
   GGACGGCCAG GGTAACCTTG GTTCCATCGA CGGCGACTCC GCCGCGGCCGA      300
   TGC GTTATAC CGAAATTCGT CTGGCGAAAA TCGCTCATGA GCTGATGGCC      350
   GATCTT                                     356
  
```

15

2) INFORMATION FOR SEQ ID NO: 1769

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 361 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear
  
```

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

     (A) ORGANISM: Klebsiella pneumoniae subsp. pneumoniae
     (B) STRAIN: ATCC 29011
  
```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769

```

   TAAGAACTCT TATCTGGATT ATGCGATGTC GGTCATTGTT GGCCGTGCGC      50
   TGCCGGATGT CCGAGATGGC CTGAAGCCGG TACACCGTCG CGTACTTTAC      100
35  GCCATGAACG TATTGGGCAA TGA CTGGAAC AAAGCCTATA AAAAATCAGC      150
   CCGTGTCGTT GGTGACGTAA TCGGTAAATA CCACCCGCAC GGCGACTCCG      200
   CGGTATACGA CACCATCGTG CGTATGGCGC AGCCGTTCTC GCTGCGTTAC      250
   ATGCTGGTGG ACGGCCAGGG TAACTTTGGT TCCATCGACG GCGACTCCGC      300
   CGCGGCGATG CGTTATACCG AAATTCGTCT GCGGAAAATC GCTCATGAGC      350
40  TGATGGCCGA T                                     361
  
```

2) INFORMATION FOR SEQ ID NO: 1770

45

(i) SEQUENCE CHARACTERISTICS:

```

     (A) LENGTH: 365 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
50  (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *rhinoscleromatis*

(B) STRAIN: ATCC 13824

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | TAAGAACTCT | TATCTGGATT | ATGCGATGTC | GGTCATTGTT | GGCCGTGCGC | 50  |
|    | TGCCGGATGT | CCGAGATGGC | CTGAAGCCGG | TACACCGTCG | CGTACTTTAC | 100 |
| 10 | GCCATGAACG | TATTGGGCAA | TGACTGGAAC | AAAGCCTATA | AAAAATCAGC | 150 |
|    | CCGTGTCGTT | GGTGACGTAA | TCGGTAAATA | CCACCCGCAC | GGCGACTCCG | 200 |
|    | CGGTATACGA | CACCATCGTG | CGTATGGCGC | AGCCGTTCTC | GCTGCGTTAC | 250 |
|    | ATGCTGGTGG | ACGGCCAGGG | TAACCTTGGT | TCCATCGACG | GCGATTCCGC | 300 |
|    | CGCGGCGATG | CGTTATACCG | AAATTCGTCT | GGCGAAAATC | GCTCATGAGC | 350 |
| 15 | TGATGGCCGA | TCTTG      |            |            |            | 365 |

## 2) INFORMATION FOR SEQ ID NO: 1771

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25

(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Klebsiella terrigena*

(B) STRAIN: ATCC 33257

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 35 | TCGTATCTGG | ATTATGCGAT | GTCGGTCATT | GTTGGCCGTG | CGCTGCCGGA | 50  |
|    | TGTCCGAGAT | GGGTGAAAC  | CGGTACACCG | TCGCGTACTT | TACGCCATGA | 100 |
|    | ACGTATTGGG | CAATGACTGG | AACAAAGCCT | ATAAAAAATC | CGCCCGTGTC | 150 |
|    | GTTGGTGACG | TAATCGGTAA | ATATCACCT  | CACGGTGATA | CGCCCGTTTA | 200 |
|    | TGACACCATT | GTACGTATGG | CGCAGCCATT | CTCCTTGCGT | TATATGCTGG | 250 |
| 40 | TCGATGGCCA | GGGTAACTTC | GGTTCTGTCT | ATGGCGACTC | CGCCGCAGCG | 300 |
|    | ATGCGTTATA | CGGAAATCCG | TATGTCGAAA | ATCGCCACG  | AGCTGATGGC | 350 |
|    | CGACCTC    |            |            |            |            | 357 |

45

## 2) INFORMATION FOR SEQ ID NO: 1772

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 968 bases

50

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*  
(B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772

```

10 CAGTACACAG GCGAGTTCTT TTTGCGATGA GTGAGTTAAG TAATGATTGG      50
   AATAAGCCGT ATAAAAAATC TGCTCGTGTA GTAGGGGATG TCATTGGTAA      100
   ATATCATCCT CATGGGGATA CAGCTGTTTA TGACACTATT GTTCGTATGG      150
   CTCAGCCCTT TTCCATGCGT TATATGCTGA TTGATGGGCA GGGTAATTTT      200
   GGCTCTGTAG ATGGAGATGC TCCAGCTGCC ATGCGTTACA CTGAAGTAAG      250
   AATGTCCAAA GTGGCGCATG CTTTACTGGC TGATTTGGAT AAGGAAACCG      300
15 TTGATTTTAG TCCTAACTAT GATGAAACAG AATTTGCTCC AGTGGTATTG      350
   CCATCGAGAA TTCCCAATTT ACTAGTTAAT GGCTCTTCCG GTATTGCGGT      400
   AGGGATGGCT ACTAATATTC CACCACATAA TCTTACCGAA GTAATCAATG      450
   CATGTATTGC TTTAGTGGAT GAACCTGACA CGAGTCTTGA AGATTTAATG      500
   GAAATTATTC CTGGCCCTGA TTTTCCTACA GCCGCAATTA TTAATGGTCG      550
20 TGCTGGAATT ATTGAAGGTT ATCGTACTGG AAAAGGGCGG GTTGTTATCA      600
   GGGCACGCAC AGAAATTGAA ACGGATGAAA GTTCAGGCCG TCAGTCAATT      650
   ATTATTCAGG AATTACCCTA TCAGGTGAAT AAAGCGCGTT TGATCGAGCG      700
   TATTGCTGAA TTGGTAAGGG ACAAGAAAAT CGAAGGAATT TCCGGCTTGA      750
   GAGATGAGTC AGACAAGCAA GGAATGAGAG TAGTCATTGA ATTAAAACGC      800
25 AATGAAGTAG CAGATGTGGT ATTGAATAAC CTGTTGCTC ATACTCAAAT      850
   GCAAAATGTA TTCGGAATTA ATATGGTTGC TCTGGTGGAT GGCCAACCGC      900
   GTACTTTGAA TTTGAAGCAA ATACTGGAAT ATTTTATAAA ACATCGAAGA      950
   GAGGTTGTTA CCAGACGC                                     968

```

30

2) INFORMATION FOR SEQ ID NO: 1773

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 967 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*  
45 (B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773

```

50 CACCGCCGAG TGCTATTTGC GATGAATGTA CTGGGAAACG ATTGGAATAA      50
   ACCTTATAAA AAATCAGCCC GTGTTGTTGG GGATGTAATC GGTAATATC      100
   ACCCGCACGG TGACAGTGCT GTCTATGAAA CGATTGTTTCG TTTAGCACAG      150
   CCTTTTTCTA TGCGCTACAT GTTGGTTGAC GGTCAGGGTA ACTTCGGGTC      200
   AGTTGATGGT GACTCCGCGG CGGCTATGCG TTATACCGAA GTTCGTATGG      250
   CGAAGATCGC CCATGAACTG CTGGCGGATT TGGAAAAAGA GACGGTCGAC      300

```

|    |             |             |            |            |            |     |
|----|-------------|-------------|------------|------------|------------|-----|
|    | TTTGTTTCCTA | ACTATGATGG  | AACAGAAAAT | ATACCGGCTG | TTATGCCAAC | 350 |
|    | CCGTATTCCA  | AACTTGTTAG  | TTAATGGCTC | TTCAGGTATT | GCCGTTGGGA | 400 |
|    | TGGCAACGAA  | TATCCCTCCG  | CATAACCTCG | GTGAAGTTAT | CGACGGTTGT | 450 |
|    | CTTGCCATATG | TTGATAATGA  | AGACATCACC | ATAGAAGAAT | TAATGGAATA | 500 |
| 5  | TATTACCGGG  | CCTGATTTTC  | CGACTGCTGC | GATTATTAAT | GGTCGCAGAG | 550 |
|    | GAATATTAGA  | TGCTTATCGT  | ACAGGGCGTG | GAAAGATTTA | TATCCGTGCT | 600 |
|    | CAGGCTGATA  | TTGAAACTGA  | TGAGAAAACA | GGTCGCGAAA | CCATTATCGT | 650 |
|    | GACAGAAATT  | CCTTATCAGG  | TGAATAAAGC | CCGTTTAATT | GAAAAAATTG | 700 |
|    | CGGAGCTTGT  | AAAAGATAAA  | CGTATTGAAG | GTATCAGCGG | ATTACGTGAC | 750 |
| 10 | GAGTCTGATA  | AAGACGGTAT  | GCGTATTGTT | GTTGAGATCA | AACGTGATGC | 800 |
|    | AGTCGGTGAA  | GTAAGTATTAA | ATCACCTCTT | TTCACAAACT | CAAATGCAAG | 850 |
|    | TCTCTTTTGG  | TATTAATATG  | GTTGCGCTTC | ATCAAGGCCA | ACCAAATTA  | 900 |
|    | TTGAACCTAA  | AAGAAATTAT  | CGCAGCCTTT | ATTGCGCATC | GTCGTGAAGT | 950 |
|    | GGTGACTCGC  | CGTACCA     |            |            |            | 967 |

## 2) INFORMATION FOR SEQ ID NO: 1774

## 20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*  
 (B) STRAIN: ATCC 9250

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CCAGTACACC | GCAGAGTATT | GTATGCGATG | AATGTATTGG | GAAATGATTG | 50  |
| 35 | GAATAAACCC | TATAAAAAAT | CTGCCCCTAT | TGTTGGGGAC | GTCATCGGTA | 100 |
|    | AATACCATCC | ACATGGTGAT | AGCGCTGTTT | ACGAGACAA  | CGTTCGTCTT | 150 |
|    | GCTCAGCCTT | TCTCAATGCG | TTACATGCTG | GTTGATGGTC | AGGGAAACTT | 200 |
|    | CGGTTCTGTT | GACGGAGACT | CCGCAGCGGC | AATGCGTTAT | ACGGAAATCC | 250 |
|    | GTATGGCGAA | AATTGCCCAT | GAACACTTGT | CTGACCTTGA | AAAAGAAACC | 300 |
| 40 | GTTGATTTCG | TTCTAACTA  | TGACGGAACA | GAGCACATTC | CTGAAGTTAT | 350 |
|    | GCCAACGAAA | ATCCCAAACC | TTTTGGTTAA | TGGGTCGTCA | GGTATTGCTG | 400 |
|    | TTGGGATGGC | AACCAATATC | CCACCTCACA | ATTTAGGGGA | GGTGATTAAT | 450 |
|    | GGTTGTCTTG | CCTATATAGA | AGACGAAGAC | ATCAGCATTG | ATGGTTTAAT | 500 |
|    | GGAACACATT | CCAGGGCCTG | ATTTCCCAAC | CGCAGCTATT | ATTAATGGCC | 550 |
| 45 | GTCGTGGGAT | TATTGATGCG | TATCGCACAG | GGCGTGGCAA | GGTCTATATC | 600 |
|    | CGTGCAAGCG | CTGAAGTGGA | AGTCGATGAG | AAAAATGGTC | GCGAAACCAT | 650 |
|    | TATTGTCAGC | GAAATTCCTT | ATCAAGTGAA | TAAAGCTCGC | TTGATTGAAA | 700 |
|    | AAATTGCTGA | GTTAGTTAAA | GACAAGCGTG | TTGAAGGTAT | CAGTGCACTG | 750 |
|    | CGTGACGAGT | CTGATAAAGA | CGGTATGCGT | ATTGTTATTG | AAATCAAACG | 800 |
| 50 | CGATGCGGGT | GGTGAAGTTG | TACTGAACAA | CTTATATTCC | CTGACCCAAT | 850 |
|    | TGCAAGTTTC | TTTTGGTATC | AATATGGTAG | CTCTACACCA | AGGGCAGCCG | 900 |
|    | AAAATACTGA | ATTTAAAAGA | TATCATTGCT | GCTTTTGTGC | GTCACCGCCG | 950 |
|    | TGAAGTCGTC | ACTCGTCGTA | CGATTTTC   |            |            | 978 |

## 2) INFORMATION FOR SEQ ID NO: 1775

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 978 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*  
 (B) STRAIN: ATCC 13315

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775

15 CCAGTACACC GTCGCGTTCT TTTCGCGATG AATGTATTAG GAAACGATTG 50  
 GAATAAACCT TATAAAAAAT CAGCCCGTGT TGTTGGGGAT GTTATCGGTA 100  
 AATATCACCC GCACGGTGAC AGTGCTGTTT ATGAAACGAT AGTTCGTTTA 150  
 20 GCACAGCCTT TTTCTATGCG TTACATGTTG GTTGACGGGC AGGGTAACTT 200  
 CGGGTCAGTT GATGGTGACT CGGCGGCTGC AATGCGTTAT ACCGAAGTTC 250  
 GTATGGCGAA AATCGCCCAT GAACTGCTGG CGGATTTGGA AAAAGAAACG 300  
 GTTGATTTTG TTCCTAACTA TGATGGAACA GAGCATATCC CGGCAGTCAT 350  
 GCCAACCCGT ATTCCAAACT TATTAGTCAA TGGTTCTTCA GGTATCGCAG 400  
 25 TCGGGATGGC AACAAACATT CCTCCGCATA ACCTAGGTGA AGTTATCGAC 450  
 GGCTGTCTTG CTTATGTTGA TAACGAAGAC ATCACTATTG AAGAGTTGAT 500  
 GGAGCATATC ACGGGGCCTG ATTTCCCAAC TGCCGCTATT ATTAATGGCC 550  
 GCAGAGGAAT TTTAGATGCT TACCGTACTG GGC GCGGAAA AATTTATATT 600  
 CGTGACACAAG CTGATGTAGA AACCGATGAG AAAACTGGTC GCGAAACAAT 650  
 30 TATCGTGACG GAAATTCCTT ATCAGGTGAA CAAAGCTCGC TTAATTGAAA 700  
 AAATTGCAGA GCTTGTTAAA GATAAACGTA TTGAAGGCAT TAGCGGATTA 750  
 CGTGATGAGT CAGATAAAGA TGGTATGCGC ATTGTTGTTG AAATTAAGCG 800  
 TGATGCTGTT GGTGAAGTTG TACTAAATCA CTTATTTTCT CAGACTCAGA 850  
 TGCAGGTTTC TTTTGGTATT AACATGGTTG CACTGCATCA AGGTCAACCG 900  
 35 AAAGTGTTAA ACCTGAAAGA AATTATTTCA GCCTTTATTC GTCACCGTCG 950  
 TGAAGTGGTG ACTCGTCGTA CTATTTTT 978

## 40 2) INFORMATION FOR SEQ ID NO: 1776

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 940 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*  
 (B) STRAIN: ATCC 9610

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | TGGGTAATGA | CTGGAATAAG | CCATACAAAA | AATCGGCCCG | TGTAGTCGGG  | 50  |
|    | GACGTTATCG | GTAAATATCA | CCCGCATGGT | GACAGCGCGG | TCTACGACAC  | 100 |
| 5  | AATTGTGCGT | ATGGCCCAGC | CGTTCTCACT | GCGCTATATG | CTGGTGGATG  | 150 |
|    | GGCAGGGCAA | CTTCGGTTCC | GTTGATGGCG | ACTCCGCCGC | AGCGATGCGT  | 200 |
|    | TATACCGAAA | TCCGTATGTC | TAAAATTGCT | CACGAATTGT | TGGCGGACTT  | 250 |
|    | AGAAAAAGAT | ACCGTCGACT | TCGTGCCGAA | CTATGACGGT | ACGGAGCAAA  | 300 |
|    | TTCTTGCCGT | AATGCCAACC | CGAATCCCTA | ACTTGCTGGT | TAACGGCTCG  | 350 |
| 10 | TCAGGTATTG | CTGTCGGTAT | GGCAACCAAT | ATTCCGCCGC | ATAACCTTTC  | 400 |
|    | TGAGGTTATT | GATGGCTGTC | TGGCCTATAT | CGAAGATGAA | AACATCACCA  | 450 |
|    | TTGAAGGGTT | GATGGAGTAC | ATCCCGGGGC | CAGATTTCCT | AACTGCTGCG  | 500 |
|    | ATTATCAATG | GTCGCCGTGG | TATTGAAGAA | GCTTATCGTA | CTGGCCGTGG  | 550 |
|    | CAAGGTGTAT | ATCCGTGCCC | GTGCTGAAGT | TGAGGCTGAC | GCTTAAACCG  | 600 |
| 15 | GTCGCGAAAC | CATTATTGTT | CACGAGATCC | CGTATCAGGT | GAACAAGGCG  | 650 |
|    | CGGTTGATTG | AAAAAATCGC | CGAGCTGGTT | AAAGAAAAAC | GCGTAGAAGG  | 700 |
|    | CATCAGTGCG | TTGCGTGATG | AGTCTGATAA | AGACGGCATG | CGTATCGTGA  | 750 |
|    | TTGAAATCAA | ACGTGATGCT | GTCGGGGAAG | TGGTTCTGAA | CAACCTCTAT  | 800 |
|    | TCTCTGACGC | AATTGCAGGT | GACTTTCGGT | ATCAATATGG | TGGCTCTGTC  | 850 |
| 20 | TCAAGGGCAG | CCTAAGTTGC | TTAACCTGAA | AGACATTTTG | GTTGCTTTTCG | 900 |
|    | TGCGCCACCG | CCGTGAAGTG | GTGACTCGCC | GTACCATTTT |             | 940 |

## 25 2) INFORMATION FOR SEQ ID NO: 1777

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 bases  
 (B) TYPE: Nucleic acid  
 30 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*  
 (B) STRAIN: ATCC 13182

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 40 | CCGTTTATTG | GCGATGGCCT | GAAGCCGGTC | CAGCGTCGCA | TCGTCTATGC | 50  |
|    | GATGTCTGAA | CTGGGTCTGA | ACGCCAGCGC | GAAGTTCAAA | AAGTCCGCCC | 100 |
|    | GCACCGTCGG | TGACGTGCTG | GGTAAATACC | ATCCCCACGG | CGACAGCGCG | 150 |
|    | TGCTATGAAG | CCATGGTGCT | GATGGCTCAG | CCCTTCTCCT | ACCGCTATCC | 200 |
| 45 | GCTGGTTGAC | GGTCAGGGAA | ACTGGGGGGC | GCCGGACGAT | CCTAAATCCT | 250 |
|    | TCGCCGCAAT | GCGTTATACC | GAATCCCGTT | TGTCGAAGTA | TGCTGAACTG | 300 |
|    | CTGCTGAGCG | AACTGGGGCA | AGGCACCGTT | GACTGGGTAC | CAAACCTCGA | 350 |
|    | CGGCACTTTG | CAGGAGCCGA | AGATGCTGCC | TGCGCGCCTG | CCCAATATTC | 400 |
|    | TGCTAAACGG | TACTACCGGC | ATTGCCGTTG | GGATGGCGAC | GGACATTCCG | 450 |
| 50 | CCGCACAACC | TGCGTGAAGT | GGCCCGGGCG | GCCATTACCC | TGATTGAAAA | 500 |
|    | GCCGCAAAC  | TCGCTGGATG | ACCTGCTGGA | TATCGTGCAG | GGGCCGGATT | 550 |
|    | ATCCTACCGA | AGCGGAAATC | ATTACCCCCC | GTGCCGAAAT | CCGCAAAATC | 600 |
|    | TACCAGAATG | GCCGCGGTTT | GGTGCGGATG | CGCGCGGTAT | GGGCCAAAGA | 650 |



AGACGGCGCG GTGGTGAT

668

## 5 2) INFORMATION FOR SEQ ID NO: 1778

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 bases  
(B) TYPE: Nucleic acid  
10 (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*  
(B) STRAIN: ATCC 33496

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778

20  
GTTTATTGGC GATGGCCTGA AGCCGGTCCA GCGTCGCATC GTCTATGCGA 50  
TGTCTGAACT GGGTCTGAAC GCCAGCGCGA AGTTCAAAAA GTCCGCCCCG 100  
ACCGTCGGTG ACGTGCTGGG TAAATACCAT CCCCACGGCG ACAGCGCGTG 150  
CTATGAAGCC ATGGTGCTGA TGGCTCAGCC CTTCTCCTAC CGCTATCCGC 200  
25 TGGTTGACGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC TAAATCCTTC 250  
GCCGCAATGC GTTATACCGA ATCCCGTTTG TCGAAGTATG CTGAACTGCT 300  
GCTGAGCGAA CTGGGGCAAG GCACCGTTGA CTGGGTACCA AACTTCGACG 350  
GCACTTTGCA GGAGCCGAAG ATGCTGCCTG CGCGCCTGCC CAATATTCTG 400  
CTAAACGGTA CTACCGGCAT TGCCGTTGGG ATGGCGACGG ACATTCCGCC 450  
30 GCACAACCTG CGTGAAGTGG CCCGGGCGGC CATTACCCTG ATTGAAAAGC 500  
CGCAAACCTC GCTGGATGAC CTGCTGGATA TCGTGCAGGG GCCGGATTAT 550  
CCTACCGAAG CGGAAATCAT TACCCCCCGT GCCGAAATCC GCAAATCTA 600  
CCAGAATGGC CGCGGTTCGG TCGGATGCG CGCGGTATGG GCCAAAGAAG 650  
ACGGCGCGGT GGTGATTAGC GCGCTGCCGC ATCAGGTTTC CGGCGCCCCG 700  
35 GTGCTTGAGC AGAT 714

## 2) INFORMATION FOR SEQ ID NO: 1779

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
45 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*  
(B) STRAIN: ATCC 11296

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | TTGGCGATGG | CTTAAAACCG | GTCCAGCGTC | GCATCGTCTA | TGCGATGTCC | 50  |
|    | GAGCTGGGGC | TGAACGCCAG | CGCGAAATTC | AAAAAGTCCG | CCCGCACCGT | 100 |
|    | CGGCGACGTG | TTGGGTAAAT | ATCACCCGCA | CGGCGACAGC | GCCTGCTATG | 150 |
| 5  | AAGCGATGGT | GCTGATGGCG | CAGCCGTTCT | CTTACCGCTA | TCCGCTGGTG | 200 |
|    | GATGGTCAGG | GAAACTGGGG | GGCGCCGGAC | GATCCCAAAT | CTTTCGCCGC | 250 |
|    | CATGCGTTAC | ACCGAATCCC | GCCTGTCGAA | GTATGCCGAG | CTGCTGCTCA | 300 |
|    | GCGAGCTGGG | GCAGGGGACG | GTCGACTGGG | TGCCAAACTT | TGACGGTACG | 350 |
|    | CTGCAGGAGC | CGAAAATGCT | GCCAGCGCGT | TTGCCGAACA | TCCTGCTGAA | 400 |
| 10 | CGGCACCACC | GGCATCGCGG | TAGGTATGGC | GACCGATATT | CCTCCGCACA | 450 |
|    | ACCTGCGGGA | AGTGGCCAAA | GCGGCGATTA | CGCTGATTGA | GCAGCCGAAA | 500 |
|    | ACCACCCTCG | ACGAACTGCT | GGATATCGTA | CAGGGGCCGG | ATTTCCCGAC | 550 |
|    | CGAGGCGGAG | ATCATCACCT | CGCGGGCGGA | AATTCGAAAA | ATCTACCAGA | 600 |
|    | ACGGGCGCGG | CTCAGTGCGC | ATGCGCGCGG | TGTGGAGTAA | AGAGGACGGC | 650 |
| 15 | GCGGTGGTGA | TCAGCGCGCT | GCCGCATCAG | GTCTCCGGCG | CCAAAGTGCT | 700 |
|    | GGAGCAGATT | GCGGCGCAGA | TG         |            |            | 722 |

20 2) INFORMATION FOR SEQ ID NO: 1780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*  
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780

|    |             |            |            |            |             |     |
|----|-------------|------------|------------|------------|-------------|-----|
| 35 | GTCCAGCGTC  | GCATCGTTTA | TGCGATGTCT | GAGCTGGGGC | TGAACGCCAG  | 50  |
|    | CGCGAAGTTC  | AAAAAGTCCG | CCCGCACCGT | GGGTGATGTG | CTGGGTAAAT  | 100 |
|    | ATCACCCGCA  | CGGCGATAGC | GCATGCTATG | AAGCTATGGT | GCTGATGGCG  | 150 |
|    | CAGCCATTCT  | CCTACCGCTA | CCCGCTGGTG | GATGGGCAGG | GAACTGGGG   | 200 |
| 40 | GGCACCGGAC  | GATCCTAAAT | CCTTCGCCGC | GATGCGTTAT | ACCGAATCCC  | 250 |
|    | GTTTGTGCGAA | GTATGCGGAA | CTGCTGCTGG | GCGAACTGGG | GCAGGGAACC  | 300 |
|    | GTCGACTGGG  | TGCCGAACTT | CGACGGGACG | ATGCAGGAGC | CGAAAAATGCT | 350 |
|    | GCCTGCGCGT  | CTGCCGAATA | TTCTGCTGAA | CGGCACTACC | GGCATCGCCG  | 400 |
|    | TCGGTATGGC  | AACCGATATT | CCTCCGCACA | ACCTGCGTGA | AGTGGCGCAG  | 450 |
| 45 | GCGGCGATTA  | CCCTGATCGA | AAAACCGCAG | ACCTCGCTCG | ACGAACTGCT  | 500 |
|    | GGATATCGTT  | CACGGACCCG | ACTACCCGAC | CGAAGCCGAA | ATCATTACTC  | 550 |
|    | CACGCGCGGA  | GATCCGCAAA | ATCTACCAGA | ACGGCCGCGG | TTCGGTGC GG | 600 |
|    | ATGCGCGCGG  | TATGGAAAAA | AGAGGACGGC | GCGGTCGTGA | TTACGGCGTT  | 650 |
| 50 | GCCGCATCAG  | GTTTCCGGCG | CCCGCGTGCT | GGAGCAAATT | GC          | 692 |

2) INFORMATION FOR SEQ ID NO: 1781

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 700 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Klebsiella pneumoniae*  
 (B) STRAIN: ATCC 27336

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781

15 GTTTATTGGC GATGGCTTAA AACCGGTCCA GCGTCGCATC GTCTATGCGA 50  
 TGTCCGAGCT GGGGCTGAAC GCCAGCGCGA AATTCAAAAA GTCCGCCCCG 100  
 ACCGTCGGCG ACGTGTTGGG TAAATATCAC CCGCACGGCG ACAGCGCCTG 150  
 CTATGAAGCG ATGGTGCTGA TGGCGCAGCC GTTCTCTTAC CGCTATCCGC 200  
 20 TGGTGGATGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC CAAATCTTTC 250  
 GCCGCCATGC GTTACACCGA ATCCCGCCTG TCGAAGTATG CCGAGCTGCT 300  
 GCTCAGCGAG CTGGGGCAGG GGACGGTCGA CTGGGTGCCA AACTTTGACG 350  
 GCACGCTGCA GGAGCCGAAA ATGCTGCCAG CGCGTTTGCC GAACATCCTG 400  
 CTGAACGGCA CCACCGGCAT CGCGGTAGGC ATGGCGACCG ATATTCCTCC 450  
 25 GCACAACCTG CGGGAAGTGG CCAAAGCGGC GATTACGCTG ATTGAGCAGC 500  
 CGAAAACAC CCTCGACGAA CTGCTGGATA TCGTACAGGG GCCGGATTTC 550  
 CCGACCGAGG CGGAGATCAT CACCTCGCGG GCGGAAATTC GCAAAATCTA 600  
 CCAAAACGGG CGCGGCTCAG TCGCATGCG CGCGGTGTGG AGTAAAGAGG 650  
 ACGGCGCGGT GGTGATCAGC GCGTGCCGC ATCAGGTCTC CGGCGCCAAA 700  
 30

## 2) INFORMATION FOR SEQ ID NO: 1782

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 726 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*  
 45 (B) STRAIN: ATCC 13883

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782

50 ATTGGCGATG GCTTAAACCG GGTCCAGCGT CGCATCGTCT ATGCGATGTC 50  
 CGAGCTGGGG CTGAACGCCA GCGCGAAATT CAAAAAGTCC GCCCGCACCG 100  
 TCGGCGACGT GTTGGGTAAA TATCACCCGC ACGGCGACAG CGCCTGCTAT 150  
 GAAGCGATGG TGCTGATGGC GCAGCCGTTC TCTTACCGCT ATCCGCTGGT 200  
 GGATGGTCAG GGAAACTGGG GGGCGCCGGA CGATCCCAAA TCTTTCGCCG 250

|    |            |            |             |            |            |     |
|----|------------|------------|-------------|------------|------------|-----|
|    | CCATGCGTTA | CACCGAATCC | CGCCTGTCTGA | AGTATGCCGA | GCTGCTGCTC | 300 |
|    | AGCGAGCTGG | GGCAGGGGAC | GGTCGACTGG  | GTGCCAAACT | TTGACGGCAC | 350 |
|    | GCTGCAGGAG | CCGAAAATGC | TGCCAGCGCG  | TCTGCCGAAC | ATCCTGCTGA | 400 |
|    | ACGGCACCAC | CGGCATCGCG | GTAGGCATGG  | CGACCGATAT | TCCTCCGCAC | 450 |
| 5  | AACCTGCGGG | AAGTGGCCAA | AGCGGCGATT  | ACGCTGATTG | AGCAGCCGAA | 500 |
|    | AACCACCCTC | GACGAACTGC | TGGATATCGT  | ACAGGGGCCG | GATTTCCCGA | 550 |
|    | CCGAGGCGGA | GATCATCACC | TCGCGGGCGG  | AAATTCGCAA | AATCTACCAG | 600 |
|    | AACGGGCGCG | GCTCAGTGCG | CATGCGCGCG  | GTGTGGAGTA | AAGAGGACGG | 650 |
|    | CGCGGTGGTG | ATCAGTGCGC | TGCCGCATCA  | GGTCTCTGGC | GCCAAAGTGC | 700 |
| 10 | TGGAGCAGAT | TGCGGCGCAG | ATGCGC      |            |            | 726 |

## 2) INFORMATION FOR SEQ ID NO: 1783

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*  
 (B) STRAIN: ATCC 29011

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 30 | GGCTTAAAAC | CGGTCCAGCG | TCGCATCGTC | TATGCGATGT | CCGAGCTGGG | 50  |
|    | GCTGAACGCC | AGCGCGAAAT | TCAAAAAGTC | CGCCCGCACC | GTCGGCGACG | 100 |
|    | TGTTGGGTAA | ATATCACCCG | CACGGCGACA | GCGCCTGCTA | TGAAGCGATG | 150 |
|    | GTGCTGATGG | CGCAGCCGTT | CTCTTACCGC | TATCCGCTGG | TGGATGGTCA | 200 |
|    | GGGAAACTGG | GGGGCGCCGG | ACGATCCCAA | ATCTTTTGCC | GCCATGCGTT | 250 |
| 35 | ACACCGAATC | CCGCCTGTCT | AAGTATGCCG | AGCTGCTGCT | CAGCGAGCTG | 300 |
|    | GGGCAGGGGA | CGGTCGACTG | GGTGCCAAAC | TTTGACGGCA | CGCTGCAGGA | 350 |
|    | GCCGAAAATG | CTGCCAGCGC | GTCTGCCGAA | CATCCTGCTG | AACGGCACCA | 400 |
|    | CCGGCATCGC | GGTAGGCATG | GCGACCGATA | TTCTCCGCA  | CAACCTGCGG | 450 |
|    | GAAGTGGCCA | AAGCGGCGAT | TACGCTGATT | GAGCAGCCGA | AAACCACCCT | 500 |
| 40 | CGACGAACTG | CTGGATATCG | TACAGGGGCC | GGATTTCCCG | ACCGAGGCGG | 550 |
|    | AGATCATCAC | CTCGCGGGCG | GAAATTCGCA | AAATCTACCA | GAACGGGCGC | 600 |
|    | GGCTCAGTGC | GATGCGCGC  | GGTGTGGAGT | AAAGAGGACG | GCGCGGTGGT | 650 |
|    | GATCAGTGCG | CTGCCGCATC | AGGTCTCCGG | CGCCAAAGTG | CTGGAGCAGA | 700 |
|    | TTGCGG     |            |            |            |            | 706 |

45

## 2) INFORMATION FOR SEQ ID NO: 1784

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.  
*rhinoscleromatis*

(B) STRAIN: ATCC 13884

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | TTGGCGATGG | CTTAAAACCG | GTCCAGCGTC | GCATCGTCTA | TGCGATGTCC  | 50  |
|    | GAGCTGGGGC | TGAACGCCAG | CGCGAAATTC | AAAAAGTCCG | CCCGCACCGT  | 100 |
|    | CGGCGACGTG | TTGGGTAAAT | ATCACCCGCA | CGGCGACAGC | GCCTGCTATG  | 150 |
| 15 | AAGCGATGGT | GCTGATGGCG | CAGCCGTTCT | CTTACCGCTA | TCCGCTGGTG  | 200 |
|    | GATGGTCAGG | GAAACTGGGG | GGCGCCGGAC | GATCCCAAAT | CTTTCGCCGC  | 250 |
|    | CATGCGTTAC | ACCGAATCCC | GCCTGTGCGA | GTATGCCGAG | CTGCTGCTCA  | 300 |
|    | GCGAGCTGGG | GCAGGGGACG | GTCGACTGGG | TGCCAAACTT | TGACGGGCACG | 350 |
|    | CTGCAGGAGC | CGAAAATGCT | GCCAGCGCGT | CTGCCGAACA | TCCTGCTGAA  | 400 |
| 20 | CGGCACCACC | GGCATCGCGG | TAGGCATGGC | GACCGATATT | CCTCCGCACA  | 450 |
|    | ACCTGCGGGA | AGTGGCCAAA | GCGGCGATTA | CGCTGATTGA | GCAGCCGAAA  | 500 |
|    | ACCACCCTCG | ACGAACTGCT | GGATATCGTA | CAGGGGCCGG | ATTTCCCGAC  | 550 |
|    | CGAGGCGGAG | ATCATCACCT | CGCGGGCGGA | AATTCGCAA  | ATCTACCAGA  | 600 |
|    | ACGGGCGCGG | CTCA       |            |            |             | 614 |

25

## 2) INFORMATION FOR SEQ ID NO: 1785

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella terrigena*

40 (B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GCCTGAAACC | GGTCCAGCGG | CGCATCGTTT | ATGCGATGTC | CGAACTGGGT | 50  |
| 45 | CTGAACGCCA | CCGCTAAATT | CAAAAAATCC | GCGCGCACCG | TCGGCGACGT | 100 |
|    | GCTGGGTAAA | TATACCCGC  | ACGGCGATAG | CGCCTGCTAT | GAGGCGATGG | 150 |
|    | TGCTGATGGC | GCAGCCGTTT | TCTTACCGCT | ACCCGCTGGT | GGACGGTCAG | 200 |
|    | GGCAACTGGG | GCGCCCCGGA | CGATCCCAA  | TCCTTCGCCG | CGATGCGTTA | 250 |
|    | TACCGAATCC | CGCCTGTCAA | AGTATGCGGA | GCTGCTGCTG | GGCGAGCTGG | 300 |
| 50 | GTCAGGGAAC | CGTTGACTGG | GTACCTAACT | TTGACGGTAC | GATGCAGGAG | 350 |
|    | CCGAAAATGC | TGCCTGCGCG | TTTGCCGAAT | ATTCTGCTCA | ACGGCACCAC | 400 |
|    | CGGTATCGCC | GTGGGGATGG | CCACCGATAT | TCCGCCGCAC | AACCTGCGCG | 450 |
|    | AAGTGCCCAA | AGCGGCCATC | ACCCTGATTG | AAAAGCCGCA | GACCTCGCTC | 500 |

|             |            |            |            |            |     |
|-------------|------------|------------|------------|------------|-----|
| GACGAACTGC  | TGGATATCGT | TCACGGGCCG | GACTACCCCA | CCGAAGCTGA | 550 |
| AATCATCACC  | CCGCGCGCCG | AGATCCGCAA | AATCTATCAG | AACGGTCGCG | 600 |
| GCTCGGTTTCG | CATGCGTGCG | GTGTGGAAAA | AAGAGGACGG | CGCGGTGGTG | 650 |
| ATTAGCGCCC  | TGCCGCAT   |            |            |            | 668 |

5

## 2) INFORMATION FOR SEQ ID NO: 1786

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacillus cereus*
  - (B) STRAIN: ATCC 7064
- 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CATTACGTTC | TAACACTCAA | GGACGCGGAA | CATTCTCTAT | GGTGTTTGAC | 50  |
| CACTATGAAG | AAGTACCAA  | GTCTGTTTCT | GAAGAAATTA | TCAAAAAAAA | 100 |
| TAAAGGTGAA | TAA        |            |            |            | 113 |

## 30 2) INFORMATION FOR SEQ ID NO: 1787

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacillus cereus*
  - (B) STRAIN: ATCC 14579
- 40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| AACGTCATTA | CGTTCTAACA | CTCAAGGACG | CGGAACATTC | TCTATGGTGT | 50  |
| TTGACCACTA | TGAAGAAGTA | CCAAAGTCTG | TTTCTGAAGA | AATTATCAAA | 100 |
| AAAAATAAAG | GTGAATAA   |            |            |            | 118 |

50

## 2) INFORMATION FOR SEQ ID NO: 1788

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*  
(B) STRAIN: CIP 9444

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788

15 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50  
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100  
AAAAAATAA AGGTGAATAA 120

20

## 2) INFORMATION FOR SEQ ID NO: 1789

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*  
(B) STRAIN: ATCC 13472

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789

AACGTCATTA CGTTCTAACA CTCAAGGACG CGGAACATTC TCTATGGTGT 50  
TTGACCACTA TGAAGAAGTA CCAAAGTCTG TTTCTGAAGA AATTATCAAA 100  
AAAAATAAAG GTGAATAA 118

40

## 2) INFORMATION FOR SEQ ID NO: 1790

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*  
(B) STRAIN: ATCC 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790

5 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50  
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100  
AAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1791

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 120 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*  
(B) STRAIN: NRRL B-617

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791

GCAACGTCAT TACGTTCTAA CACGCAAGGA CGCGGAACAT TCTCAATGAC 50  
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATCA 100  
30 AAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1792

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Bacillus cereus*  
(B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792

50 CGTCATTACG TTCTAACACT CAAGGACGCG GAACATTCTC TATGGTGTTT 50  
GACCACTATG AAGAAGTACC AAAGTCTGTT TCTGAAGAAA TTATCAAAAA 100  
AAATAAAGGT GAATAA 116



## 2) INFORMATION FOR SEQ ID NO: 1793

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 9440

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GCAACGTCAT | TACGTTCTAA | CACTCAAGGA | CGCGGAACAT | TCTCTATGGT | 50  |
| GTTTGACCAC | TATGAAGAAG | TACCAAAGTC | TGTTTCTGAA | GAAATTATCA | 100 |
| AAAAAATAA  | AGGTGAATAA |            |            |            | 120 |

## 2) INFORMATION FOR SEQ ID NO: 1794

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CACTCAAGGA | CGCGGAACAT | TCTCTATGGT | GTTTGATCAC | TATGAAGAAG | 50  |
| TACCAAAGTC | TGTTTCTGAA | GAAATTATCA | AAAAAATAA  | AGGTGAATAA | 100 |

## 2) INFORMATION FOR SEQ ID NO: 1795

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Bacillus weihenstephanensis*  
(B) STRAIN: WSBC 10204

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795

GCAACGGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50  
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCTGAA GAAATTATTA 100  
AAAAAAATAA AGGTGAATAA 120

## 2) INFORMATION FOR SEQ ID NO: 1796

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear  
20 (ii) MOLECULE TYPE: Genomic DNA  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Bacillus mycoides*  
25 (B) STRAIN: ATCC 6462

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796

GCGACAGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50  
30 ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATTA 100  
AAAAAAATAA AGGCGAATAA 120

## 35 2) INFORMATION FOR SEQ ID NO: 1797

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 bases  
(B) TYPE: Nucleic acid  
40 (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: Genomic DNA  
(vi) ORIGINAL SOURCE:  
45 (A) ORGANISM: *Bacillus thuringiensis*  
(B) STRAIN: ATCC 10792

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797

50 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50  
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100  
AAAAAAATAA AGGTGAATAA 120

## 2) INFORMATION FOR SEQ ID NO: 1798

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*  
(B) STRAIN: WSBC 10204

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGAGACGCAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCCATATAAA 100  
CTAAGGAGGA ATTTAGA 117

## 2) INFORMATION FOR SEQ ID NO: 1799

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*  
(B) STRAIN: ATCC 10792

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100  
CTAAGGAGGA ATTTAGA 117

## 2) INFORMATION FOR SEQ ID NO: 1800

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Bacillus anthracis*  
(B) STRAIN: ATCC 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100  
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1801

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycooides*  
(B) STRAIN: NRRL B-617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGGGACTTAA GTTTCACCTTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100  
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1802

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*  
(B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100

CTAAGGAGGA ATTTAGA

117

## 5 2) INFORMATION FOR SEQ ID NO: 1803

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*  
(B) STRAIN: ATCC 7064

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803

20 TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGAGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100  
CTAAGGAGGA ATTTAGA 117

25

## 2) INFORMATION FOR SEQ ID NO: 1804

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## 35 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM *Bacillus cereus*  
(B) STRAIN: ATCC 49064

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGGGACGCAA GTTTCACCTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100  
45 CTAAGGAGGA ATTTAGA 117

50

## 2) INFORMATION FOR SEQ ID NO: 1805

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus anthracis*  
(B) STRAIN: CIP 9440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 10 | ATGGCTAAAG | CTAAATTCGA | ACGTTCTAAA | CCCCATGTTA | ACATCGGTAC | 50  |
|    | AATCGGCCAC | GTTGACCATG | GTAAAACTAC | ATTAAGTCTG | GCGATCACTA | 100 |
|    | CAGTACTTGC | AAAAGCTGGT | GGTGCTGAAG | CACGCGGATA | CGATCAAATC | 150 |
|    | GATGCTGCTC | CAGAAGAAAG | AGAGCGCGGT | ATCACAATCT | CAACTGCACA | 200 |
|    | CGTTGAGTAC | GAAACTGAAA | CTCGTCACTA | TGCACACGTT | GACTGCCCAG | 250 |
| 15 | GTCACGCTGA | CTATGT     |            |            |            | 266 |

2) INFORMATION FOR SEQ ID NO: 1815

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacillus cereus*  
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 35 | ATGGCTAAAG | CTAAATTCGA | ACGTTCTAAA | CCCCATGTTA | ACATCGGTAC | 50  |
|    | AATCGGCCAC | GTTGACCATG | GTAAAACTAC | ATTAAGTCTG | GCGATCACTA | 100 |
|    | CAGTACTTGC | AAAAGCTGGT | GGTGCTGAAG | CACGCGGATA | CGATCAAATC | 150 |
|    | GATGCTGCTC | CAGAAGAAAG | AGAGCGCGGT | ATCACAATCT | CAACTGCACA | 200 |
|    | CGTTGAGTAC | GAAACTGAAA | CTCGTCACTA | TGCACACGTT | GACTGCCCAG | 250 |
| 40 | GTCACGCTGA | CTATGTTAA  |            |            |            | 269 |

2) INFORMATION FOR SEQ ID NO: 1816

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
- (B) STRAIN: ATCC 6462

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805

|          |       |         |       |         |     |         |       |         |      |     |
|----------|-------|---------|-------|---------|-----|---------|-------|---------|------|-----|
| TTGATTTT | TA    | TCAATTG | TTC   | GAGTATA | ACT | ACTTATG | TAA   | GCTTAGA | AAAG | 50  |
| TGGGACG  | TAA   | GTTTCG  | CTTT  | CTAGTCT | AAA | TATAAA  | AATAA | CCTATAT | AAA  | 100 |
| CTAAGG   | GAGGA | ATT     | TTAGA |         |     |         |       |         |      | 117 |

15

2) INFORMATION FOR SEQ ID NO: 1806

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 14579

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806

|          |       |         |       |         |     |         |       |         |      |     |
|----------|-------|---------|-------|---------|-----|---------|-------|---------|------|-----|
| TTGATTTT | TA    | TCGATTG | TTC   | AAGTATA | ACT | ACTTATG | TAA   | GCTTAGA | AAAG | 50  |
| TGGGACG  | TAA   | GTTTCA  | CTTT  | CTAGTCT | AAA | TATAAA  | AATAA | CCTATAT | AAA  | 100 |
| CTAAGG   | GAGGA | ATT     | TTAGA |         |     |         |       |         |      | 117 |

35

40 2) INFORMATION FOR SEQ ID NO: 1807

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807

5 TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100  
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1808

10

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Bacillus cereus*  
(B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808

25 TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100  
CTAAGGAGGA ATTTAGA 117

30

2) INFORMATION FOR SEQ ID NO: 1809

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 117 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*  
(B) STRAIN: CIP 9440

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50  
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100  
CTAAGGAGGA ATTTAG 117

50

2) INFORMATION FOR SEQ ID NO: 1810



## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 278 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Bacillus mycoides*  
 (B) STRAIN: ATCC 6462

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810

15 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50  
 AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA 100  
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150  
 GACGCTGCTC CAGAAGAAAG AGAGCGCGGA ATCACAATCT CAACTGCACA 200  
 20 CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250  
 GTCACGCTGA CTATGTTAAA AACATGAT 278

## 25 2) INFORMATION FOR SEQ ID NO: 1811

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases  
 (B) TYPE: Nucleic acid  
 30 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Bacillus thuringiensis*  
 (B) STRAIN: ATCC 10792

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811

40 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50  
 AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA 100  
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150  
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200  
 45 CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250  
 GTCACGCTGA CTATGTTAAA AACATGAT 278

## 50 2) INFORMATION FOR SEQ ID NO: 1812

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| ATGGCTAAAG    | CTAAATTCGA | ACGTTCTAAA | CCCCATGTTA | ACATCGGTAC | 50  |
| AATCGGCCAC    | GTTGACCATG | GTAAACTAC  | ATTAAGTCT  | GCGATCACTA | 100 |
| 15 CAGTACTTGC | AAAAGCTGGT | GGTGCTGAAG | CACGCGGATA | CGATCAAATC | 150 |
| GATGCTGCTC    | CAGAAGAAAG | AGAGCGCGGT | ATCACAATCT | CAACTGCACA | 200 |
| CGTTGAGTAC    | GAAACTGAAA | CTCGTCACTA | TGCACACGTT | GACTGCCCAG | 250 |
| GTCACGCTGA    | CTATGTTAAA |            |            |            | 270 |

20

2) INFORMATION FOR SEQ ID NO: 1813

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
- (B) STRAIN: WSBC 10204

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| ATGGCTAAAG    | CTAAATTCGA | ACGTTCTAAA | CCCCATGTTA | ACATCGGTAC | 50  |
| AATCGGCCAC    | GTTGACCATG | GTAAACTAC  | ATTAAGTCT  | GCGATCACTA | 100 |
| 40 CAGTTCTTGC | AAAAGCTGGT | GGTGCTGAAG | CACGCGGATA | CGATCAAATC | 150 |
| GACGCTGCTC    | CAGAAGAAAG | AGAGCGCGGA | ATCACAATCT | CAACTGCACA | 200 |
| CGTTGAGTAC    | GAAACTGAAA | CTCGTCACTA | TGCACACGTT | GACTGCCCAG | 250 |
| GTCATGCTGA    | CTATGTTAAA | AACATGAT   |            |            | 278 |

45

2) INFORMATION FOR SEQ ID NO: 1814

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 266 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 13472

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50  
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCT GCGATCACTA 100  
CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150  
10 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200  
CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250  
GTCACGCTGA CTATGTTA 268

15

## 2) INFORMATION FOR SEQ ID NO: 1817

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 bases  
20 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50  
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCT GCGATCACTA 100  
CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150  
35 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200  
CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250  
GTCACGCTGA CTATGTAAA AACATGAT 278

40

## 2) INFORMATION FOR SEQ ID NO: 1818

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 bases  
45 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 14579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818

```

5  ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
   AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA      100
   CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
   GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
   CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG      250
   GTCACGCTGA CTATGTTA          268
10

```

## 2) INFORMATION FOR SEQ ID NO: 1819

```

15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 278 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Bacillus anthracis
25          (B) STRAIN: CIP 9444

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819

```

30 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
   AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA      100
   CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
   GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
   CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG      250
   GTCACGCTGA CTATGTTAAA AACATGAT          278
35

```

## 2) INFORMATION FOR SEQ ID NO: 1820

```

40  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 278 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
45
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Bacillus pseudomycoides
50          (B) STRAIN: NRRL B-617

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820

```

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCT GCGATCACTA      100
CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGACCAAATC      150
GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
5  CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
GTCACGCTGA CTATGTTAAA AACATGAT      278

```

10 2) INFORMATION FOR SEQ ID NO: 1821

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 263 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Bacillus cereus
    (B) STRAIN: ATCC 49064

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821

```

25 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCT GCGATCACTA      100
CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
30 CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
GTCACGCTGA CTA      263

```

35 2) INFORMATION FOR SEQ ID NO: 1822

(i) SEQUENCE CHARACTERISTICS:

```

40 (A) LENGTH: 1668 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Streptococcus oralis
    (B) STRAIN: ATCC 35037

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822

```

50 CAATCGAAGT ACAACGTTCT CTTGCGGTAT TGGACGGTGC GGTTACTGTT      50
CTTGACTCAC AATCAGGTGT TGAGCCTCAA ACTGAAACAG TTTGGCGTCA      100
AGCAACTGAG TACGGAGTTC CACGTATCGT ATTTGCTAAC AAAATGGACA      150

```

|    |            |            |            |            |             |      |
|----|------------|------------|------------|------------|-------------|------|
|    | AAATCGGTGC | TGACTTCCTT | TACTCAGTAA | GCACACTTCA | CGACCGTCTT  | 200  |
|    | CAAGCAAACG | CACACCCAAT | CCAATTGCCA | ATCGGTGCTG | AAGATGACTT  | 250  |
|    | CCGTGGTATC | ATCGACTTGA | TCAAGATGAA | AGCTGAAATC | TATACTAACG  | 300  |
|    | ACCTTGGTAC | AGATATCCTT | GAAGAAGATA | TTCCAGCTGA | ATACCTTGAC  | 350  |
| 5  | CAAGCTCAAG | AATACCGTGA | AAAATTGGTT | GAAGCAGTCG | CTGAAACTGA  | 400  |
|    | TGAAGACTTG | ATGATGAAAT | ACCTTGAAGG | TGAAGAAATC | ACTAACGAAG  | 450  |
|    | AATTGAAAGC | TGCTATCCGT | AAAGCAACTA | TCAACGTTGA | ATTCTTCCCA  | 500  |
|    | GTATTGTGTG | GTTCTGCCTT | CAAGAACAAG | GGTGTTCAAT | TGATGCTTGA  | 550  |
|    | TGCGGTTATC | GACTACCTTC | CAAGCCCACT | TGATATCCCA | GCGATCAAAG  | 600  |
| 10 | GTATCAACCC | AGATWCAGAT | GAAGAAGAAA | CTCGTCCAGC | ATCTGACGAA  | 650  |
|    | GAGCCATTTC | CAGCTCTTGC | CTTCAAGATC | ATGACGGACC | CATTTGTAGG  | 700  |
|    | TCGTTTGACA | TTCTTCCGTG | TATACTCARG | TGTTCTCCAA | TCARGKTCTT  | 750  |
|    | ACGTATTGAA | CACATCTAAA | GGTAAACGTG | AACGTATCGG | ACGTATCCTT  | 800  |
|    | CAAATGCACG | CTAACAGCCG | TCAAGAAATT | GACACTGTTT | ACTCAGGTGA  | 850  |
| 15 | TATCGCTGCT | GCCGTTGGTT | TGAAAGATAC | TYCAACTGGT | GACTCATTGM  | 900  |
|    | CAGATGAAAA | AGCTAAAATC | ATCCTTGAGT | CAATCAACGT | TCCAGAMCCA  | 950  |
|    | GTTATCCAAT | TGATGGTTGA | GCCAAAATCT | AAAGCTGACC | AAGATAAGAT  | 1000 |
|    | GGGTATCGCC | CTTCAAAAAT | TGGCTGAAGA | AGATCCAACA | TTCCGCGTTG  | 1050 |
|    | AAMCAAACGT | TGAAACTGGT | GAAMCAGTTA | TCTCAGGTAT | GGGTGAGCTT  | 1100 |
| 20 | CACTTGAGCG | TCCTTGTTGA | CCGTATGCGT | CGTGAGTTCA | AAGTGGAAGC  | 1150 |
|    | GAACGTAGGT | GCTCCTCAAG | TATCTTACCG | TGAAACATTC | CGCGCTTCTA  | 1200 |
|    | CTCAAGCACG | TGGATTCTTC | AAACGTCAGT | CTGGTGGTAA | AGGTCAATTC  | 1250 |
|    | GGTGATGTAT | GGATTGAATT | TACTCCAAAC | GAAGAAGGTA | AAGGATTCTGA | 1300 |
|    | ATTCGAAAAC | GCAATCGTCG | GTGGTGTGGT | TCCTCGTGAA | TTTATCCCAG  | 1350 |
| 25 | CGGTTGAAAA | AGGTTTGGTA | GAATCTATGG | CTAACGGTGT | TCTTGCAGGT  | 1400 |
|    | TACCCAATGG | TTGACGTTAA | AGCTAAGCTT | TACGATGGTT | CATACCACGA  | 1450 |
|    | TGTCGACTCA | TCTGAAACTG | CCTTCAAGAT | CGCGGCTTCA | CTTGCCCTTA  | 1500 |
|    | AAGAAGCTGC | TAAGTCAGCA | CAACCAGCTA | TCCTTGAGCC | AATGATGCTT  | 1550 |
|    | GTAACCATCA | CTGTTCCAGA | AGAAAACCTT | GGTGATGTTA | TGGGTCACGT  | 1600 |
| 30 | AACTGCTCGT | CGTGGACGTG | TAGATGGTAT | GGAAGCACWC | GGTAACAGCC  | 1650 |
|    | AAATCGTTTC | TGCTTACG   |            |            |             | 1668 |

## 35 2) INFORMATION FOR SEQ ID NO: 1823

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 115 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*  
(B) STRAIN: ATCC 35567

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 50 | AGACCTGCGT | TCACAAACAC | AGGGTCGTGC | TTCTTACTCT | ATGGAGTTCT | 50  |
|    | TGAAGTACAA | CGAAGCGCCA | AACAACGTTG | CTACAGCAAT | CATTGAAGCT | 100 |
|    | CGTAAGGCTA | GATAA      |            |            |            | 115 |

## 2) INFORMATION FOR SEQ ID NO: 1824

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Buttiauxella agrestis*  
(B) STRAIN: ATCC 33320

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824

CTGCGTTCAC TGACCAAGGT CGTGCACTTT ACTCCATGGA ATTCCTGAAG 50  
TATGATGACG CGCCAAACAA CGTAGCTCAG GCCGTAATCG AAGCTCGCGG 100  
TAAATAA 107

## 2) INFORMATION FOR SEQ ID NO: 1825

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*  
(B) STRAIN: ATCC 13182

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825

TTACTCCATG GAGTTCCTGA AGTATGATGA TGCGCCGAAC AACGTTGCTC 50  
AGGCCGTAAT CGAAGCCCGT GGTAAATAA 79

## 2) INFORMATION FOR SEQ ID NO: 1826

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Plesiomonas shigelloides*

(B) STRAIN: ATCC 14029

## 5. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826

CAGCTGCGTT CTCTGACCAA AGGTCGTGCA TCATACACTA TGG AATTCCT 50  
GAAGTATGAT GATGCGCCAA ACAACGTTGC TCAGGCCGTT ATTGAAGCCC 100  
GTGGTAAGTA A 111

## 2) INFORMATION FOR SEQ ID NO: 1827

## 15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shewanella putrefaciens*

25 (B) STRAIN: ATCC 8071

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827

GATTTGCGCT CTGCAACTCA TGGGCGTGCT TCGTACTCCA TGGAGTTCTT 50  
30 GAAGTACTCT GATGCACCGC AAAACATTGC GAAAGCGATT ATTGAATCTC 100  
GTAGCTAA 108

## 35 2) INFORMATION FOR SEQ ID NO: 1828

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## 45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Obesumbacterium proteus*

(B) STRAIN: ATCC 12841

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828

50

CTCAGCTGCG TTCTCTGACC AAAGGTCGTG CATCTTACTC CATGGAATTC 50  
CTGAAGTATG ATGATGCGCC TAACAACGTT GCTCAGGCCG TTATTGAAGC 100  
TCGTGGCAAA TAA 113



## 2) INFORMATION FOR SEQ ID NO: 1829

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*  
(B) STRAIN: ATCC 13182

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829

GCCGCAGGGT TAAACCAAA GTCCCGTGCT CTCTCCTGAA GGGGAGAGCA 50  
CTATAGTAAG GAATATAGCC 70

## 2) INFORMATION FOR SEQ ID NO: 1830

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*  
(B) STRAIN: ATCC 35567

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830

GCCTCGGGTA AACTTATAT CCCAGTCCCC CTCGTATAGA GGGGGATAGA 50  
GTAAAGGAAG ATAATC 66

## 2) INFORMATION FOR SEQ ID NO: 1831

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*  
(B) STRAIN: ATCC 14029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831

TCCACAGGAT TAAACCCAG GTTTAAACCT AAGTCCCGTG CTCTCTCCTC 50  
AGGGGAGAGC ACAATAGTAA GGAATATAGC C 81

2) INFORMATION FOR SEQ ID NO: 1832

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*  
(B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832

GCTACTAGTT TAAACATTG ATCCCGTGCT CTCTCTATGA AGGGAGAGCA 50  
CAAGAGTAAG GAATAAAGCC 70

2) INFORMATION FOR SEQ ID NO: 1833

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*  
(B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833

TTTCCAGTTA CGACATAAAT GTTATTATGG TCCAGCTTTG ACTGGACTAT 50  
TCTGAAAAGA AAGGAATATA TC 72

2) INFORMATION FOR SEQ ID NO: 1834

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Buttiauxella agrestis*  
 (B) STRAIN: ATCC 33320

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834

GCCCCGGGTT TTAAAAACA TTGATCCCGT GCTCTCTCCA GAAGGGGAGA 50  
 GCGCAACAGT AAGGAATATA GCC 73

## 2) INFORMATION FOR SEQ ID NO: 1835

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*  
 (B) STRAIN: ATCC 43479

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835

CTGCAGCTGA TGGTCCTATG CCACAAACTA GAGAGCACAT CCTTCTATCA 50  
 CGCCAAGTAG GTGTTCCATA TATCGTTGTA TTTATGAATA AAGCAGATAT 100  
 GGTTGATGAT GCTGAACTTT TAGAATTGGT TGAAATGGAA ATTAGAGAAT 150  
 40 TATTAAGCTC TTATGATTTT CCAGGTGATG ACACACCTAT TATTTTCAGGT 200  
 TCTGCTTTAA AAGCTCTTGA AGAAGCAAAA GCTGGACAAG ATGGCGAATG 250  
 GTCAGCGAAA ATTATGGATC TTATGGCTGC TGTGATAGC TATATTCCAA 300  
 CTCCAACCTCG TGACACTGAA AAAGATTTCT TAATGCCAAT TGAAGATGTT 350  
 TTCTCAATTT CAGGTCGTGG TACTGTTGTT ACAGGTAGAA TTGAAAAAGG 400  
 45 TATTGTAAAA GTTGGTGATA CTATAGAAAT CGTTGGTATT AAAGATACTC 450  
 AAACAACAAC TGTAACCTGGC GTTGAAATGT TTAGAAAAGA AATGGACCAA 500  
 GGTGAAGCAG GGGATAATGT TGGTGTCTT CTTCGTGGTA CAAAAAAGA 550  
 AGAAGTTATC CGCGGTATGG TTCTTGCTAA ACCAAAATCA ATTACTCCAC 600  
 ATACTGATTT CGAAGCTGAA GTTTATATCC TAAATAAAGA TGAGGGTGGT 650  
 50 AGACATACTC CATTCTTTAA TAACTATAGA CCGCAATTCT ATGTAAGAAC 700  
 AACAGATGTA ACAGGTCTA TTAAATTAGC TGATGGCGTT GAAATGGTTA 750  
 TGCCTGGTGA AAATGTAAGA ATTACTGTAA GCTTGATTGC ACCAG 795

## 2) INFORMATION FOR SEQ ID NO: 1836

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*  
 (B) STRAIN: ATCC 25936

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836

15 GCCATACTAG TTGTTTCTGC AGCTGATGGC CCAATGCCAC AACTAGAGA 50  
 GCACATTTTG CTATCTCGTC AAGTTGGTGT TCCATATATA GTTGTTTTTA 100  
 TGAACAAAGC TGATATGGTA GATGACGCAG AGTTGCTAGA ATTAGTTGAA 150  
 20 ATGGAGATCA GAGAGTTATT AAGCGAATAT GACTTCCCTG GTGATGATAC 200  
 TCCTATTATA AGCGGATCAG CACTTCAAGC TCTTGAAGAA GCTAAAGCTG 250  
 GTAATGATGG CGAATGGTCA GCTAAGATTA TGGATCTTAT GGCTGCTGTT 300  
 GATAGCTACA TACCAACTCC AGTTCGTGCT ACTGATAAAG ATTTCTTAAT 350  
 GCCGATTGAA GACGTATTCT CAATTTCTGG CCGTGGTACT GTTGTTACTG 400  
 25 GTAGAATTGA AAAAGGTATA GTTAAAGTTG GTGATACTAT CGAAATCGTA 450  
 GGTATTAGAG ATACACAAAC TACAACAGTT ACCGGCGTTG AAATGTTTAG 500  
 AAAAGAAATG GATCAAGGCG AGGCTGGTGA TAACGTTGGT GTTCTTTTAC 550  
 GCGGTACAAA GAAAGAAGAC GTTGAAAGAG GTATGGTTCT TTGTAAGCCA 600  
 AAATCAATTA CTCCTCATA TAAATTTGAG GGAGAAGTTT ATATCTTGAC 650  
 30 TAAGGAAGAG GCGGGTAGAC ATACTCCATT CTTCAACAAC TATAGACCAC 700  
 AATTTTATGT AAGAACAACA GATGTTACTG GATCAATCAC TCTTCCAGAG 750  
 GGTACTGAGA TGGTTATGCC TGGTGATAAC TTAAAAATCA CTGTTGAGTT 800  
 AATCAACCCA GTTGCTC 817

## 2) INFORMATION FOR SEQ ID NO: 1837

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 798 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*  
 (B) STRAIN: ATCC 33561

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837

CCATACTAGT TGTTTCTGCA GCTGATGGCC CAATGCCACA AACTAGAGAG 50

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CACATTTTGC | TATCTCGTCA | AGTTGGTGTT | CCATATATAG | TTGTTTTTAT | 100 |
|    | GAACAAAGCT | GATATGGTAG | ATGACGCAGA | GTTGCTAGAA | TTAGTTGAAA | 150 |
|    | TGGAGATCAG | AGAGTTATTA | AGCGAATATG | ACTTCCCTGG | TGATGATACT | 200 |
|    | CCTATTATAA | GCGGATCAGC | ACTTCAAGCT | CTTGAAGAAG | CTAAAGCTGG | 250 |
| 5  | TAATGATGGC | GAATGGTCAG | CTAAGATTAT | GGATCTTATG | GCTGCTGTTG | 300 |
|    | ATAGCTACAT | ACCAACTCCA | GTTCGTGCTA | CTGATAAAGA | TTTCTTAATG | 350 |
|    | CCGATTGAAG | ACGTATTCTC | GATTTCTGGC | CGTGGTACTG | TTGTTACTGG | 400 |
|    | TAGAATTGAA | AAAGGTATAG | TTAAAGTTGG | TGATACTATC | GAAATCGTAG | 450 |
|    | GTATTAGAGA | TACACAAACT | ACAACAGTTA | CCGGCGTTGA | AATGTTTAGA | 500 |
| 10 | AAAGAAATGG | ATCAAGGCGA | GGCTGGTGAT | AACGTTGGTG | TTCTTTTACG | 550 |
|    | CGGTACAAAG | AAAGAAGACG | TTGAAAGAGG | TATGGTTCTT | TGTAAGCCAA | 600 |
|    | AATCAATTAC | TCCTCATACT | AAATTTGAGG | GAGAAGTTTA | TATCTTGACT | 650 |
|    | AAGGAAGAGG | GCGGTAGACA | TACTCCATTC | TTCAACAACT | ATAGACCACA | 700 |
|    | ATTTTATGTA | AGAACAACAG | ATGTTACTGG | ATCAATCACT | CTTCCAGAGG | 750 |
| 15 | GTACTGAGAT | GGTTATGCCT | GGTGATAACT | TAAAAATCAC | TGTTAGTT   | 798 |

## 2) INFORMATION FOR SEQ ID NO: 1838

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Buttiauxella agrestis*
- (B) STRAIN: ATCC 33320

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 35 | GTGTCTAAAG | AAAAATTTGA | ACGTACAAAA | CCGCACGTCA | ACGTCGGTAC | 50  |
|    | TATCGGCCAC | GTTGACCATG | GTAAACTAC  | TCTGACTGCA | GCAATCACTA | 100 |
|    | CCGTTCTGGC | TAAACCTAC  | GGCGGTTCTG | CACGCGCATT | CGACCAGATC | 150 |
|    | GATAACGCAC | CAGAAGAAAA | AGCTCGTGGT | ATCACCATCA | ACACTTCCCA | 200 |
|    | CGTTGAATAT | GACACCCCGA | CTCGTCACTA | CGCGCACGTT | GACTGCCCAG | 250 |
| 40 | GGCACGCCGA | CTACGTTAAA | AACATGATCA | CCGGTGCTGC | TCAGATGGAC | 300 |
|    | GGCGCTATCC | TGGTTGTTGC | TGCGACTGAT | GGCCCGATGC | CACAGACTCG | 350 |
|    | TGAGCACATC | CTGCTGGGTC | GCCAGGTTGG | CGTTCCATTC | ATGATCGTGT | 400 |
|    | TCATGAACAA | ATGTGACATG | GTTGATGACG | AAGAGCTGCT | GGAAGTGGTA | 450 |
|    | GAAATGGAAG | TTCGTGAACT | TCTGTCTGCT | TATGATTTCC | CGGGCGACGA | 500 |
| 45 | CATCCCAGTG | GTTCTGTGGT | CAGCTCTGAA | AGCGCTGGAA | GGCGAAGCAG | 550 |
|    | AGTGGGAAGC | TAAAATCATC | GAGCTGGCTG | GTCACCTGGA | TAAGTACATC | 600 |
|    | CCAGAACCAG | AGCGTGCTAT | CGACAAGCCA | TTCTGCTGCT | CAATCGAAGA | 650 |
|    | CGTATTCTCC | ATCTCCGGCC | GTGGTACTGT | TGTTACTGGT | CGTGTAGAGC | 700 |
|    | GTGGTATCAT | TAAAGTTGGT | GAAGAAGTAG | AAATCGTTGG | TATCAAAGAT | 750 |
| 50 | ACCGTGAAAT | CTACCTGTAC | TGGCGTTGAA | ATGTTCCGCA | AACTGCTGGA | 800 |
|    | CGAAGGCCGT | GCTGGTGAGA | ACGTTGGTGT | TCTGCTGCGT | GGTATTAAAC | 850 |
|    | GTGAAGATAT | CGAACGTGGT | CAGGTTCTGG | CTAAGCCAGG | CTCTATCAAG | 900 |
|    | CCGCACACTC | AGTTCGAATC | AGAAGTTTAT | ATCCTGTCCA | AAGATGAAGG | 950 |

|            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------|
| CGGCCGTCAT | ACTCCGTTCT | TCAAAGGCTA | CCGTCCACAG | TTCTACTTCC | 1000 |
| GTACAACTGA | CGTGACTGGC | ACCATCGAAC | TGCCAGAAGG | CGTTGAGATG | 1050 |
| GTAATGCCGG | GCGACAACAT | TCAAATGGTT | GTTACCCTGA | TCCACCCAAT | 1100 |
| CGCAATGGAC | GACGGT     |            |            |            | 1116 |

5

## 2) INFORMATION FOR SEQ ID NO: 1839

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
- (B) STRAIN: ATCC 13182

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839

|               |            |            |            |            |      |
|---------------|------------|------------|------------|------------|------|
| GTGTCTAAAG    | AAAAATTTGA | ACGTACAAAA | CCGCACGTCA | ACGTCGGTAC | 50   |
| 25 TATCGGCCAC | GTTGACCATG | GTAAAACTAC | TCTGACCGCT | GCAATCACTA | 100  |
| CCGTTCTGGC    | TAAACCTAC  | GGTGGTGCTG | CTCGCGCATT | CGACCAGATC | 150  |
| GATAACGCGC    | CGGAAGAAAA | AGCTCGTGGT | ATCACCATCA | ACACTTCCCA | 200  |
| CGTTGAATAT    | GACACCCCGA | CTCGCCACTA | CGCGCACGTA | GACTGCCCCG | 250  |
| GCCACGCCGA    | CTATGTTAAA | AACATGATCA | CCGGTGCTGC | GCAGATGGAC | 300  |
| 30 GCGCGGATCC | TGGTTGTTGC | TGCGACTGAC | GGCCCGATGC | CGCAGACTCG | 350  |
| TGAGCACATC    | CTGCTGGGTC | GTCAGGTAGG | CGTTCCGTAC | ATCATCGTGT | 400  |
| TCCTGAACAA    | GTGCGACATG | GTTGATGACG | AAGAGCTGCT | GGAAGTGGTT | 450  |
| GAAATGGAAG    | TTCGTGAACT | TCTGTCTCAG | TACGATTTCC | CGGGCGACGA | 500  |
| CACTCCGATC    | GTTCGTGGTT | CTGCTCTGAA | AGCTCTGGAA | GGCGACGCTG | 550  |
| 35 AGTGGAATC  | TAAAATCATC | GAAGTGGCTG | GCTTCCTGGA | TTCTTATATT | 600  |
| CCGGAACCAG    | AGCGTGCGAT | TGACAAGCCG | TTCCTGCTGC | CGATCGAAGA | 650  |
| CGTATTCTCC    | ATCTCCGGTC | GTGGTACCGT | TGTTACCGGT | CGTGTAGAGC | 700  |
| GCGGTATCAT    | CAAAGTTGGC | GAAGAAGTTG | AAATCGTTGG | TATCAAAGAC | 750  |
| ACTGCTAAGT    | CTACCTGTAC | TGGCGTTGAA | ATGTTCCGCA | AACTGCTGGA | 800  |
| 40 CGAAGGCCGT | GCTGGTGAGA | ACGTTGGTGT | TCTGCTGCGT | GGTATCAAAC | 850  |
| GTGAAGAAAT    | CGAACGTGGT | CAGGTACTGG | CTAAGCCGGG | CTCTATCAAG | 900  |
| CCGCACACCA    | AGTTCGAATC | TGAAGTTTAT | ATCCTGTCCA | AAGACGAAGG | 950  |
| CGGCCGTCAC    | ACTCCGTTCT | TCAAAGGCTA | CCGTCCGCAG | TTCTACTTCC | 1000 |
| GTACAACTGA    | CGTGACTGGC | ACCATCGAAC | TGCCGGAAGG | CGTAGAGATG | 1050 |
| 45 GTTATGCCGG | GCGACAACAT | CAAATGGTT  | GTTACCCTGA | TCCACCCGAT | 1100 |
| CGCGATGGA     |            |            |            |            | 1109 |

## 50 2) INFORMATION FOR SEQ ID NO: 1840

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
- (B) STRAIN: ATCC 14029

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840

|    |            |            |            |            |             |      |
|----|------------|------------|------------|------------|-------------|------|
|    | GTGTCTAAAG | AAAAATTTGA | ACGTACTAAA | CCGCACGTTA | ACGTTGGTAC  | 50   |
|    | TATCGGCCAC | GTTGACCACG | GTAAAACTAC | CCTGACTGCA | GCTATCACTA  | 100  |
| 15 | CCGTACTGTC | TAAAGTATAC | GGTGGTCAGG | CTCGTGCAAT | CGATCAGATC  | 150  |
|    | GATAACGCGC | CAGAAGAAAA | AGCTCGTGGT | ATCACCATCA | ACACTTCTCA  | 200  |
|    | CGTAGAGTAC | GACACCCCAA | CTCGTCACTA | CGCGCACGTT | GACTGCCCCAG | 250  |
|    | GTCACGCCGA | CTACGTGAAG | AACATGATCA | CTGGTGCTGC | TCAGATGGAC  | 300  |
|    | GGCGCTATCC | TGGTAGTAGC | TGCGACTGAC | GGCCCAATGC | CTCAGACTCG  | 350  |
| 20 | TGAGCACATC | CTGCTGGGTC | GTCAGGTAGG | CGTTCCTTAC | ATCATCGTGT  | 400  |
|    | TCCTGAACAA | GTGTGACATG | GTTGATGACG | AAGAGCTGCT | GGAAGTGGTA  | 450  |
|    | GAAATGGAAG | TACGTGAGCT | GCTGTCTCAG | TACGACTTCC | CAGGCGACGA  | 500  |
|    | TACTCCAGTT | GTTCGCGGTT | CTGCACTGAA | AGCGCTGGAA | GGCGATGCTC  | 550  |
|    | AGTGGGAAGA | GAAGATTGTT | GAAGTGGCAG | GCTACCTGGA | CAGCTACATC  | 600  |
| 25 | CCTGAGCCAG | AGCGTGCTAT | CGACAAGCCA | TTCCTGCTGC | CAATCGAAGA  | 650  |
|    | CGTATTCTCT | ATCTCCGGCC | GTGGTACTGT | AGTAACTGGT | CGTGTAGAGC  | 700  |
|    | GCGGTATCAT | CAAAGTTGGT | GAAGAAGTAG | AAATCGTTGG | TATCAAAGAG  | 750  |
|    | ACTACCAAGA | CTACTTGTAC | TGGCGTTGAA | ATGTTCCGTA | AGCTGCTGGA  | 800  |
|    | CGAAGGTCGT | GCGGGCGAGA | ACGTAGGTGT | TCTGCTGCGT | GGTACCAAGC  | 850  |
| 30 | GTGATGACGT | AGAGCGTGGT | CAGGTTCTGG | CTAAGCCAGG | CTCAATCAAC  | 900  |
|    | CCACACACCA | ACTTTGTAGC | AGAAGTTTAT | ATTCTGTCCA | AAGATGAAGG  | 950  |
|    | TGGTCGTCAC | ACTCCATTCT | TCAAAGGCTA | CCGTCCACAG | TTCTACTTCC  | 1000 |
|    | GTACAACTGA | CGTGACCGGT | ACCATCGAAC | TGCCAGAAGG | CGTAGAGATG  | 1050 |
|    | GTAATGCCAG | GTGACAACAT | TCAAATGGTT | GTTACCCTGA | TTGCACCAAT  | 1100 |
| 35 | CGCGATGG   |            |            |            |             | 1108 |

2) INFORMATION FOR SEQ ID NO: 1841

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | TGGCAAAAGC | TAAATTTGAA | CGTATTAAGC | CTCACGTAAA | CGTGGGCACC | 50   |
|    | ATTGGTCACG | TTGACCATGG | TAAAACCACT | CTGACTGCAG | CTATCTCTCA | 100  |
|    | CGTACTGGCT | AAGACCTACG | GTGGCGAAGC | TAAAGACTTC | TCTCAAATCG | 150  |
| 5  | ATAACGCTCC | AGAAGAGCGT | GAGCGCGGTA | TTACCATCAA | TACCTCTCAC | 200  |
|    | ATCGAATATG | ACACGCCATC | ACGCCACTAC | GCCCACGTAG | ACTGCCCAGG | 250  |
|    | CCACGCTGAC | TATGTTAAAA | ACATGATCAC | TGGTGCTGCA | CAGATGGACG | 300  |
|    | GCGCGATTCT | GGTAGTCGCT | TCAACAGACG | GTCCAATGCC | ACAGACTCGT | 350  |
|    | GAGCACATCC | TGCTTTCTCG | TCAGGTTGGC | GTACCATTCA | TCATCGTATT | 400  |
| 10 | CATGAACAAA | TGTGACATGG | TAGATGACGA | AGAGCTGTTA | GAGCTAGTTG | 450  |
|    | AGATGGAAGT | GCGTGAAGT  | TTATCAGAA  | ACGATTTCCC | AGGTGATGAC | 500  |
|    | TTACCGGTAA | TCCAAGGTT  | AGCTCTGAAA | GCGCTAGAAG | GCGAGCCAGA | 550  |
|    | GTGGGAAGCA | AAAATCCTTG | AATTAGCAGC | GCGCTGGAT  | TCTTACATTC | 600  |
|    | CAGAACCACA | ACGTGACATC | GATAAGCCGT | TCCTACTGCC | AATCGAAGAC | 650  |
| 15 | GTATTCTCAA | TTTCAGGCCG | TGGTACAGTA | GTAACAGGTC | GTGTTGAGCG | 700  |
|    | TGGTATTGTA | CGCGTAGGCG | ACGAAGTTGA | AATCGTTGGT | GTACGTGCGA | 750  |
|    | CAACTAAGAC | AACGTGTA   | GGTGTAGAAA | TGTTCCGTAA | ACTGCTTGAC | 800  |
|    | GAAGGTCGTG | CAGGTGAGAA | CTGTGGTATT | TTGTTACGTG | GTACTAAGCG | 850  |
|    | TGATGACGTA | GAACGTGGTC | AAGTATTAGC | GAAGCCAGGT | TCAATCAACC | 900  |
| 20 | CACACACTAC | TTTTGAATCA | GAAGTTTACG | TACTGTCAA  | AGAAGAAGGT | 950  |
|    | GGTCGTCACA | CGCCATTCTT | CAAAGGCTAC | CGTCCACAGT | TCTACTTCCG | 1000 |
|    | TACAACTGAC | GTAACCGGTA | CTATCGAACT | GCCAGAAGGC | GTAGAGATGG | 1050 |
|    | TAATGCCAGG | CGATAACATC | AAGATGGTAG | TGACACTGAT | TTGCCCAATC | 1100 |
|    | GCGATGG    |            |            |            |            | 1107 |
| 25 |            |            |            |            |            |      |

## 2) INFORMATION FOR SEQ ID NO: 1842

|    |  |
|----|--|
| 30 | (i) SEQUENCE CHARACTERISTICS:                |
|    | (A) LENGTH: 1116 bases                       |
|    | (B) TYPE: Nucleic acid                       |
|    | (C) STRANDEDNESS: Double                     |
|    | (D) TOPOLOGY: Linear                         |
| 35 |  |
|    | (ii) MOLECULE TYPE: Genomic DNA              |
|    |  |
|    | (vi) ORIGINAL SOURCE:                        |
|    | (A) ORGANISM: <i>Obesumbacterium proteus</i> |
| 40 | (B) STRAIN: ATCC 12841                       |

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1842

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GTGTCTAAAG | AAAAATTTGA | ACGTACAAAA | CCGCACGTTA | ACGTTGGTAC | 50  |
| 45 | AATCGGCCAC | GTTGACCACG | GTAAAACTAC | CCTGACTGCT | GCAATCACTA | 100 |
|    | CCGTTCTGGC | TAAAACCTAC | GGTGGTTCTG | CACGTGCATT | CGACCAGATC | 150 |
|    | GATAACGCGC | CAGAAGAAAA | AGCTCGTGGT | ATCACCATCA | ACACTTCTCA | 200 |
|    | CGTTGAATAT | GACACCCCGA | CTCGCCACTA | CGCACACGTA | GACTGCCCAG | 250 |
|    | GCCACGCCGA | CTATGTTAAA | AACATGATCA | CCGGTGCTGC | GCAGATGGAC | 300 |
| 50 | GGCGCGATCC | TGGTTGTTGC | TGCGACTGAC | GGCCCTATGC | CTCAGACTCG | 350 |
|    | TGAGCACATC | CTGCTGGGTC | GTCAGGTTGG | CGTTCCTTAC | ATCATCGTAT | 400 |
|    | TCCTGAACAA | ATGCGACATG | GTTGATGATG | AAGAGCTGCT | GGAGCTGGTA | 450 |
|    | GAAATGGAAG | TTCGTGAACT | TCTGTCTCAG | TACGACTTCC | CAGGCAATGA | 500 |



|    |             |            |            |            |            |      |
|----|-------------|------------|------------|------------|------------|------|
|    | TACTCCAATC  | ATCCGTGGTT | CTGCTCTGAA | AGCGCTGGAA | GGCGAAGCTG | 550  |
|    | AGTGGGAAGC  | TAAGATCGTA | GAAGTGGCTG | AAACTCTGGA | TTCTTACATC | 600  |
|    | CCAGAACCAG  | AACGTGCTAT | CGACAAGCCA | TTCCTGCTGC | CAATCGAAGA | 650  |
|    | CGTATTCTCA  | ATCTCTGGCC | GTGGTACTGT | TGTTACCGGT | CGTGTAGAGC | 700  |
| 5  | GCGGTATCGT  | TAAAGTTGGT | GAAGAAGTTG | AGATTGTTGG | TATCAAAGAT | 750  |
|    | ACCGTTAAAT  | CAACTTGTAC | CGGCGTTGAA | ATGTTCCGTA | AACTGCTGGA | 800  |
|    | CGAAGGTCGT  | GCAGGCGAGA | ACGTTGGTGT | TCTGCTGCGT | GGTATCAAGC | 850  |
|    | GTGAAGACAT  | CGAACGTGGT | CAGGTTCTGG | CTAAACCAGG | TTCTATCAAA | 900  |
|    | CCACACACCA  | AGTTCGAATC | AGAAGTTTAT | ATTCTGAGCA | AAGATGAAGG | 950  |
| 10 | CGGCCGTCAT  | ACTCCGTTCT | TCAAAGGCTA | CCGTCCACAG | TTCTACTTCC | 1000 |
|    | GTACAACCTGA | CGTGACCGGT | ACCATCGAAC | TGCCAGAAGG | CGTGGAAATG | 1050 |
|    | GTAATGCCAG  | GCGATAACAT | CAAATGATC  | GTTACCCTGA | TCCACCCAAT | 1100 |
|    | CGCAATGGAC  | GATGGT     |            |            |            | 1116 |

15

## 2) INFORMATION FOR SEQ ID NO: 1843

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1129 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Budvicia aquatica*

(B) STRAIN: ATCC 35567

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843

|    |             |             |            |            |             |      |
|----|-------------|-------------|------------|------------|-------------|------|
|    | GTGTCTAAAG  | AAAAATTTGA  | ACGTACAAAA | CCGCACGTTA | ACGTTGGTAC  | 50   |
|    | TATCGGCCAC  | GTTGACCACG  | GTAAAACAAC | TCTGACTGCT | GCTATCACCA  | 100  |
| 35 | GCGTTTTAGC  | TAAAACTTAT  | GGCGGTAACG | CTCGTGCATT | CGATCAAATC  | 150  |
|    | GATAATGCAC  | CAGAAGAAAA  | AGCACGTGGT | ATCACCATCA | ACACTTCTCA  | 200  |
|    | CGTTGAGTAT  | GATACTCCTG  | CTCGCCACTA | CGCACACGTA | GACTIONCCAG | 250  |
|    | GACACGCCGA  | CTATGTGAAA  | AACATGATCA | CCGGTGCTGC | TCAAATGGAC  | 300  |
|    | GGCGCGATCT  | TAGTTGTTGC  | GGCAACTGAT | GGTCCTATGC | CACAGACTCG  | 350  |
| 40 | TGAGCACATC  | CTGTTAGGTC  | GTCAGGTTGG | CGTTCCTTAC | ATCATCGTGT  | 400  |
|    | TCCTGAACAA  | GTGTGACATG  | GTTGATGACG | AAGAACTGTT | AGAATTAGTT  | 450  |
|    | GAAATGGAAG  | TTCGTGAGCT  | TCTTTCTGCT | TATGATTTCC | CTGGTGACGA  | 500  |
|    | TACTCCAGTT  | GTTCTGTGGT  | CTGCGCTGAA | AGCGTTAGAA | GGCGAAGCTG  | 550  |
|    | AGTGGGAAGC  | TAAGATCATT  | GAATTAGCCG | GATATCTGGA | TAGCTACATC  | 600  |
| 45 | CCAGAGCCAG  | AGCGTGCGAT  | TGACCGTCCG | TTCCTGCTGC | CAATCGAAGA  | 650  |
|    | CGTATTCTCT  | ATTTTCAGGCC | GTGGTACAGT | TGTTACCGGT | CGTGTAGAGC  | 700  |
|    | GCGGAATCGT  | TAAAGTCGGT  | GAAGCCGTTG | AGATTGTTGG | TATCAAAGAT  | 750  |
|    | ACCGTACAAA  | CTACCTGTAC  | TGGCGTTGAA | ATGTTCCGTA | AGTTACTTGA  | 800  |
|    | CGAAGGCCGT  | GCTGGTGAGA  | ACGTTGGTGT | TCTGCTGCGT | GGTACTAAGC  | 850  |
| 50 | GTGAAGAAAT  | CGAACGCGGT  | CAAGTACTGG | CTAAGCCAGG | TTCAATCAAC  | 900  |
|    | CCGCACACCA  | ACTTTGTATC  | AGAAGTTTAT | ATTCTGAGCA | AAGATGAAGG  | 950  |
|    | TGGTCGTCAT  | ACTCCATTCT  | TCAAAGGCTA | CCGTCCACAG | TTCTACTTCC  | 1000 |
|    | GTACAACCTGA | CGTGACCGGT  | ACTATCGAAC | TGCCAGAAGG | CGTAGAGATG  | 1050 |

GTGATGCCTG GTGACAACAT TCAGATGACT GTAACCTCTGA TTGCACCAAT 1100  
CGCGATGGAC GAAGGTTTAC GCTTCGCTA 1129

5

## 2) INFORMATION FOR SEQ ID NO: 1844

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*  
(B) STRAIN: ATCC 49175

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844

ATATTCATAA TGCATTACAA GTTGTGAAAA CAACAAGTGA CGGAAGTGAA 50  
AAGACTGTTA CATTGGAAAC TGCTGTAGAA TTAGGGGATG GTGCAGTTCG 100  
TACGATTGCC ATGGAATCTA CAGATGGTTT GCAACGTGGC ATGAAAGTAG 150  
25 TGGACTTAGG ACGCACAAAT AGCGTTCCTG TGGGACCTGA AACATTAGGT 200  
CGTGTATTCA ACGTTTTAGG AGATACAATC GACTTGAAAG AACCATTCCC 250  
AGAAGACTTT ACAAGACATG AAATCCATAA ACCAGCACCA AAATTTGAAG 300  
AATTAAACAG TCAATATGAA ATTCTACAAA CAGGGATTAA AGTTATTGAC 350  
CTTTTAGCAC CTTATCTTAA AGGTGGTAAA ATCGGTTTAT TCGGTGGTGC 400  
30 CGGTGTAGGG AAAACCGTAT TAATTCAAGA ATTAATTCAT AATATCGCTG 450  
AAGAACTTGG TGGTATTTCA GTATTTACAG GGGTAGGGGA ACGTACTCGT 500  
GAAGGGAATG ACCTTTACCA TGAAATGCAA GAATCAGGCG TATCTGCTAA 550  
AACAGCGATG GTGTTTGGGC AAATGAACGA ACCACCAGGA GCTCGTATGC 600  
GTGTAGCACT AACAGGGTTA ACTATTGCGG AATACTTCCG TGATATGGAA 650  
35 AAACAAGACG TGCTTTTATT CATCGATAAC ATTTATCGTT TCACGCAAGC 700  
AGGTTTCAGAA GTGTCAGCGT TACTTGGTCG TATGCCTTCT GCCGTAGGGT 750  
ATCAACCAAC ATTAGCGACA GAAATGGGTC AATTACAAGA ACGTATCAGT 800  
TCAACTAAAG 810

40

## 2) INFORMATION FOR SEQ ID NO: 1845

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 815 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*

(B) STRAIN: ATCC 9345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845

|    |            |             |            |             |            |     |
|----|------------|-------------|------------|-------------|------------|-----|
| 5  | TGCTCTGCCA | GAAATTAACA  | ACGCCCTCCT | CACCGAAGTA  | GACCTCTCCG | 50  |
|    | GCCAAGGCGA | AGGCGAAAGC  | GTTCTCAAGA | TGACTCTTGA  | GGTTGCTCAG | 100 |
|    | CACCTCGGCG | ATAACATCGT  | CCGTACCATC | GCCATGAAGC  | CAACCGACGG | 150 |
|    | TCTGGTTCGC | GGCGCCACCG  | TTATCGATAC | CGGCGCCCCA  | ATCACCGTGC | 200 |
|    | CAGTTGGCGA | CGCAACTAAA  | GGTCATGTTT | TCAACGTGAC  | CGGTGATGTC | 250 |
| 10 | CTAAACTTGG | GCGAAGGCGA  | AACCCTTGAC | GTCAAGGAAC  | GGTGGCCAAT | 300 |
|    | CCACCGCAAG | GCTCCACAGT  | TCGACGAACT | CGAACC GGAA | ACCAAGATGT | 350 |
|    | TCGAAACAGG | CATCAAGGTG  | ATCGATCTCC | TCACCCCAT A | CGTACAGGGC | 400 |
|    | GGCAAGATCG | GTCTGTTTGG  | CGGTGCTGGT | GTTGGTAAGA  | CCGTTCTTAT | 450 |
|    | CCAGGAAATG | ATCCAGCGTG  | TTGCACAGGA | TCATGGCGGT  | GTGTCCGTGT | 500 |
| 15 | TCGCGGGTGT | GGGTGAACGT  | ACCCGTGAAG | GTAACGATCT  | TATCCACGAA | 550 |
|    | ATGGAAGATG | CGGGCGTTCT  | TGATAAGACC | GCGCTTGTGT  | TCGGCCAGAT | 600 |
|    | GGATGAACCG | CCAGGGGGTTC | GTTTGCGTAT | TGCACTTTCC  | GGCCTGACCA | 650 |
|    | TGGCGGAATA | CTTCCGTGAC  | GTGCAAAACC | AGGACGTGCT  | TTTGTTCATC | 700 |
|    | GATAACATCT | TCCGCTTCAC  | CCAGGCAGGT | TCGGAAGTGT  | CCACGTTGCT | 750 |
| 20 | TGGCCGTATG | CCATCAGCAG  | TGGGCTACCA | GCCGACCTTG  | GCAGATKAAA | 800 |
|    | TGGGCGCATT | GCAGG       |            |             |            | 815 |

25 2) INFORMATION FOR SEQ ID NO: 1846

(i) SEQUENCE CHARACTERISTICS:

|    |                          |
|----|--------------------------|
|    | (A) LENGTH: 1073 bases   |
|    | (B) TYPE: Nucleic acid   |
| 30 | (C) STRANDEDNESS: Double |
|    | (D) TOPOLOGY: Linear     |

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

|  |   |
|--|---|
|  | (A) ORGANISM: <i>Basidiobolus ranarum</i> |
|  | (B) STRAIN: ATCC 24670                    |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846

|    |            |             |              |            |             |     |
|----|------------|-------------|--------------|------------|-------------|-----|
| 40 | ACCTTCCTCC | TATCTTGA AH | GCCCTGGAGG   | TCCAAAACCA | CAGCTCTCGY  | 50  |
|    | TTAGTTTTAG | AGGTGTC CCA | GCATTTGGGT   | GAAAACACCG | TTCGTACTAT  | 100 |
|    | TGCTATGGAC | GGTACTGAAG  | GATTGGTTTCG  | TGGTCAAAAT | GTCGTAGATA  | 150 |
|    | CCGGATATCC | TATTAGAGTT  | CCTGTGCGGT C | CTGAATGTTT | GGGTCGTATC  | 200 |
| 45 | ATGAACGTTA | TTGGCGAGCC  | TGTTGATGAG   | CGCGGYCCTA | TCAAGACCAA  | 250 |
|    | GAAGCTTGCA | CCCATCCACG  | CTTCTCCCCC   | CGAGTTCGTY | GACCAATCCA  | 300 |
|    | CCACCCCCGA | AATCTTGGAG  | ACTGGTATTA   | AGGTTGTCGA | TTTGTG TGCC | 350 |
|    | CCTTACGCTC | GTGGTG GTAA | GATCGGTCTT   | TTCGGTGGTG | CCGGTGT CGG | 400 |
|    | TAAGACTGTG | TTTATCCAGG  | AGTTGATYAA   | CAACGTTGCC | AAGGCCCACG  | 450 |
| 50 | GTGGTTACTC | CGTGTT CGCT | GGTGTTGGTG   | AGCGTACTCG | TGAGGGTAAC  | 500 |
|    | GATTTGTACC | ACGAGATGAT  | TCAA ACTGGT  | GTCATCAAGC | TTGATGGCCA  | 550 |
|    | ATCCAAGGCT | GCCCTTGTCT  | ACGGMCAAAT   | GAACGAGCCC | CCAGGTGCTC  | 600 |
|    | GTGCCCGMGT | CGCTTTGACC  | GGTCTTACCG   | TTGCTGAATA | CTTCCGTGAT  | 650 |

|   |            |            |            |             |            |      |
|---|------------|------------|------------|-------------|------------|------|
|   | GAGGAAGGHC | AAGATGTGTT | GCTCTTCATT | GACAAACATTT | TCCGTTTCAC | 700  |
|   | CCAAGCTGGT | TCTGAAGTGT | CYGCCTTGTT | GGGTCGTATC  | CCCTCCGCTG | 750  |
|   | TCGGTTACCA | ACCCACCTTG | GCCACCGATA | TGGGTGTCAT  | GCAAGAGCGT | 800  |
|   | ATTACCACCA | CCAAGAAGGG | TTCCATTACC | TCTGTCCAGG  | CCATTTACGT | 850  |
| 5 | CCCTGCTGAT | GATTTGACCG | ATCCCCTCC  | TGCCACTACT  | TTTGCCCATC | 900  |
|   | TTGACGCCAC | CACCGTGTTG | TCTCGTTCCA | TCTCTGAGTT  | GGGTATTAC  | 950  |
|   | CCCGCTGTCG | ATCCCCTCGA | CTCCAAGTCT | CGTATGTTGG  | ATCCYCGTAT | 1000 |
|   | TGTCGGTGAA | GAGCACTACG | ACATCGCCAC | TGGTGTTCAG  | AAGATTCTCC | 1050 |
|   | ARTCTTACAA | GTCTCTCCAG | GAT        |             |            | 1073 |

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## 2) INFORMATION FOR SEQ ID NO: 1847

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*  
 (B) STRAIN: ATCC 56220

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | TGTCTTTATC | CAGGAGTTGA | TTGTACGTCT | TGCCTCACCC | TTTGGGTATT  | 50  |
| 30 | TTGCGAATAC | TAATTATAGT | AGAACAACAT | TGCCAAGGCT | CACGGTG GTT | 100 |
|    | ACTCTGTCTT | CACTGGTGTC | GGTGAACGTA | CTCGTGAGGG | TAACGATTTG  | 150 |
|    | TACCACGAAA | TGCAGGAAAC | TGGTGTCATT | CAGCTCGAGG | GTGAATCCAA  | 200 |
|    | GGTCGCCCTC | GTGTTCCGTC | AGATGAACGA | GCCCCCTGGT | GCCCGTGCCC  | 250 |
|    | GTGTCGCTCT | TACTGGTTTG | ACCATTGCCG | AGTACTTCCG | TGACGAGGAG  | 300 |
| 35 | GGTCAAGATG | TGCTTCTCTT | CATTGACAAC | ATTTTCCGTT | TCACTCAGGC  | 350 |
|    | CGGTTCTGAG | GTGTCTGCCC | TTTTGGGTCG | TATCCCCTCT | GCCGTCGGTT  | 400 |
|    | ACCAGCCCAC | TCTCGCCGTC | GACATGGGTG | TCATGCAGGA | GCGTATTACC  | 450 |
|    | ACCACCACCA | AGGGTTCCAT | CACCTCCGTC |            |             | 480 |

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## 2) INFORMATION FOR SEQ ID NO: 1848

## 45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 50 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
| 5  | TGTCTTCATT | CAGGAGTTGA | TTGTACGTCC | CTTCCTCTCT  | ACAAATGACG | 50  |
|    | GGCGAGGAAA | ATTTTGGCT  | TTTTCTAATA | GTCGTTATA   | GAACAACATT | 100 |
|    | GCCAAAGCCC | ACGGTGGTTA | CTCCGTTTTC | ACTGGTGTCTG | GCGAGCGGAC | 150 |
|    | CCGTGAAGGA | AACGATTTGT | ACCACGAGAT | GCAGGAAACC  | CGTGTTATCC | 200 |
|    | AGCTCGATGG | CGAGTCTAAG | GTCGCACTCG | TCTTCGGTCA  | GATGAACGAG | 250 |
| 10 | CCCCCGGAG  | CCCGTGCCCG | TGTTGCCCTC | ACTGGCCTGA  | CCATTGCTGA | 300 |
|    | ATATTTCCGT | GACGAGGAAG | GTCAAGACGG | TATGTATTCA  | TATAAATTAC | 350 |
|    | TCCGGGCAAA | TTGACTCAGA | ACCGCACTCA | CTCACACATA  | TATTAGTGCT | 400 |
|    | TCTCTTTATC | GACAACATTT | TCCGCTTCAC | CCAGGCCGGT  | TCCGAAGTGT | 450 |
|    | CCGCCCTGCT | TGGTCGTATT | CCCTCCGCCG | TCGGTTACCA  | ACCCACTCTC | 500 |
| 15 | GCCGTCGACA | TGGGTGGTAT | GCAGGAACGT | ATCACAACCA  | CCACCAAGGG | 550 |
|    | CTCCATTACC | TYCGTG     |            |             |            | 566 |

20 2) INFORMATION FOR SEQ ID NO: 1849

(i) SEQUENCE CHARACTERISTICS:

|    |                          |
|----|--------------------------|
|    | (A) LENGTH: 817 bases    |
|    | (B) TYPE: Nucleic acid   |
| 25 | (C) STRANDEDNESS: Double |
|    | (D) TOPOLOGY: Linear     |

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

|  |   |
|--|---|
|  | (A) ORGANISM: <i>Campylobacter coli</i> |
|  | (B) STRAIN: ATCC 43479                  |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849

|    |            |            |             |             |            |     |
|----|------------|------------|-------------|-------------|------------|-----|
| 35 | AATGAAGCCA | TTGTTGTAAA | TTTTGAAAGT  | GAAGGC AAAA | AACAAAAACT | 50  |
|    | TGTTTTAGAA | GTAGCAGCAC | ACTTGGGCGA  | TAATAGAGTT  | AGAACTATTG | 100 |
|    | CTATGGATAT | GACAGATGGC | TTGGTAAGAG  | GACTTAAAGC  | AGAAGCTTTG | 150 |
|    | GGTGCTCCTA | TTAGCGTTCC | TGTGGGTGAA  | AAAGTTTTAG  | GAAGAATTTT | 200 |
| 40 | TAATGTTACG | GGAGATTTGA | TCGATGAAGG  | TGAAGAAATT  | TCTTTTGATA | 250 |
|    | AAAAATGGGC | AATTCATAGA | GATCCACCAG  | CTTTTGAAGA  | TCAAAGCACA | 300 |
|    | AAAAGTGAGA | TTTTTGAAAC | AGGGATTAAA  | GTTGTGGATT  | TACTTGCTCC | 350 |
|    | TTATGCAAAA | GGTGGTAAAG | TAGGTCTTTT  | TGGTGGTGCA  | GGTGTGGTA  | 400 |
|    | AAACTGTTAT | TATTATGGAG | CTTATT CACA | ATGTTGCATT  | TAAACATAGC | 450 |
| 45 | GGCTATTCTG | TATTTGCAGG | TGTAGGTGAG  | AGAACTCGTG  | AAGGAAATGA | 500 |
|    | CCTTTATAAT | GAAATGAAAG | AAAGTAATGT  | TTTAGACAAA  | GTTGCTCTAT | 550 |
|    | GTTATGGACA | AATGAATGAA | CCACCAGGGG  | CAAGAAATCG  | TATTGCTTTA | 600 |
|    | ACAGGTTTAA | CAATGGCTGA | GTATTTTAGA  | GATGAAATGG  | GTCTTGATGT | 650 |
|    | GCTTATGTTT | ATTGATAATA | TCTTTAGATT  | TTCACAATCA  | GGTTCTGAAA | 700 |
| 50 | TGTCAGCACT | TTTAGGAAGA | ATTCCATCAG  | CTGTGGGTTA  | TCAACCAACC | 750 |
|    | CTAGCAAGTG | AAATGGGTAA | ATTCCAAGAA  | AGAATTACTT  | CAACTAAAAA | 800 |
|    | AGGATCAATT | ACTTCAG    |             |             |            | 817 |

## 2) INFORMATION FOR SEQ ID NO: 1850

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*  
 (B) STRAIN: ATCC 25936

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850

```

AAGGCAACAC GCATAAACTT ATTTTAGAGA CTGCTGCACA CCTTGGAGAT      50
AATCGTGTA  GAACATATCGC TATGGATATG AGCGAAGGAC TTACAAGAGG      100
GTTAGATGCT ATAGCGCTTG GGTCGCCTAT CAGTGTCCTT GTTGGAGAAA      150
AAGTTTTTAGG AAGAATATTC AACGTAATTG GTGATCTTAT AGACGAAGGC      200
GAAGAAGAAA AATTTGATAA AAAATGGTCG ATTCATAGAG ATCCGCCGGC      250
ATTTGAAGAT CAAAGCACAA AAAGTGAAAT TTTTGAAACA GGTATAAAAG      300
TCGTAGATCT TTTGGCTCCT TATGCAAAAG GCGGTAAAGT TGGACTATTT      350
GGCGGTGCCG GCGTTGGTAA AACAGTTATC ATTATGGAAC TTATCCACAA      400
CGTTGCATTC AAACACAGCG GCTATTCGGT ATTTGCCGGT GTCGGTGAAA      450
GAACAAGAGA GGGTAACGAT CTTTATAATG AAATGAAAGA ATCCGGCGTT      500
TTGGATAAAG TTGCCCTTATG TTATGGACAA ATGAATGAAC CGCCGGGTGC      550
AAGAAACCGT ATAGCGCTTA CTGGTCTTAC AATGGCTGAG TATTTTCGTG      600
ACGAGATGGG ACTAGATGTT CTTATGTTTA TCGATAACAT CTTCCGTTTC      650
TCACAATCAG GCTCAGAGAT GTCGGCTCTT CTTGGACGTA TCCCAAGTGC      700
GGTTGGTTAT CAACCAACGT TAGCTAGCGA AATGGGAAGA CTTCAAGAAA      750
GAATCACATC AACTAAAAAA GGTTC                                     775

```

## 2) INFORMATION FOR SEQ ID NO: 1851

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*  
 (B) STRAIN: ATCC 33561

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851

```

CGAAGCTATT GAAGTAAATT TTACAGTAGA AGGCAACACG CATAAACTTA      50
TTTTAGAGAC TGCTGCACAC CTTGGAGATA ATCGTGTAAG AACTATCGCT      100

```

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGGATATGA | GCGAAGGACT | TACAAGAGGG | TTAGATGCTA | TAGCGCTTGG | 150 |
|    | GTCGCCTATC | AGTGTTCCTG | TTGGAGAAAA | AGTTTTAGGA | AGAATATTCA | 200 |
|    | ACGTAATTGG | TGATCTTATA | GACGAAGGCG | AAGAAGAAAA | ATTTGATAAA | 250 |
|    | AAATGGTCGA | TTCATAGAGA | TCCGCCGGCA | TTTGAAGATC | AAAGCACAAA | 300 |
| 5  | AAGTGAAATT | TTTGAAACAG | GTATAAAAGT | CGTAGATCTT | TTGGCTCCTT | 350 |
|    | ATGCAAAAGG | CGGTAAAGTT | GGACTATTTG | GCGGTGCCGG | CGTTGGTAAA | 400 |
|    | ACAGTTATCA | TTATGGAAC  | TATCCACAAC | GTTGCATTCA | AACACAGCGG | 450 |
|    | CTATTCGGTA | TTTGCCGGTG | TCGGTGAAAG | AACAAGAGAG | GGTAACGATC | 500 |
|    | TTTATAATGA | AATGAAAGAA | TCCGGCGTTT | TGGATAAAGT | TGCCTTATGT | 550 |
| 10 | TATGGACAAA | TGAATGAACC | GCCGGGTGCA | AGAAACCGTA | TAGCGCTTAC | 600 |
|    | TGGTCTTACA | ATGGCTGAGT | ATTTTCGTGA | CGAGATGGGA | CTAGATGTTC | 650 |
|    | TTATGTTTAT | CGATAACATC | TTCCGTTTCT | CACAATCAGG | CTCAGAGATG | 700 |
|    | TCGGCTCTTC | TTGGACGTAT | CCCAAGTGCG | GTTGGTTATC | AACCAACGTT | 750 |
|    | AGCTAGCGAA | ATGGGAAGAC | TTCAAGAAAG | AATCACATCA | ACT        | 793 |
| 15 |            |            |            |            |            |     |

## 2) INFORMATION FOR SEQ ID NO: 1852

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 825 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter gracilis*
  - 30 (B) STRAIN: ATCC 33236

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852

|    |            |            |            |             |            |     |
|----|------------|------------|------------|-------------|------------|-----|
|    | GGACTATTTA | CCGAAGATTA | ACGAAGCTAT | CGAGGTTAAA  | TTTGACGTCG | 50  |
| 35 | AGGGCGCTCA | TCGCAGGCTG | ATCCTAGAGG | TAGCCGCGCA  | CCTTGAGAGC | 100 |
|    | AATCGCGTCC | GCACGATCGC | TATGGATATG | AGCGATGGAC  | TTAGGCGAGG | 150 |
|    | GCTTGAGGCC | GTCGCTTTGG | GCGCGCCTAT | TACGGTGCCCT | GTGGGCGAGA | 200 |
|    | AAGTTTTGGG | TAGAATTTTT | AATGTTACGG | GCGATCTGAT  | CGACGAAGGC | 250 |
|    | GAGGATGAAA | AATTTGAAAC | CCGCTGGTCG | ATCCACAGAG  | ATCCGCCTAG | 300 |
| 40 | CTTTGAAAAT | CAAAGCACGA | AGAGTGAAAT | TTTTGAAACC  | GGCATTAAGG | 350 |
|    | TAGTCGATCT | GCTCGCCCCT | TATGCAAAGG | GCGGTAAGGT  | AGGACTATTC | 400 |
|    | GGCGGTGCTG | GCGTCGGTAA | GACCGTCATC | ATCATGGAAC  | TGATTACAAA | 450 |
|    | CGTCGCTTTC | AAACACAGCG | GCTACTCCGT | ATTTGCGGGT  | GTCGGCGAGC | 500 |
|    | GAACGAGAGA | GGGAAACGAC | CTTTATAACG | AGATGAAAGA  | ATCGGGCGTT | 550 |
| 45 | TTGGATAAAG | TCGCCTTGAC | CTATGGTCAG | ATGAACGAAC  | CGCCGGGAGC | 600 |
|    | GAGAAACCGT | ATCGCGCTAA | CCGTCCTTAC | GATGGCCGAG  | TATTTCCGCG | 650 |
|    | ACGAGCTAGG | GCTTGACGTT | TTGATGTTTA | TTGATAATAT  | CTTCCGCTTC | 700 |
|    | TCGCAGTCGG | GTTCGGAGAT | GTCCGCGCTT | TTAGGACGAA  | TTCCGTCCGC | 750 |
|    | GGTCGGTTAT | CAGCCTACGC | TTGCCAGCGA | AATGGGTAAA  | TTACAGGAGC | 800 |
| 50 | GCATTACTTC | TACTAAGAAG | GGCTC      |             |            | 825 |

## 2) INFORMATION FOR SEQ ID NO: 1853

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*  
 (B) STRAIN: ATCC 33560

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TTTACCTCAA | ATTAATGAAG | CAATTGTTGT | AAATTTTGAA | AGCGAAGGAA | 50  |
| AAAAACATAA | ACTTGTTTTA | GAAGTAGCAG | CTCATTTAGG | AGATAATAGA | 100 |
| GTTAGAATA  | TTGCTATGGA | TATGACAGAT | GGTTTGGTAA | GGGGCTTAAA | 150 |
| AGCTGAGGCT | TTAGGTGCTC | CTATTAGTGT | TCCTGTTGGT | GAGAAAGTTT | 200 |
| TAGGAAGAAT | TTTCAATGTT | ACTGGAGATT | TGATCGATGA | AGGTGAAGAA | 250 |
| ATTTCTTTTG | ATAAAAAATG | GGCAATTCAT | AGAGATCCGC | CAGCTTTTGA | 300 |
| AGATCAAAGC | ACAAAAAGTG | AGATTTTTGA | AACAGGGATT | AAAGTTGTAG | 350 |
| ATTTGCTTGC | TCCTTATGCA | AAAGGTGGTA | AAGTAGGTCT | TTTTGGTGGT | 400 |
| GCAGGTGTTG | GTAAAACGTG | TATTATTATG | GAGCTTATTC | ACAATGTTGC | 450 |
| ATTTAAGCAT | AGCGGCTATT | CTGTATTTGC | AGGTGTGGGT | GAGAGAAGTC | 500 |
| GTGAAGGAAA | TGACCTTTAT | AATGAAATGA | AAGAAAGTAA | TGTTTTAGAC | 550 |
| AAAGTTGCTC | TATGTTATGG | ACAAATGAAT | GAACCACCAG | GAGCAAGAAA | 600 |
| TCGTATTGCT | TTAACAGGTT | TAACAATGGC | TGAGTATTTT | AGAGATGAAA | 650 |
| TGGGTCTTGA | TGTGCTTATG | TTTATTGATA | ATATCTTTAG | ATTTTCACAA | 700 |
| TCAGGTTCTG | AAATGTCAGC | ACTTTTAGGA | AGAATTCCAT | CAGCTGTGGG | 750 |
| TTATCAACCA | ACCCTAGCAA | GTGAAATGGG | TAAATTCCAA | GAAAGAATTA | 800 |
| CTTCAACTAA | AAAAGGCT   |            |            |            | 818 |

## 2) INFORMATION FOR SEQ ID NO: 1854

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*  
 (B) STRAIN: ATCC 43198

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854

|            |            |            |            |            |    |
|------------|------------|------------|------------|------------|----|
| ATTACCTGAT | ATCAACAACG | CCTTATTGGT | CTATAAAAAT | GATGAACAAA | 50 |
|------------|------------|------------|------------|------------|----|



|    |             |             |            |            |            |     |
|----|-------------|-------------|------------|------------|------------|-----|
|    | AAAGTAAAAT  | TGTGCTAGAA  | GCTGCCTTAG | AATTAGGTGA | TGGCATCATT | 100 |
|    | CGTACAATTG  | CCATGGAATC  | AACGGATGGT | TTACAACGTG | GGATGGAAGT | 150 |
|    | TGTCGATACT  | GGTAAACCAA  | TTTCAGTTCC | AGTTGGTAAA | GAAACGCTAG | 200 |
|    | GACGTGTCTT  | TAACGTTTTA  | GGGGATACGA | TTGATATGCA | AGAACCATTT | 250 |
| 5  | GCACAAGATG  | CAGATCGTTC  | TGCAATTCAT | AAAGCTGCAC | CAAAATTTGA | 300 |
|    | AGACTTAAGT  | ACAAGTACTG  | AAATTTTAGA | AACAGGGATT | AAAGTTATCG | 350 |
|    | ACTTATTAGC  | ACCATATTTA  | AAAGGTGGTA | AAGTCGGTCT | ATTCGGGGGT | 400 |
|    | GCCGGAGTAG  | GTAAAACCGT  | TTTAATCCAA | GAATTAATCC | ATAATATTGC | 450 |
|    | ACAAGAACAT  | GGTGGGATTT  | CTGTATTTAC | CGGTGTTGGT | GAACGTACAC | 500 |
| 10 | GTGAAGGAAA  | TGACTTGTAT  | CATGAAATGC | GTGATTCAGG | AGTTATTGAA | 550 |
|    | AAAAC TGCCA | TGGTGT TTGG | TCAAATGAAC | GAACCACCTG | GAGCTCGTAT | 600 |
|    | GCGTGTTGCT  | TTAACTGGGT  | TAACGATTGC | TGAATATTTT | CGTGATGTAG | 650 |
|    | AAGGACAAGA  | TGTGTTGCTA  | TTTATTGATA | ACATCTTCCG | TTTCACTCAA | 700 |
|    | GCGGGTTCTG  | AAGTATCAGC  | CTTGCTTGGT | CGTATGCCAT | CTGCCGTGGG | 750 |
| 15 | TTATCAACCT  | ACATTGGCTA  | CAGAAATGGG | TCAATTACAA | GAACGTATCA | 800 |
|    | CTTCAACTAA  | GAAGGGCTCT  | ATCACTTCTA |            |            | 830 |

20 2) INFORMATION FOR SEQ ID NO: 1855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*  
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855

|    |             |            |             |            |            |     |
|----|-------------|------------|-------------|------------|------------|-----|
| 35 | TCTTTACCAG  | ATATCAATAA | TGCGCTTATT  | GTCTATAAAA | ATGATGAACA | 50  |
|    | AAAAAGTAAA  | ATCGTGCTTG | AAGCTGCTTT  | AGAGCTAGGA | GATGGCATT  | 100 |
|    | TTCGTACGAT  | TGCAATGGAA | TCAACTGATG  | GATTGCAACG | TGGAATGGAA | 150 |
|    | GTTTTTCGATA | CAGGTAAGCC | AATTTTCAGTA | CCAGTAGGTC | GTGAAACATT | 200 |
| 40 | AGGTCGTGTA  | TTTAATGTTT | TAGGTGATAC  | CATTGATACG | CAAGAAGCTT | 250 |
|    | TTCCTGCTGA  | TGCGAATCGT | GATGCGATT   | ATAAATCAGC | TCCAGCTTTT | 300 |
|    | GAAGAATTAA  | GTACAAGTAC | TGAAATCCTA  | GAAACAGGGA | TTAAAGTTAT | 350 |
|    | CGACTTACTA  | GCACCATACT | TAAAAGGTGG  | GAAAGTTGGT | CTATTCCGGT | 400 |
|    | GTGCCGGTGT  | AGGTAAAACC | GTATTAATTC  | AAGAATTAAT | TCATAATATC | 450 |
| 45 | GCCCAAGAAC  | ATGGGGGTAT | TTCAGTATTT  | ACCGGTGTTG | GTGAACGTAC | 500 |
|    | ACGTGAAGGA  | AATGACTTGT | ATCACGAAAT  | GCGTGATTCA | GGCGTTATCG | 550 |
|    | AAAAAACTGC  | TATGGTGTTT | GGGCAAATGA  | ACGAACCACC | TGGAGCACGT | 600 |
|    | ATGCGTGTTG  | CGCTAACTGG | ACTAACTATT  | GCGGAATACT | TCCGTGATGT | 650 |
|    | TGAAGGCCAA  | GACGTATTGC | TATTTATTGA  | TAATATCTTC | CGTTTTACTC | 700 |
| 50 | AAGCAGGTTT  | TGAAGTTTCT | GCCTTACTTG  | GTCGTATGCC | TTCTGCGGTA | 750 |
|    | GGTTATCAAC  | CTACTTTGGC | TACTGAAATG  | GGTCAATTGC | AAGAACGGAT | 800 |
|    | TACATCAACG  | AAGAAAGGTT | CGA         |            |            | 823 |

## 2) INFORMATION FOR SEQ ID NO: 1856

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*  
 (B) STRAIN: ATCC 51266

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856

|            |            |            |            |             |     |
|------------|------------|------------|------------|-------------|-----|
| TTACCAGACA | TTAATAATGC | CTTGGTTGTC | TATAAAAATG | ACGAACAAAA  | 50  |
| AACCAAGATT | GTATTAGAAG | CTGCCTTAGA | ACTAGGAGAT | GGTGTGATTC  | 100 |
| GAAGTATCGC | CATGGAATCT | ACTGATGGCT | TACAACGGGG | AATGGAAGTT  | 150 |
| GTCGATACTG | GCAGTTCCAT | TTCTGTACCG | GTAGGAAAAG | AAACATTGGG  | 200 |
| TCGTGTATTT | AACGTTTTAG | GAAATACAAT | TGACTTAGAA | GAACCTTTTC  | 250 |
| CAGCGGATGC | TAAACGTAGT | GGTATCCATA | AAAAAGCGCC | TGATTTTGAT  | 300 |
| GAATTAAGCA | CTAGTACAGA | AATTTTAGAA | ACAGGGATTA | AAGTTATTGA  | 350 |
| CCTATTAGCC | CCTTATTTAA | AAGGTGGTAA | AGTCGGATTA | TTCGGTGGTG  | 400 |
| CCGGAGTTGG | TAAAACCGTT | TTAATTCAAG | AATTAATTCA | TAATATTGCC  | 450 |
| CAAGAACATG | GTGGGATTTC | TGTTTTTACT | GGTGTGGTG  | AAAGAACACG  | 500 |
| TGAAGGTAAT | GACTTGTATT | ATGAAATGAA | AGAATCTGGC | GTTATCGAAA  | 550 |
| AAACTGCCAT | GGTATTTGGT | CAAATGAATG | AGCCACCTGG | TGCCCCGGATG | 600 |
| CGGGTTGCTT | TAACCGGACT | TACCATTGCG | GAATACTTCC | GGGACGTTGA  | 650 |
| AGGACAAGAT | GTATTGCTCT | TTATCGATAA | TATTTTCCGT | TTTACCCAAG  | 700 |
| CTGGTTCAGA | AGTATCTGCC | TTATTAGGAC | GGATGCCCTC | TGCCGTTGGT  | 750 |
| TATCAACCAA | CTTTGGCTAC | TGAAATGGGA | CAACTTCAAG | AACGGATTAC  | 800 |
| CTCAACGAAA | AAAGGTTCTA | TTACAT     |            |             | 826 |

## 2) INFORMATION FOR SEQ ID NO: 1857

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*  
 (B) STRAIN: ATCC 43197

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857

|            |            |            |            |            |    |
|------------|------------|------------|------------|------------|----|
| TCCTTACCAG | ACATCAACAA | TGCGTTGATT | GTTTACAAAA | AAAATAAAAC | 50 |
|------------|------------|------------|------------|------------|----|

|    |             |             |            |            |            |     |
|----|-------------|-------------|------------|------------|------------|-----|
|    | AAAAGTTGTT  | CTTGAAGCTG  | CTTTGGAAC  | TGGTGATGGT | GTTATCCGCA | 100 |
|    | CGATCTCTAT  | GGAATCAACA  | GATGGCTTGC | AACGTGGAAT | GGAAGTTGTC | 150 |
|    | GATACAGGCA  | AACCAATCTC  | AGTTCCCGTT | GGTAAAGAAA | CTTTAGGTCG | 200 |
|    | TGTGTTTAAAC | GTATTAGGTG  | AAACAATCGA | CAAAGAAGCG | CCTTTTCCAG | 250 |
| 5  | AAGATGCAGT  | AAAAAGCGGT  | ATTCATAAAA | AAGCGCCGGC | TTTTGAAGAA | 300 |
|    | CTTAGTACCA  | GTAATGAAAT  | TTTAGAAACA | GGGATCAAAG | TTATCGACTT | 350 |
|    | ATTAGCTCCT  | TACTTAAAGG  | GTGGTAAAGT | CGGACTATTT | GGTGGTGCCG | 400 |
|    | GTGTTGGTAA  | AACCGTCTTG  | ATCCAAGAAT | TGATTCATAA | TATCGCCCAA | 450 |
|    | GAACACGGTG  | GTATTTTCACT | GTTTACGGGT | GTTGGTGAAC | GTACTCGTGA | 500 |
| 10 | AGGGAACGAC  | CTTTATTATG  | AAATGAAGGA | ATCAGGCGTT | ATTGAGAAAA | 550 |
|    | CTGCCATGGT  | GTTTGGACAA  | ATGAACGAGC | CGCCAGGTGC | GCGTATGCGT | 600 |
|    | GTTGCCTTGA  | CTGGTTTGAC  | ATTGGCTGAA | TATTTCCGAG | ATGAAGAAGG | 650 |
|    | ACAAGATGTG  | CTGTTGTTTA  | TCGACAACAT | CTTCCGTTTC | ACTCAAGCCG | 700 |
|    | GTTCTGAAGT  | TTCTGCCTTG  | CTTGGCCGGA | TGCCTTCAGC | CGTTGGCTAC | 750 |
| 15 | CAACCAACTT  | TGGCAACTGA  | AATGGGTCAA | TTGCAAGAAC | GAATCACTTC | 800 |
|    | AACGAAGAAG  | GGCT        |            |            |            | 814 |

## 20 2) INFORMATION FOR SEQ ID NO: 1858

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*  
 (B) STRAIN: ATCC 43186

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 35 | CGCATTAGTT | GTTTATAAAA | ATGATGAGCA | AAAATCAAAA | GTTGTTCTTG | 50  |
|    | AAGCAGCATT | AGAATTAGGT | GACGGTGTGA | TCCGTACGAT | CGCAATGGAA | 100 |
|    | TCGACGGATG | GACTACAACG | TGGAATGGAA | GTCATCGACA | CAAGCAAAGC | 150 |
|    | GATCTCTGTA | CCAGTTGGAA | CAGAAACATT | AGGTCGTGTG | TTCAACGTGT | 200 |
| 40 | TAGGTGAAAC | AATCGATTTG | GAAGCACCAT | TTCCAGAGGA | TGCCCCAAGA | 250 |
|    | AGCGAGATCC | ACAAGAAAGC | ACCAAATTTT | GATGAATTAA | GCACAAGTAC | 300 |
|    | AGAGATTCTT | GAAACTGGGA | TCAAAGTCAT | TGACTTATTA | GCACCTTATT | 350 |
|    | TAAAAGGTGG | GAAAGTTGGA | TTGTTTGGGG | GTGCCGGTGT | TGGTAAAACC | 400 |
|    | GTACTGATCC | AAGAATTGAT | CCATAATATC | GCCCAAGAAC | ATGGGGGAAT | 450 |
| 45 | CTCAGTGTTT | ACCGGTGTAG | GGGAACGTAC | CCGTGAAGGA | AACGATCTGT | 500 |
|    | ATTACGAAAT | GAAAGATTCA | GGCGTAATCG | AAAAAACAGC | GATGGTGTTT | 550 |
|    | GGACAAATGA | ATGAGCCACC | AGGTGCTCGT | ATGCGTGTCT | CACTAACTGG | 600 |
|    | ATTGACGATT | GCGGAATATT | TCCGTGATGT | CGAAGGACAA | GACGTGCTCT | 650 |
|    | TATTTATTGA | TAATATTTTC | CGTTTCACCC | AAGCAGGTTC | AGAAGTATCT | 700 |
| 50 | GCCTTACTAG | GACGTATGCC | ATCAGCGGTT | GGTTATCAAC | CAACCTTAGC | 750 |
|    | GACTGAAATG | GGACAACTCC | AAGAACGGAT | CACTTCAACG | A          | 791 |

## 2) INFORMATION FOR SEQ ID NO: 1859

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*  
 (B) STRAIN: ATCC 49427

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859

|            |             |            |            |            |     |
|------------|-------------|------------|------------|------------|-----|
| TCCTTACCAG | ACATCAACAA  | TGCGTTGATT | GTTTATAAAA | AAGATAAAAC | 50  |
| AAAAGTTGTT | CTTGAAGCTG  | CTTTGGAAC  | TGGTGATGGT | GTTATTCGCA | 100 |
| CAATCGCCAT | GGAATCAACG  | GATGGATTAC | AACGTGGAAT | GGAAGTTGTC | 150 |
| GATACTGGCA | AGCCTATTTT  | TGTTCCAGTA | GGAAAAGAAA | CTCTAGGTCG | 200 |
| TGTATTTAAT | GTATTAGGTG  | AAACAATCGA | CAAGGAAGCG | CCTTTTCCAG | 250 |
| AAGATGCAGA | AAAAAGTGGT  | ATTCAACAAG | AAGCACCAAC | TTTCGAAGAA | 300 |
| CTTAGCACAA | GTAATGAGAT  | CTTAGAAACA | GGAATCAAAG | TTATTGACTT | 350 |
| GTTAGCTCCT | TACTTAAAAG  | GTGGTAAAGT | TGGATTATTT | GGTGGTGCCG | 400 |
| GTGTTGGTAA | AACAGTCTTG  | ATTCAAGAGC | TAATTCATAA | TATCGCTCAA | 450 |
| GAACATGGTG | GTATTTCTGT  | GTTTACTGGT | GTTGGTGAAC | GTACTCGTGA | 500 |
| AGGGAACGAC | CTTTATTATG  | AAATGAAAGA | TTCTGGTGTT | ATTGAGAAAA | 550 |
| CTGCTATGGT | GTTCGGTCAA  | ATGAACGAGC | CGCCAGGTGC | ACGTATGCGT | 600 |
| GTTGCCTTAA | CTGGTTTAAAC | CTTAGCCGAA | TACTTCCGTG | ATGAAGAAGG | 650 |
| ACAAGATGTG | TTGCTATTTA  | TTGACAACAT | TTTCCGTTTC | ACTCAAGCCG | 700 |
| GATCAGAAGT | TTCTGCCTTA  | CTTGGCCGTA | TGCCGTCAGC | AGTTGGTTAC | 750 |
| CAACCGACTT | TAGCAACTGA  | AATGGGTCAA | TTACAAGAAC | GTATTACGTC | 800 |
| GACGAAAAAA | GGTTCAA     |            |            |            | 817 |

## 2) INFORMATION FOR SEQ ID NO: 1860

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Globicatella sanguis*  
 (B) STRAIN: ATCC 51173

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860

|            |            |            |            |            |    |
|------------|------------|------------|------------|------------|----|
| CCTGACATTC | ATAATGCATT | AATTGTAACG | AACGCTGATA | TGGCGGATGT | 50 |
|------------|------------|------------|------------|------------|----|

|    |            |             |            |            |             |     |
|----|------------|-------------|------------|------------|-------------|-----|
|    | AATGCAAGAA | AATATTTTCGG | ATGAAGAAAA | ATTATTAACC | TTAGAAGTTG  | 100 |
|    | CACTGGATTT | AGGTCATGGA  | ATGGTCCGGA | CAATTGCGAT | GGAATCAACC  | 150 |
|    | GATGGTTTGG | AACGCGGCAT  | GACAGTTGTG | GATTATTTAA | CACCGATTAA  | 200 |
|    | AGTGCCAGTA | GGCGAAGCCA  | CTTTAGGTAG | AGTATTCAAT | GTTTTAGGTG  | 250 |
| 5  | AGACAATTGA | TGAACTAGAA  | CCGGTTGGCG | ACGATGTTGA | ACTCAAAAGT  | 300 |
|    | ATTCATCGTG | AAGCCCCTAA  | ATATGAGGAC | TTAGATAATA | GTTTTTCATGT | 350 |
|    | TTTAGAAACC | GGAATTAAGG  | TCATCGATTT | ATTAGCTCCT | TATATTAAAG  | 400 |
|    | GGGGAAAAAT | CGGTTTATTC  | GGTGGTGCCG | GAGTGGGTAA | AACGGTCTTA  | 450 |
|    | ATTCAAGAAT | TAATTCATAA  | TATTGCAGAA | CAATTAGGAG | GTATCTCAGT  | 500 |
| 10 | TTTCACTGGG | GTTGGAGAAC  | GTACCCGTGA | AGGGAATGAC | CTCGTTTTTG  | 550 |
|    | AAATGCGAGA | GTCAGGTGTA  | AGCAAGAAGA | CGGCCATGGT | TTTCGGTCAA  | 600 |
|    | ATGAATGAAC | CACCTGGAGC  | ACGTATGCGT | GTTGTCTTAA | CAGGACTTAC  | 650 |
|    | AATGGCGGAA | TATTTCCGTG  | ACGAATTGAA | ACAAGACGTC | TTATTATTTA  | 700 |
|    | TTGATAATAT | TTATCGTTTT  | ACTCAAGCAG | GTTCCGAAGT | GTCAGCCTTA  | 750 |
| 15 | TTAGGTCGTA | TGCCTTCAGC  | AGTAGGGTAT | CAACCAACTT | TAGCAAGTGA  | 800 |
|    | AATGGGACAA | ATGCAAGAAC  | GTATTACGTC | WACGAAGCRC | GGTTCCATTA  | 850 |
|    | CA         |             |            |            |             | 852 |

20

## 2) INFORMATION FOR SEQ ID NO: 1861

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus garvieae*  
 (B) STRAIN: ATCC 49156

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
|    | GCGCGACTCT  | TCCTGAGATT | AATAACGCAC | TCATCGTTTA | CAAAGATGTA | 50  |
|    | GACGGCGTTA  | AAACTAAAAT | CGTCCTTGAA | GTGGCGTTGG | AACTTGGTGA | 100 |
|    | TGGTGCCGTA  | CGTACCATCG | CTATGGAATC | AACTGATGGC | TTGACACGTG | 150 |
| 40 | GACTTGAAGT  | TCTCGATACA | GGTAAAGCAA | TCAGCGTACC | TGTTGGTCAA | 200 |
|    | GAAACACTTG  | GACGTGTCTT | CAATGTACTT | GGAGATGCTA | TTGATGGAGG | 250 |
|    | GGAAGCATTT  | GCTGAAAATG | CAGAACGCAG | CCCTATCCAT | AAAAAAGCCC | 300 |
|    | CATCTTTTGA  | TGAACTTTCA | ACAGCAAATG | AAATTCTGGT | GACAGGGATT | 350 |
|    | AAAGTTATTG  | ACTTGCTTGC | CCCATACCTT | AAAGGTGGTA | AGATTGGGTT | 400 |
| 45 | GTTCCGGTGGT | GCCGGAGTTG | GTAAAACCGT | CCTTATCCAA | GAGTTGATTC | 450 |
|    | ACAATATTGC  | CCAAGAACAC | GGTGGTATTT | CCGTATTTAC | TGGTGTTGGG | 500 |
|    | GAACGTACAC  | GTGAAGGGAA | TGACCTTTAC | TGGGAAATGA | AAGAATCAGG | 550 |
|    | CGTTATCGAA  | AAAACAGCCA | TGGTCTTCGG | TCAAATGAAT | GAACCACCTG | 600 |
|    | GAGCACGTAT  | GCGTGTTGCT | CTTACTGGTT | TGACAATTGC | TGAATATTTT | 650 |
| 50 | CGTGATGTAG  | AAAACAAGA  | CGTTTTGCTT | TTCATTGATA | ATATCTTCCG | 700 |
|    | TTTCAACCAA  | GCCGGTTCAG | AAGTATCTGC | CCTCTTAGGA | CGTATGCCAT | 750 |
|    | CAGCCGTTGG  | TTACCAACCT | ACGCTTGCAA | CTGAAATGGG | TCAACTTCAA | 800 |
|    | GAACGTATCA  | CTTCAACAAA | ACAAGGTT   |            |            | 828 |

## 2) INFORMATION FOR SEQ ID NO: 1862

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis*  
 (B) STRAIN: ATCC 11454

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| AATTGCCTGA | RATTAACAAT | GCCTTGATTG | TCTACAAAGA | TGTCAATGGC | 50  |
| CTAAAAACAA | AAATTACTCT | TGAAGTTGCT | TTGGAACCTG | GTGATGGTGC | 100 |
| AGTTCGTACA | ATCGCTATGG | AATCTACTGA | TGGCTTGACT | CGTGGACTTG | 150 |
| AAGTCCTTGA | TACAGGTAAA | GCAGTCAGCG | TTCCTGTTGG | GGAAGCCACT | 200 |
| CTTGGTCGTG | TTTTTAACGT | TCTTGGTGAT | GTTATTGACG | GTGGGGAAGA | 250 |
| ATTTGCTGCT | GATGCAGAAC | GTAATCCTAT | CCATAAAAAA | GCTCCAACAT | 300 |
| TTGACGAATT | GTCAACTGCA | AACGAAGTTC | TCGTAACCTG | GATTAAAGTT | 350 |
| GTCGATTTGC | TTGCACCTTA | CCTTAAAGGT | GGTAAAGTTG | GACTTTTCGG | 400 |
| TGGTGCCGGA | GTTGGTAAAA | CCGTCCTTAT | TCAAGAATTG | ATTCACAACA | 450 |
| TCGCCCAAGA | ACACGGAGGT | ATTTCTGTGT | TTACCGGTGT | TGGGGAACGT | 500 |
| ACTCGTGAAG | GGAATGACCT | TTACTGGGAA | ATGAAAGAAT | CAGGCGTTAT | 550 |
| TGAAAAAACT | GCCATGGTCT | TTGGTCAAAT | GAATGAACCA | CCAGGAGCAC | 600 |
| GTATGCGTGT | TGCCCTTACT | GGTTTGACAA | TTGCTGAATA | TTTCCGTGAT | 650 |
| GTTCAAGGTC | AAGACGTACT | GCTTTTCATT | GACAACATCT | TCCGTTTCAC | 700 |
| ACAAGCTGGT | TCAGAAGTTT | CTGCCCTTTT | GGGACGTATG | CCTTCTGCCG | 750 |
| TTGGTTACCA | ACCAACACTT | GCTACTGAAA | TGGGGCAATT | GCAAGAACGT | 800 |
| ATCACTTCTA | CTAAGAAGGG | TTCTGTTA   |            |            | 828 |

## 2) INFORMATION FOR SEQ ID NO: 1863

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*  
 (B) STRAIN: ATCC 19119

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863

|            |            |            |            |            |    |
|------------|------------|------------|------------|------------|----|
| CTTACCTGAA | ATCTACAACG | CCCTAGTTAT | TGAATATAAA | TCTGATGCAG | 50 |
|------------|------------|------------|------------|------------|----|

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
|    | AAGAAGCACC  | AACTAGCCAA | CTTACTTTAG | AAGTAGCCAT | TCAATTAGGT | 100 |
|    | GATGACGTTG  | TTCGTACAAT | TGCAATGGCA | TCAACTGATG | GTGTTCAAAG | 150 |
|    | AGGTATGGAA  | GTTATTGATA | CTGGGAGCCC | AATCACAGTT | CCAGTTGGTA | 200 |
|    | CAGTAACACT  | TGGTCGTGTA | TTTAACGTAT | TAGGAAACAC | TATCGATTTG | 250 |
| 5  | GATGAGCCAC  | TTCCAAGCGA | TATCAAGCGT | AATAAAATTC | ACCGTGAAGC | 300 |
|    | ACCAACATTT  | GACCAATTAG | CAACAACACT | TGAAATTCTT | GAAACAGGAA | 350 |
|    | TAAAAGTTGT  | AGACTTGCTA | GCCCCATATT | TAAAAGGTGG | TAAAATTGGT | 400 |
|    | TTGTTTCGGCG | GAGCGGGTGT | TGGTAAAACC | GTTTTAATCC | AAGAACTTAT | 450 |
|    | TCATAATATC  | GCTCAAGAAC | ATGGTGGTAT | TTCTGTGTTC | GCTGGTGTTC | 500 |
| 10 | GAGAACGTAC  | TCGTGAAGGG | AACGATCTTT | ACTTTGAAAT | GAAAGACTCT | 550 |
|    | GGTGTAATTG  | AAAAAACTGC | CATGGTATTC | GGTCAAATGA | ACGAACCACC | 600 |
|    | AGGTGCTCGT  | ATGCGTGTAG | CTTTAACAGG | TCTTACAATC | GCTGAATATT | 650 |
|    | TCCGTGATGA  | AGAACACCAA | GATGTACTTC | TATTCATTGA | TAATATTTTC | 700 |
|    | CGCTTTACTC  | AAGCTGGTTC | AGAGGTTTCG | GCTTTACTAG | GTCGTATGCC | 750 |
| 15 | ATCTGCAGTA  | GGTTATCAAC | CAACTCTAGC | TACCGAAATG | GGACAATTAC | 800 |
|    | AAGAACGTAT  | TACTTCTACT | AATGT      |            |            | 825 |

## 20 2) INFORMATION FOR SEQ ID NO: 1864

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*  
 (B) STRAIN: ATCC 19716

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 35 | GTCATATTCC | AGAGCTTTAT | GACGCTCTGG | AGGTAAAGGG | CGATGGTAAG | 50  |
|    | CATCGTTTCA | ACCTAGTTCT | TGAGGTTCAA | CAGCAGATTG | GCGGTGGTGT | 100 |
|    | GGTACGCTGC | ATTGCCATGG | GTTCTTCTGA | CGGTTTGAGC | AGAGGAATTG | 150 |
|    | AGGCTGTAAA | TACTGGTGCC | GGTGTTAAGG | TTCCAGTTGG | TCGTGAGACC | 200 |
| 40 | CTAGGACGTA | TTATGAACGT | TTTAGGTCAG | CCTGTAGATG | AGAGAGGTCC | 250 |
|    | TATCGGACAG | AAAGAGGATT | GGGAAATTCA | CCGTCCAGCT | CCTACCTATG | 300 |
|    | CTGAGCAGTC | ATCAACTACA | GAAATTCTAG | AAACCGGTAT | TAAGGTTATG | 350 |
|    | GACCTTATCT | GCCCATTTGC | TAAGGGTGGT | AAAGTTGGTC | TGTTCGGTGG | 400 |
|    | TGCCGGTGTG | GGTAAGACAG | TTAACATGAT | GGAGCTTATC | AATAACATTG | 450 |
| 45 | CTAAGGCTCA | CTCAGGTCTA | TCTGTATTTA | CCGGTGTTGG | TGAGCGTACT | 500 |
|    | CGTGAGGGTA | ACGACTTCTA | CCACGAAATG | CAGGAATCAA | AGGTTATCGA | 550 |
|    | TAAGGTATCA | ATGATTTACG | GTCAGATGAA | CGAGCCTCCA | GGGAACCGTC | 600 |
|    | TACGTGTTGC | TCTGACAGGT | CTGACTGTTG | CTGAGAAGTT | CCGTGACGAA | 650 |
|    | GGTCTGGATG | TGCTTCTGTT | CATCGATAAC | ATCTATCGTT | ATACACTGGC | 700 |
| 50 | TGGTACAGAG | GTATCTGCTC | TGTTAGGCCG | TATGCCTTCA | GCTGTGGGTT | 750 |
|    | ACCAGCCTAC | ACTGGCTGAG | GAAATGGGTG | TATTACAGGA | GCGTATTGCT | 800 |
|    | TCAACTAAGA | AAGGTTCTAT | T          |            |            | 821 |

## 2) INFORMATION FOR SEQ ID NO: 1865

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*  
 (B) STRAIN: ATCC 33315

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865

|    |             |            |             |            |            |     |
|----|-------------|------------|-------------|------------|------------|-----|
|    | TGATACTTTA  | CCAGATATCA | ATAATGCATT  | AGCCGTATAT | AAAAATGATG | 50  |
|    | AGAACAAGAC  | GCGTGTTGTA | TTGGAAGCTA  | CTTTAGAACT | TGGAGATGGG | 100 |
|    | GTAATTCGTG  | CCATTTCTAT | GGGGTCTACT  | GACGGCTTGC | AACGTGGCAT | 150 |
| 20 | GGAAGTTGTG  | GATACACAAG | AACCTATTTT  | TGTTCCGGTA | GGAAATGATA | 200 |
|    | CTTTAGGTCG  | TGTATTTAAT | GTGTTAGGAG  | AAACAATAGA | TAATCAGGAG | 250 |
|    | CCATTTCTCTG | AAGATGCTGA | AAAAAGTGGT  | ATTCACAAAA | AAGCCCCTAG | 300 |
|    | TTTTGATGAA  | TTAAGTACTA | GTTTCGGAAAT | ATTAGAAACA | GGGATCAAAG | 350 |
|    | TGATTGATTT  | ATTAGAACCT | TATCTAAGAG  | GCGGTAAAGT | CGGATTGTTT | 400 |
| 25 | GGAGGCGCCG  | GTGTTGGAAG | AACGGTGCTA  | ATTCAAGAAT | TGATCAATAA | 450 |
|    | TGTTGCCCAA  | GAACACGGGG | GTATTTCCGT  | GTTTAATGGT | GTAGGTGAAC | 500 |
|    | GTAATCGTGA  | AGGTAATGAC | TTGTATTATG  | AAATGCAGGA | TTCAGGCGTT | 550 |
|    | ATCGAAAAAA  | CAGCCATGGT | GTTTGGTCAA  | ATGAACGAAC | CACCAGGTGC | 600 |
|    | TCGTATGCGT  | GTTGCTTTAA | CTGGCCTAAC  | ACTGGCAGAA | TATTTTCGAG | 650 |
| 30 | ATGTTGAAGG  | TCAAGACGTA | TTATTATTTA  | TTGATAATAT | TTTCCGTTTT | 700 |
|    | ACACAAGCAG  | GTACCGAAGT | TTCCGCTTTA  | CTTGGTAGAA | TGCCATCTGC | 750 |
|    | TGTTGGCTAT  | CAACCCACAC | TAGCAACTGA  | AATGGGGCAA | CTGCAAGAAC | 800 |
|    | GGATTACGTC  | AACGGATAAG | GG          |            |            | 822 |

## 2) INFORMATION FOR SEQ ID NO: 1866

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*  
 (B) STRAIN: ATCC 25936

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866

|  |            |            |            |           |            |    |
|--|------------|------------|------------|-----------|------------|----|
|  | ATCTCCTCAG | GATCKATAGG | ACTTGATATA | GCTCTTGGA | TAGGCGGCGT | 50 |
|--|------------|------------|------------|-----------|------------|----|



|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | ACCAAAAGGA | AGAATAGTCG | AAATTTATGG | GCCAGAAAGC | TCTGGTAAAA  | 100 |
|    | CAACTCTTAC | TTTGCATTTA | ATAGCAGAAT | CTCAAAAAGT | CGGCGGAGTT  | 150 |
|    | TGCGCGTTTG | TAGATGCAGA | GCATGCACTT | GATGTAAAT  | ATGCTAAAAA  | 200 |
|    | TTTAGGCGTT | GATACGGATA | ACTTATATAT | TTCTCAACCG | GACTTCGGAG  | 250 |
| 5  | AGCAAGCTCT | TGATATAGTA | GAAACTCTAG | CTAGAAGCGG | CGCCGTTGAT  | 300 |
|    | CTTATAGTAA | TAGATAGCGT | AGCAGCTYTA | ACACCAAAAA | GCGAAATAGA  | 350 |
|    | AGGCGATATG | GGAGATCAGC | ACGTAGGGCT | GCAAGCAAGA | CTCATGAGTC  | 400 |
|    | AAGCACTTAG | AAAATTAACC | GGAGTTGTCC | ATAAAATGGG | AACTACAGTT  | 450 |
|    | GTATTTATAA | ACCAAATTCG | TATGAAAATC | GGCGCTATGG | GCTATGGCAC  | 500 |
| 10 | TCCTGAAACT | ACTACTGGCG | GAAATGCGCT | TAAATTTTAC | GCTTCAGTTA  | 550 |
|    | GACTTGACGT | ACGTAAAATA | GCTACTTTAA | AACAGAGCGA | TGAGCCAATC  | 600 |
|    | GGAAACCGCG | TAAAAGTAAA | AGTAGTAAAA | AACAAAGTCG | CTCCTCCTTT  | 650 |
|    | TAGACAAGCC | GAATTTGATA | TCATGTTTGG | AGAAGGTATC | AGCAAAGAAG  | 700 |
|    | GAGAGATAAT | AGATTACGGC | GTAAAACTTG | ATATTATCGA | TAAAAGCGGC  | 750 |
| 15 | GCTTGGTTTA | GCTATGATAA | TTCAAAATTA | GGTCAAGGCA | GAGAAAACCTC | 800 |
|    | AAAAGCGTTT | TTAAAAGA   |            |            |             | 818 |

## 20 2) INFORMATION FOR SEQ ID NO: 1867

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*  
 (B) STRAIN: ATCC 33561

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
| 35 | TCTCCTCAGG | ATCKATAGGA | CTTGATATAG | CTCTTGGTAT | AGGCGGCGTA  | 50  |
|    | CCAAAAGGAA | GAATAGTCGA | AATTTATGGG | CCAGAAAGCT | CTGGTAAAAC  | 100 |
|    | AACTCTTACT | TTGCATTTAA | TAGCAGAATC | TCAAAAAGTC | GGCGGAGTTT  | 150 |
|    | GCGCGTTTGT | AGATGCAGAG | CATGCACTTG | ATGTTAAATA | TGCTAAAAAT  | 200 |
| 40 | TTAGGCGTTG | ATACGGATAA | CTTATATATT | TCTCAACCGG | ACTTCGGAGA  | 250 |
|    | GCAAGCTCTT | GATATAGTAG | AAACTCTAGC | TAGAAGCGGC | GCCGTTGATC  | 300 |
|    | TTATAGTAAT | AGATAGCGTA | GCAGCTYTAA | CACCAAAAAG | CGAAATAGAA  | 350 |
|    | GGCGATATGG | GAGATCAGCA | CGTAGGGCTG | CAAGCAAGAC | TCATGAGTCA  | 400 |
|    | AGCACTTAGA | AAATTAACCG | GAGTTGTCCA | TAAAATGGGA | ACTACAGTTG  | 450 |
| 45 | TATTTATAAA | CCAAATTCGT | ATGAAAATCG | GCGCTATGGG | CTATGGCACT  | 500 |
|    | CCTGAAACTA | CTACTGGCGG | AAATGCGCTT | AAATTTTACG | CTTCAGTTAG  | 550 |
|    | ACTTGACGTA | CGTAAATAG  | CTACTTTAAA | ACAGAGCGAT | GAGCCAATCG  | 600 |
|    | GAAACCGCGT | AAAAGTAAAA | GTAGTAAAAA | ACAAAGTCGC | TCCTCCTTTT  | 650 |
|    | AGACAAGCCG | AATTTGATAT | CATGTTTGGG | GAAGGTATCA | GCAAAGAAGG  | 700 |
| 50 | AGAGATAATA | GATTACGGCG | TAAAACCTTG | TATTATCGAT | AAAAGCGGCG  | 750 |
|    | CTTGGTTTAT | CTATGATAAT | TCAAAATTAG | GTCAAGGCAG | AGAAAACCTCA | 800 |
|    | AAAGCGTTTT | TAAA       |            |            |             | 814 |

## 2) INFORMATION FOR SEQ ID NO: 1868

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni jejuni*  
 (B) STRAIN: ATCC 33560

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868

```

GATAGCATAG GCWCAGGTTC AGTTGGACTT GATCTTGCTT TAGGTATAGG      50
CGGTGTTCCA AAAGGAAGAA TTATAGAAAT TTATGGGCTT GAAAGTTCAG      100
GTAAAACTAC TCTAACTCTA CACATTATCG CAGAATGCCA AAAAGCAGGT      150
GGGGTTTGTG CTTTTATCGA TGCAGAACAT GCACTTGATG TGAAATATGC      200
TAAAAATTTA GGTGTAAATA CAGATGATTT GTATGTTTCT CAACCTGATT      250
TTGGAGAGCA AGCCTTAGAA ATTGTAGAAA CTATAGCWAG AAGTGGTGCA      300
GTAGATCTTA TWGTAGTAGA TAGCGTTGCA GCWCTTACCC CAAAAGCAGA      350
AATTGAAGGC GATATGGGCG ATCARCATGT AGGACTTCAA GCAAGACTTA      400
TGTCTCAAGC TCTAAGAAAA CTTACAGGTA TAGTTCATAA AATGAATACC      450
ACAGTAATTT TCATCAACCA AATTCGTATG AAAATCGGTG CTATGGGTTA      500
TGGTACTCCT GAAACCACAA CAGGTGGAAA TGCATTAAAA TTTTATGCTT      550
CTGTGCGTTT AGATGTTAGA AAAGTAGCAA CCTTAAAMCA AAACGWAGAM      600
CCTATAGGAA ACCGCGTTAA AGTAAAAGTA GTTAAAAATA AAGTTGCTCC      650
TCCATTCAGM CAAGCTGAAT TTGATGTGAT GTTTGGAGAG GGTTTAAGCC      700
GTGAAGGTGA ATTGATCGAT TATGGTGTA AACTTGATAT CGTAGATAAA      750
AGTGGTGCGT GGTTTCTTA TAAAGATAAA AAACCTGGAC AAGGTAGAGA      800
AAATTCAAAA GCTTTCTTAA AAGA                                     824

```

## 2) INFORMATION FOR SEQ ID NO: 1869

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*  
 (B) STRAIN: ATCC 14025

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869

```

AGAAAGTTCT GGTAACAACAA CGGTTGCACT GCATGCGATT GCAGAAGTTC      50

```

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| AAAAACATGG    | CGGGACGGCA | GCCTTTATTG | ATGCCGAGCA | CGCGTTGGAC | 100 |
| CCTCAATACG    | CACAACGTCT | AGGTGTAAAC | ATTGATGAAT | TGCTGCTATC | 150 |
| ACAACCAGAT    | ACTGGGGAAC | AAGGCTTAGA | AATTGCAGAT | GCTTTAGTTT | 200 |
| CAAGTGGCGC    | AGTCGATATT | ATCGTTATTG | ACTCGGTGGC | CGCGCTAGTC | 250 |
| 5 CCCC GTGCTG | AAATCGATGG | CGAGATGGGT | GATGCGCACG | TTGGTCTGCA | 300 |
| GGCTCGTTTG    | ATGTCACAAG | CATTGCGCAA | GCTGTCAGGC | TCTATCAACA | 350 |
| AAACAAAGAC    | TATCGCCGTC | TTTATTAACC | AAATTCGT   |            | 388 |

2) INFORMATION FOR SEQ ID NO: 1870

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| TGAAAGTTCA    | GGTAAAACAA | CAGTTGCACT | ACACGCTATT | GCAGAAGTAC | 50  |
| AAAAAAATGG    | CGGAACGGCC | GCTTTCATTG | ATGCTGAGCA | TGCGTTAGAT | 100 |
| CCGCAATATG    | CACAAAAATT | AGGTGTGAAT | ATCGATGAAC | TACTTCTTTC | 150 |
| 30 ACAGCCTGAC | ACAGGAGAAC | AAGGTCTAGA | GATCGCTGAT | GCTTTAGTAT | 200 |
| CAAGTGGGGC    | TGTAGATATC | GTAGTAGTCG | ATTCAGTTGC | TGCTTTAGTT | 250 |
| CCACGAGCAG    | AAATCGACGG | CGAAATGGGT | GACTCACATG | TCGGGTTACA | 300 |
| AGCACGTTTG    | ATGTCTCAAG | CATTGCGTAA | ACTCTCTGGT | TCGATCAACA | 350 |
| 35 AAACAAAAAC | AATCGCTATT | TTCATCAACC | AAATCCGT   |            | 388 |

2) INFORMATION FOR SEQ ID NO: 1871

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*  
 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871

|   |            |            |            |            |            |     |
|---|------------|------------|------------|------------|------------|-----|
|   | AGAGAGTTCC | GGTAAAACAA | CTGTTGCGCT | TCATGCAATT | GCGGAAGTAC | 50  |
|   | AAGCACAAGG | CGGAACAGCA | GCATTTATCG | ATGCTGAGCA | TGCGTTGGAT | 100 |
|   | CCGGCTTATG | CTAAAAACCT | AGGTGTAAAT | ATTGATGAAT | TATTACTATC | 150 |
|   | TCAACCAGAT | ACAGGAGAAC | AAGCTTTAGA | GATTGCTGAA | GCTTTAGTTA | 200 |
| 5 | GAAGTGGTGC | AGTTGATATG | TTAGTAATTG | ACTCCGTTGC | AGCACTTGTA | 250 |
|   | CCACGTGCTG | AAATCGAAGG | CGAGATGGGC | GATGCTCATG | TTGGATTACA | 300 |
|   | AGCACGTTTA | ATGTCCCAAG | CATTGCGTAA | ACTTTCTGGT | GTTATTAATA | 350 |
|   | AATCAAAAAC | CATTGCTATT | TTCATTAACC | AAATTCGT   |            | 388 |

10

## 2) INFORMATION FOR SEQ ID NO: 1872

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 388 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*  
 (B) STRAIN: ATCC 49456

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872

|    |             |            |            |            |            |     |
|----|-------------|------------|------------|------------|------------|-----|
|    | AGAGTCATCT  | GGTAAGACAA | CGGTTGCCCT | TCATGCAGTT | GCGCAAGCAC | 50  |
|    | AAAAAGAAGG  | TGGTATTGCT | GCCTTTATCG | ATGCGGAACA | TGCCCTTGAT | 100 |
| 30 | CCAGCTTATG  | CTGCGGCCCT | TGGTGTCAAC | ATTGACGAAT | TGCTCTTGTC | 150 |
|    | ACAACCAGAC  | TCAGGAGAGC | AAGGTCTTGA | GATTGCAGGA | AAATTGATTG | 200 |
|    | ACTCAGGAGC  | CGTGGATCTT | GTCGTAGTCG | ACTCAGTTGC | GGCCCTTGTC | 250 |
|    | CCTCGTGCGG  | AAATTGATGG | AGATATCGGT | GATAGCCACG | TTGGTTTGCA | 300 |
|    | GGCTCGTATG  | ATGAGCCAGG | CTATGCGTAA | ACTTGGTGCT | TCTATCAATA | 350 |
| 35 | AAACCAAAAAC | AATTGCCATC | TTTATCAACC | AATTGCGT   |            | 388 |

## 2) INFORMATION FOR SEQ ID NO: 1873

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus oralis*  
 (B) STRAIN: ATCC 35037

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GAACATGACG | CCGACTTTTT | CACGCAATTG | GTTGATAAAG | ATGGCAATTG | 50  |
|    | TTTTGGTTTT | ATTGATAGAA | GCTCCGAGTT | TACGCATGGC | CTGGCTCATC | 100 |
|    | ATTCGAGCCT | GCAAACCAAC | GTGACTGTCT | CCAATATCCC | CATCAATTTT | 150 |
| 5  | CGCACGAGGT | ACAAGGGCCG | CAACTGAGTC | GATAACGACA | AGGTCAACTG | 200 |
|    | CACCTGAGTC | AATCAATTTT | CCAGCAATTT | CAAGACCTTG | TTCACCTGAG | 250 |
|    | TCTGGTTGTG | ACAAGAGCAA | TTCGTCAATA | TTCACACCAA | GGGCTGCAGC | 300 |
|    | ATAGGCTGGG | TCAAGAGCAT | GTTCCGCATC | GATAAAGGCT | GCAATACCAC | 350 |
|    | CTTCTTTCTG | TGCTTGCGCA | ACAGCGTGAA | GGGCAACCGT | TGTCTTACCA | 400 |
| 10 | GATGATTCTG | GCGCRTACAY | TTCGATGATA |            |            | 430 |

## 2) INFORMATION FOR SEQ ID NO: 1874

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*  
 (B) STRAIN: ATCC 64746

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 30 | TTGTCGTTGT | TGCTGCCTCC | GACGGTCAGA | TGTAGGTGGA | ACATCTTGGG | 50  |
|    | AAATACGTCG | TAAAACACGT | CGCTTACGTT | TTCGCGAATA | GGCCCCAGAC | 100 |
|    | TCGTGAGCAT | TTGCTGCTCG | CCCGCCAGGT | TGGTGTCCAG | AAGATCGTTG | 150 |
|    | TCTTCGTCAA | CAAAATCGAT | GCTATTGATG | ATCCGGAGAT | GCTGGAAGT  | 200 |
|    | GTCGAACTCG | AGATGCGTGA | GCTGCTGAAC | AGCTACGGTT | TCGAGGGTGA | 250 |
| 35 | AGAGACTCCG | ATCATTTTCG | GTTCCGCTCT | CTGTGCTCTC | GAAGGACGCC | 300 |
|    | GTGACGACAT | CGGTAAAGAC | AGAATTGAGC | AGCTTATGAA | CGCTGTCGAC | 350 |
|    | ACCTGGATCC | CCACTCCTCA | GCGTGACCTC | GACAAACCTT | TCTTGATGTC | 400 |
|    | TGTCGAGGAA | GTGTTCTCTA | TCGCCGGCCG | TGGTACCGTG | GCTTCTGGTC | 450 |
|    | GTGTCGAGCG | TGGTATCTTG | AAGAAGGACT | CTGAGGTGTA | GATTGTTGGA | 500 |
| 40 | GGCTCCTTCG | AACCCAAGAA | GACCAAAGTC | ACCGACATTG | AAACCTTCAA | 550 |
|    | GAAGAGCTGT | GATGAATCGC | GTGCTGGTGA | CAACTCTGGT | CTCCTCCTGC | 600 |
|    | GTGGTATCCG | ACGTGAAGAC | GTCAAGCGTG | GTATGGTCAT | TGCTGTTCCC | 650 |
|    | GGCAGCACCA | AGGCTCACGA | CAAGTTCCTC | GTCTCCATGT | ACGTCCTGAC | 700 |
|    | CGAGGCGGAG | GGTGGTCGTC | GTAAGGCTT  | CGGTGCCAAC | TACCGTCCCC | 750 |
| 45 | AAGTCTTCAT | CCGTACTGCA | GGTAAGTTCC | CGCACACCGT | GTCCAGATCT | 800 |
|    | TCCGAGAGAT | TAGCGATATA | TGCTAATGAT | TCATCAGACG | AGGCTGCTGA | 850 |
|    | CCTCAGCTTC | CCTGACGGCG | ACCAATCTCG | CAGAGTTATG | CCTGGTGACA | 900 |
|    | ACGTCGAGAT | GATCCTGAAG | ACCCACCACC | CTGTTGCTGC | TGAGGCT    | 947 |

50

## 2) INFORMATION FOR SEQ ID NO: 1875

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus versicolor*  
 (B) STRAIN: WSA-175

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875

```

15  GCTGCTTCCG ATGGTCAAAT GTACGTCAAC CTTATATACA CCCTCTGATA      50
    TGACAGAATG TCGCCTAACA GCACGCGTGA ACTAGGCCCC AAACCCGTGA      100
    GCACTTGCTG CTTGCCCCGCC AGGTCGGTGT CCAGAAGATT GTTGTGTTCG      150
    TCAACAAGGT TGATGCCGTC GATGACCCTG AGATGTTGGA ACTTGTGAG      200
    CTGGAAATGC GTGAGCTTCT CAGCACTTAC GGCTTCGAAG GCGAGGAGAC      250
20  CCCTATCATC TTCGGTTCCG CCCTATGCGC CCTCGAGGGT CGCCGCCCCG      300
    ATATCGGTAC TGAGCGAATT GACAGCCTTC TTGAGGCCGT TGACACCTGG      350
    ATCCCTACCC CTCAGCGTGA CCTGGACAAG CCTTTCCTGA TGTCTGTCGA      400
    GGAGGTCTTC TCCATTGCCG GTCGTGGTAC CGTTGCCTCT GGCCGTGTTG      450
    AGCGTGGTCT CCTTAAGAAG GACAGCGAGG TCGAGATTCT CGGAGGTGGT      500
25  CAGGTCATGA AGACCAAGGT CACTGACATT GAGACATTCA AGAAGCACTG      550
    TGACGAATCC CGTGCTGGTG ACAACTCCGG TCTTCTTCTC CGTGGTATCC      600
    GCCGTGAGGA TGTCAAGCGC GGTATGGTTA TTGCTGCTCC CGCCTCTATC      650
    AAGGCCCACA AGAAGTTCAT GGTCTCCATG TACGTCCTCA CTGAGGCAGA      700
    AGGTGGCCGT CGCAGTGGCT TCGGTGTCAA CTATCGTCCC CAGGCTTACA      750
30  TTCGCACTGC TGGTAAGTTT TCAAAACATT CGACCTCTCG CCTTAGAAGA      800
    AGAATACCTC TAACCTGTAT TTAGACGAGG CTTGCGACCT TTCTTTCCCC      850
    GATGGCGACA TGAGCCGCCG TGTCATGCCT GGTGACAACG TGGAATGAT      900
    CCTCAACCTC AACAACCCTG TCG                                923
  
```

## 2) INFORMATION FOR SEQ ID NO: 1876

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Basidiobolus ranarum*  
 (B) STRAIN: ATCC 24670

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876

```

CATCATTGTT GTGTCCGCCA CTGATGGTCA AATGCCTCAA ACTCGTGAGC      50
  
```

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATTTGTTGTT | GGCTCGCCAA | GTTGGTGTCC | AACACTTGGT | TGTCTTCATC | 100 |
|    | AACAAGGTTG | ATGCCGTTGA | TGATCCTGAA | ATGTTGGAGT | TGGTCGAGAT | 150 |
|    | GGAAATGCGT | GATTTGCTTT | CCCAATACGG | TTTCCCCGGA | GACAACGTCC | 200 |
|    | CCATTATCCA | GGGTTCGCT  | CTCTGCGCTC | TTGAGGACCG | CAACCCCGAG | 250 |
| 5  | ATCGGCCGTA | ACGCCATCAT | GAAGTTGATG | GAGGCTGTTG | ATAGCAGCAT | 300 |
|    | CCCCACCCCT | GCCCGTGATT | TGGACAAACC | TTTCCTCATG | CCCGTTGAAG | 350 |
|    | ATGTGTTCTC | CATCTCTGGC | CGTGGTACTG | TTGCCACTGG | ACGTGTTGAG | 400 |
|    | CGTGGTATGG | TCACCAAGGG | TACTGAAGTT | GAAATCGTCG | GTATGGGCGA | 450 |
|    | GCACTTCAAG | ACCACCTTGA | CCGGTATTGA | AATGTTCCAC | AAGGAATTGG | 500 |
| 10 | ACAAGGGTAT | GGCTGGTGAC | AACATGGGTT | GCTTGCTTCG | TGGTGTCAAG | 550 |
|    | CGTGAGCAAG | TCCGTCTGGG | TATGGTTATC | TGTGCCCCCG | GATCCGTCAA | 600 |
|    | GCCACATAAG | AAGTTCATGG | CTCAGCTCTA | CATTCTCACC | AAGGATGAGG | 650 |
|    | GAGGCCGCCA | CACTCCCTTC | GTCAACAACT | ACCGCCCACA | AATGTTCTTC | 700 |
|    | AGAACTGTTG | ATGTTACCGC | CATCCTTAAG | CACCCCCCTG | GTACCCCCGA | 750 |
| 15 | TGCTGATGAG | AAGATGGTCA | TGCCCGGAGA | CAACGTTCAA | CTCGAGTGCG | 800 |
|    | AGCTCTT    |            |            |            |            | 807 |

20 2) INFORMATION FOR SEQ ID NO: 1877

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter gracilis*  
 (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877

|    |            |            |             |             |            |     |
|----|------------|------------|-------------|-------------|------------|-----|
| 35 | AGTTGTTTCT | GCTGCGGATG | GTCCTATGCC  | TCAAACCTCGC | GAGCATATCT | 50  |
|    | TGCTTCTCTG | TCAAGTAGGC | GTTCCATACA  | TCGTAGTTTT  | CCTAAACAAA | 100 |
|    | ACCGATATGG | TCGATGATCC | GGATCTTTTA  | GAGTTAGTTG  | AAGAGGAAGT | 150 |
|    | TAGAGATCTT | TTAAAAGAGT | ATAAATTCCT  | TGGCGACGAA  | ACCCCAATCA | 200 |
| 10 | TTAAGGGTTC | TGCTCTTAAG | GCTCTTGAGG  | AAGCTAAGGC  | CGGACAAGAC | 250 |
|    | GGCGAATGGT | CTGCAAAGAT | TATGGAGCTT  | ATGGACGCGG  | TTGATAGCTA | 300 |
|    | TATTCCAACT | CCTGTTTCGG | ATACTGATAA  | AGATTTCTCT  | CTTCCGATCG | 350 |
|    | AAGATATTTT | CTCGATTTCC | GGTCGCGGTA  | CCGTTGTAAAC | CGGTAGAATC | 400 |
|    | GAAAAAGGTA | TCGTTAAAGT | TGGTGATACT  | ATCGAGATCG  | TAGGTATTAA | 450 |
| 15 | ACCTACTCAG | ACTACTACCG | TCACTGGCGT  | TGAGATGTTT  | AGAAAAGAGA | 500 |
|    | TGGATCAAGG | TGAAGCCGGC | GATAATGTAG  | GTGTTTTATT  | GCGCGGTACT | 550 |
|    | AAGAAAGAGG | AAGTAGAGCG | CGGTATGGTT  | TTATGCAAAC  | CAAAATCGAT | 600 |
|    | CACTCCTCAT | ACTAAATTTG | AGGGCGAGGT  | TTATATCCTA  | ACTAAAGAAG | 650 |
|    | AAGGCGGACG | CCATACTCCA | TTCTTTAATA  | ATTATAGACC  | GCAGTTTTAC | 700 |
| 30 | GTTCGTACGA | CAGATGTTAC | CGGTTTCGATT | ACTCTTCCTG  | AAGGAACCGA | 750 |
|    | GATGGTTATG | CCGGGCGACA | ACGTTAAAT   | CACCGTTGAG  | CTAATCGCTC | 800 |
|    | CGATCG     |            |             |             |            | 806 |

## 2) INFORMATION FOR SEQ ID NO: 1878

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni jejuni*  
 (B) STRAIN: ATCC 33292

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878

|            |             |            |             |            |     |
|------------|-------------|------------|-------------|------------|-----|
| GCTGCAGATG | GCCCTATGCC  | ACAAACTAGA | GAGCACATTC  | TTCTTTCTCG | 50  |
| TCAAGTAGGC | GTTCCATATA  | TTGTTGTTTT | TATGAATAAA  | GCAGATATGG | 100 |
| TTGATGATGC | TGAACTTTTA  | GAGTTAGTTG | AAATGGAAAT  | TAGAGAATTA | 150 |
| TTAAGCTCTT | ATGATTTCCC  | AGGCGATGAT | ACACCTATTA  | TTTCTGGTTC | 200 |
| TGCTTTAAAA | GCTCTTGAAG  | AAGCTAAAGC | TGGACAAGAT  | GGTGAATGGT | 250 |
| CAGCAAAAAT | TATGGATCTT  | ATGGCTGCAG | TTGATAGCTA  | TATTCCAAC  | 300 |
| CCAACTCGTG | ATACTGAAAA  | AGACTTCTTG | ATGCCAATTG  | AAGATGTTTT | 350 |
| CTCAATTTCA | GGTCGTGGTA  | CTGTTGTAC  | AGGTAGAATT  | GAAAAAGGTG | 400 |
| TTGTAAAAGT | AGGTGATACT  | ATCGAAATCG | TTGGTATTAA  | AGATACTCAA | 450 |
| ACAACAAC   | TAACAGGTGT  | TGAAATGTTC | AGAAAAGAAA  | TGGATCAAGG | 500 |
| CGAAGCAGGA | GATAACGTAG  | GTGTTCTTCT | TCGTGGTACT  | AAAAAAGAAG | 550 |
| AAGTTATCCG | TGGTATGGTT  | CTTGCTAAAC | CAAAATCAAT  | TACTCCACAC | 600 |
| ACTGACTTCG | AAGCTGAAGT  | TTATATCTTA | AATAAAGATG  | AAGGTGGTAG | 650 |
| ACATACTCCA | TTCTTTAACA  | ACTATAGACC | ACAGTTTTTAT | GTAAGAACAA | 700 |
| CTGATGTTAC | AGGTTTCGATT | AAATTAGCTG | ATGGTGTTGA  | AATGGTTATG | 750 |
| CCAGGTGAAA | ATGTGAGAAT  | TACTGTAAGC | TTGATCGCTC  | CAGTAGCACT | 800 |
| TGAAGA     |             |            |             |            | 806 |

## 2) INFORMATION FOR SEQ ID NO: 1879

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*  
 (B) STRAIN: WSA-222

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879

|            |            |            |            |            |    |
|------------|------------|------------|------------|------------|----|
| ATGTATGCAA | CCGAGAGCAC | TCCCGGATCT | TGGTTTAAAT | GGCACTAATA | 50 |
|------------|------------|------------|------------|------------|----|



|    |            |             |             |            |             |     |
|----|------------|-------------|-------------|------------|-------------|-----|
|    | TAAGACAGGC | CTCAAAC TCG | AGAGCATTTA  | CTTCTCGCCC | GTCAGATCGG  | 100 |
|    | TATCCAAAAA | ATCGTCGTCT  | TCGTGAACAA  | GGTTGATGCC | ATCGAGGACA  | 150 |
|    | AAGAGATGTT | GGAGCTTGTT  | GAATTGGAGA  | TGCGTGAACT | CCTAACCAGC  | 200 |
|    | TACGGTTTCS | AGGGTGAAGA  | AACTCCCATC  | ATTTTTGGCT | CTGCTCTCTG  | 250 |
| 5  | TGCCCTCSAA | GGAAGACAAC  | CCGAGATCGG  | TGTTACCAAG | ATTGATGAGC  | 300 |
|    | TCTTGCAGGC | CGTCGACACC  | TGGATTCCCA  | CTCCTCAGCG | TGAGACTGAC  | 350 |
|    | AAGCCCTTCT | TGATGTCCAT  | TGAGGAAGTG  | TTCTCTATTT | CCGGACGAGG  | 400 |
|    | AACCGTTGTC | TCCGGCCGTG  | TGGAGCGTGG  | TATCCTCAAG | AAGGACTCCG  | 450 |
|    | AAGTTGAAAT | TGTCGGCGGT  | TCGCCCAGAG  | CAATCAAAAC | CAAGGTTACC  | 500 |
| 10 | GATATCGAAA | CCTTTAAGAA  | GTCTTGCGAC  | GAGTCTCGCG | CTGGTGATAA  | 550 |
|    | CTCCGGCTTG | CTCCTACGAG  | GCGTTAAGCG  | TGAAGATATT | AGCCGTGGCA  | 600 |
|    | TGGTCGTCGC | TGTACCAGGA  | AGTGTC AAGG | CCCATACTGA | ATTCTTAGTT  | 650 |
|    | TCGCTTTACG | TCCTCACC GA | AGCTGAGGGT  | GGGCGCAAAT | CTGGATT CAG | 700 |
|    | CAGCAAGTAC | CGCCCACAGA  | TGTTCAATCG  | CACTGCCGGT | ATGTAATACT  | 750 |
| 15 | GTGATAATTT | CGTTGACATG  | GTA CTGATTG | AATTCTATAG | ACGAAGCGGC  | 800 |
|    | TCAGCTCAGC | TGGCCCGGAG  | AAGATCAAGA  | CAAGATGGCT | ATGCCAGGAG  | 850 |
|    | ACAATATCGA | AATGATTTGC  | ACCACCTTGC  | ACCCAGTTGC | CGCCGA      | 896 |

20

## 2) INFORMATION FOR SEQ ID NO: 1880

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*  
 (B) STRAIN: ATCC 14976

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880

|    |            |             |            |            |            |     |
|----|------------|-------------|------------|------------|------------|-----|
|    | CTGGTAGTTG | CTGCGACTGA  | CGGCCCAATG | CCTCAGACYC | GTGAGCACAT | 50  |
|    | CCTGCTGGGT | CGCCAGGTTG  | GCGTGCCATA | CATCATCGTG | TTCTTGAACA | 100 |
|    | AATGTGACAT | GGTTGATGAT  | GAAGAGCTGC | TGGAGCTGGT | TGAAATGGAA | 150 |
| 10 | GTMCGTGACC | TGCTGTCACA  | GTACGACTTC | CCAGGCGACG | ACACGCCAAT | 200 |
|    | CGTGCRYGGT | TCTGCGCTGA  | AAGCGCTGGA | RGGCGAAGCA | GAGTGGGAAG | 250 |
|    | CGAAGATCAT | CGAACTGGCT  | GGCCATCTGG | ATAACTACAT | CCCGGAACCA | 300 |
|    | GAGCGTGCGA | TTGACAAACC  | GTTCTTGCTG | CCAATTGAAG | ACGTGTTCTC | 350 |
|    | CATCTCTGGC | CGTGGTACCG  | TTGTTACCGG | TCGTGTAGAG | CGCGGTRTSG | 400 |
| 15 | TTAAAGTGGG | TGAAGAAGTT  | GAAATCGTTG | GTATCAAAGA | TACCGTGAAA | 450 |
|    | TCAACCTGTA | CCGGCGTTGA  | GATGTTCCGT | AAGCTGCTGG | ACGAAGGCCG | 500 |
|    | TGCGGGTGAG | AACTGTGGTA  | TCCTGCTGCG | CGGTATCAAG | CGCGAAGATA | 550 |
|    | TCCAGCGTGG | TCAGGTCTCTG | GCGAAGCCAG | GCACCATCAA | GCCACACACC | 600 |
|    | AAGTTCGAGT | CAGAAGTTTA  | TATTCTGTCT | AAAGACGAAG | GCGGCCGTCA | 650 |
| 30 | TACTCCGTTT | TTCAAAGGCT  | ACCGTCCACA | GTTCTACTTC | CGTACTACTG | 700 |
|    | ACGTGACCGG | GACTATCGAA  | CTGCCAGAAG | GCGTTGAGAT | GGTGATGCCA | 750 |
|    | GGCGACAACA | TTCAGATGGT  | TGTGACCCTG | ATCCACCCGA | TCGCCATG   | 798 |

## 2) INFORMATION FOR SEQ ID NO: 1881

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Typhimurium  
 (B) STRAIN: ATCC 14028

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | ATCCTGGTTG | TTGCTGCGAC | TGACGGYCCG | ATGCCGCAGA | CCCGTGAGCA  | 50  |
|    | CATCCTGCTG | GGTCGTCAGG | TAGGCGTTCC | GTACATCATC | GTGTTCTCTGA | 100 |
| 20 | ACAAATGCGA | CATGGTTGAT | GACGAAGAGC | TGCTGGAAC  | GGTTGAAATG  | 150 |
|    | GAAGTTCGYG | AACTGCTGTC | TCAGTACGAC | TTCCCGGGCG | ACGACACTCC  | 200 |
|    | GATCGTTCGT | GGTTCTGCTC | TGAAAGCGCT | GGAAGGCGAC | GCAGAGTGGG  | 250 |
|    | AAGCGAAAAT | CATCGAACTG | GCTGGCTTCC | TGGATTCTTA | CATYCCGGAA  | 300 |
|    | CCAGAGCGTG | CGATTGACAA | GCCGTTCTTG | CTGCCGATCG | AAGACGTATT  | 350 |
| 25 | CTCCATCTCC | GGTCGTGGTA | CCGTTGTAC  | CGGTCGTGTA | GARCGCGGTA  | 400 |
|    | TCATCAAAGT | GGGCGAAGAA | GTTGAAATCG | TTGGTATCAA | AGAGACTCAG  | 450 |
|    | AAGTCTACCT | GTAAGGCGT  | TGAAATGTTT | CGCAAATGCT | TGGACGAAGG  | 500 |
|    | CCGTGCCGGT | GAGAACGTAG | GTGTTCTGCT | GCGTGATATC | AAACGTGAAG  | 550 |
|    | AAATCGAACG | TGGTCAGGTA | CTGGCTAAGC | CGGGCACCAT | CAAGCCGCAC  | 600 |
| 30 | ACCAAGTTCG | AATCTGAAGT | GTACATTCTG | TCCAAAGATG | AAGGCGGCCG  | 650 |
|    | TCATACTCCG | TTCTTCAAAG | GCTACCGTCC | GCAGTTCTAC | TTCCGTACTA  | 700 |
|    | CTGACGTGAC | TGGCACCATC | GAAGTCCCGG | AAGGCGTAGA | GATGGTAATG  | 750 |
|    | CCGGGCGACA | ACATCAAAT  | GGTTGTTACC | CTGATCCACC | CGATCGCGAT  | 800 |
| 35 | GGACGACGGT |            |            |            |             | 810 |

## 2) INFORMATION FOR SEQ ID NO: 1882

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*  
 (B) STRAIN: BM10711  
 (C) ACCESSION NUMBER : AF015628

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | ATGAATTTTT | ATTTAGAGGA | GTTTAACTTG | TCTATTCCCG | ATTCAGGTCC  | 50  |
|    | ATACGGTATA | ACTTCATCAG | AAGACGGAAA | GGTATGGTTC | ACACAACATA  | 100 |
|    | AGGCAAACAA | AATCAGCAGT | CTAGATCAGA | GTGGTAGGAT | AAAAGAATTC  | 150 |
| 5  | GAAGTTCCTA | CCCCTGATGC | TAAAGTGATG | TGTTTAATTG | TATCTTCACT  | 200 |
|    | TGGAGACATA | TGGTTTACAG | AGAATGGTGC | AAATAAAATC | GGAAAGCTCT  | 250 |
|    | CAAAAAAAGG | TGGCTTTACA | GAATATCCAT | TGCCACAGCC | GGATTCTGGT  | 300 |
|    | CCTTACGGAA | TAACGGAAGG | TCTAAATGGC | GATATATGGT | TTACCCAATT  | 350 |
|    | GAATGGAGAT | CGTATAGGAA | AGTTGACAGC | TGATGGGACT | ATTTATGAAT  | 400 |
| 10 | ATGATTTGCC | AAATAAGGGA | TCTTATCCTG | CTTTTATTAC | TTTAGGTTCG  | 450 |
|    | GATAACGCAC | TTTGGTTTAC | GGAGAACCAA | AATAATTCTA | TTGGAAGGAT  | 500 |
|    | TACAAATACA | GGGAAATTAG | AAGAATATCC | TCTACCAACA | AATGCAGCGG  | 550 |
|    | CTCCAGTGGG | TATCACTAGT | GGTAACGATG | GTGCACTCTG | GTTTGTCTGAA | 600 |
|    | ATTATGGGCA | ACAAAATAGG | TCGAATCACT | ACAACCTGGT | AGATTAGCGA  | 650 |
| 15 | ATATGATATT | CCAACTCCAA | ACGCACGTCC | ACACGCTATA | ACCGCGGGGA  | 700 |
|    | AAAATAGCGA | AATATGGTTT | ACTGAATGGG | GGGCAAATCA | AATCGGCAGA  | 750 |
|    | ATTACAAACG | ACAAAACAAT | TCAAGAATAT | CAACTTCAA  | CAGAAAATGC  | 800 |
|    | GGAACCTCAT | GGTATTACCT | TTGGAAAAGA | TGGATCCGTA | TGGTTTGCAT  | 850 |
|    | TAAAATGTAA | AATTGGGAAG | CTGAATTTGA | ACGAATGA   |             | 888 |

20

## 2) INFORMATION FOR SEQ ID NO: 1883

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883

35 AGCCGCTTGA GCAAATTAAA CTA

23

## 2) INFORMATION FOR SEQ ID NO: 1884

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884

50

GTATCCCGCA GATAAATCAC CAC

23

## 2) INFORMATION FOR SEQ ID NO: 1885

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885

AGCGAAAAAC ACCTTGCCGA C

21

## 2) INFORMATION FOR SEQ ID NO: 1886

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886

GACGCCCCGCG CCACCACT

18

## 2) INFORMATION FOR SEQ ID NO: 1887

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887

GACGCCCCGCG ACACCACTA

19

## 2) INFORMATION FOR SEQ ID NO: 1888

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888

GACGCCCCGCA ACACCACTA

19

10

2) INFORMATION FOR SEQ ID NO: 1889

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889

GTTCGCAACT GCAGCTGCTG

20

25

2) INFORMATION FOR SEQ ID NO: 1890

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 19 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890

40

TTCGCAACGG CAGCTGCTG

19

2) INFORMATION FOR SEQ ID NO: 1891

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891

CCGGAGCTGC CGAICGGG

18

5

2) INFORMATION FOR SEQ ID NO: 1892

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892

CGGAGCTGCC AARCGGGG

18

20

2) INFORMATION FOR SEQ ID NO: 1893

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893

35 GGAGCTGGCG ARCGGGGT

18

2) INFORMATION FOR SEQ ID NO: 1894

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894

50

GACCGGAGCT AGCGARCG

18

## 2) INFORMATION FOR SEQ ID NO: 1895

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895

CGGAGCTAGC AARCGGGGT

19

## 2) INFORMATION FOR SEQ ID NO: 1896

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896

GAAACGGAAC TGAATGAGGC G

21

## 2) INFORMATION FOR SEQ ID NO: 1897

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897

CATTACCATG GGCGATAACA G

21

## 2) INFORMATION FOR SEQ ID NO: 1898

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898

CCATTACCAT GAGCGATAAC AG

22

10

2) INFORMATION FOR SEQ ID NO: 1899

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: 15571
- (C) ACCESSION NUMBER: AF124984

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 30 | ATGCGTTATA | TTCGCCTGTG | TATTATCTCC | CTGTTAGCCA | CCCTGCCGCT | 50  |
|    | GGCGGTACAC | GCCAGCCCGC | AGCCGCTTGA | GCAAATTAAA | CTAAGCGAAA | 100 |
|    | GCCAGCTGTC | GGGCCGCGTA | GGCATGATAG | AAATGGATCT | GGCCAGCGGC | 150 |
|    | CGCACGCTGA | CCGCCTGGCG | CGCCGATGAA | CGCTTTCCCA | TGATGAGCAC | 200 |
|    | CTTTAAAGTA | GTGCTCTGCG | GCGCAGTGCT | GGCGCGGGTG | GATGCCGGTG | 250 |
| 35 | ACGAACAGCT | GGAGCGAAAG | ATCCACTATC | GCCAGCAGGA | TCTGGTGGAC | 300 |
|    | TACTCGCCGG | TCAGCGAAAA | ACACCTTGCC | GACGGCATGA | CGGTCGGCGA | 350 |
|    | ACTCTGCGCC | GCCGCCATTA | CCATGAGCGA | TAACAGCGCC | GCCAATCTGC | 400 |
|    | TACTGGCCAC | CGTCGGCGGC | CCCGCAGGAT | TGACTGCCTT | TTTGCGCCAG | 450 |
|    | ATCGGCGACA | ACGTCACCCG | CCTTGACCGC | TGGGAAACGG | AACTGAATGA | 500 |
| 40 | GGCGCTTCCC | GGCGACGCCC | GCGACACCAC | TACCCCGGCC | AGCATGGCCG | 550 |
|    | CGACCCTGCG | CAAGCTGCTG | ACCAGCCAGC | GTCTGAGCGC | CCGTTGCGAA | 600 |
|    | CGGCAGCTGC | TGCAGTGGAT | GGTGGACGAT | CGGGTCGCCG | GACCGTTGAT | 650 |
|    | CCGCTCCGTG | CTGCCGCGCG | GCTGGTTTAT | CGCCGATAAG | ACCGGAGCTG | 700 |
|    | GCGAGCGGGG | TGCGCGCGGG | ATTGTCGCCC | TGCTTGGCCC | GAATAACAAA | 750 |
| 45 | GCAGAGCGCA | TTGTGGTGAT | TTATCTGCGG | GATACCCCGG | CGAGCATGGC | 800 |
|    | CGAGCGAAAT | CAGCAAATCG | CCGGGATCGG | CGCGGCGCTG | ATCGAGCACT | 850 |
|    | GGCAACGCTA | A          |            |            |            | 861 |

50

2) INFORMATION FOR SEQ ID NO: 1900

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 780 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: SLK-47
- (C) ACCESSION NUMBER: Y11069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900

```

15 CTGTTAGCCA CCCTGCCGCT GGCGGTACAC GCCAGCCCGC AGCCGCTTGA      50
   GCAAATTAAA CTAAGCGAAA GCCAGCTGTC GGGCCGCGTA GGCATGATAG      100
   AAATGGATCT GGCCAGCGGC CGCACGCTGA CCGCCTGGCG CGCCGATGAA      150
   CGCTTTCCCA TGATGAGCAC CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT      200
   GGCGCGGGTG GATGCCGGTG ACGAACAGCT GGAGCGAAAG ATCCACTATC      250
20 GCCAGCAGGA TCTGGTGGAC TACTCGCCGG TCAGCGAAAA ACACCTTGCC      300
   GACGGCATGA CGGTCGGCGA ACTCTGCGCC GCCGCCATTA CCATGAGCGA      350
   TAACAGCGCC GCCAATCTGC TACTGGCCAC CGTCGGCGGC CCCGCAGGAT      400
   TGACTGCCTT TTTGCGCCAG ATCGGCGACA ACGTCACCCG CCTTGACCGC      450
   TGGGAAACGG AACTGAATGA GGCGCTTCCC GGCGACGCCG GCGCCACCAC      500
25 TACCCCGGCC AGCATGGCCG CGACCCTGCG CAAGCTGCTG ACCAGCCAGC      550
   GTCTGAGCGC CCGTTCGCAA CGGCAGCTGC TGCAGTGGAT GGTGGACGAT      600
   CGGGTCGCCG GACCGTTGAT CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT      650
   CGCCGATAAG ACCGGAGCTG GCGAGCGGGG TGCGC GCGGG ATTGTCGCCC      700
   TGCTTGGCCC GAATAACAAA GCAGAGCGCA TTGTGGTGAT TTATCTGCGG      750
30 GATACCCCGG CGAGCATGGC CGAGCGAAAT      780

```

2) INFORMATION FOR SEQ ID NO: 1901

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: U92041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901

```

50 ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT      50
   GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA      100
   GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC      150
   CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC      200

```

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CTTTAAAGTA | GTGCTCTGCG | GCGCAGTGCT | GGCGCGGGTG | GATGCCGGTG | 250 |
|    | ACGAACAGCT | GGAGCGAAAG | ATCCACTATC | GCCAGCAGGA | TCTGGTGGAC | 300 |
|    | TACTCGCCGG | TCAGCGAAAA | ACACCTTGCC | GACGGCATGA | CGGTCGGCGA | 350 |
|    | ACTCTGCGCC | GCCGCCATTA | CCATGAGCGA | TAACAGCGCC | GCCAATCTGC | 400 |
| 5  | TACTGGCCAC | CGTCGGCGGC | CCCGCAGGAT | TGACTGCCTT | TTTGCGCCAG | 450 |
|    | ATCGGCGACA | ACGTCACCCG | CCTTGACCGC | TGGGAAACGG | AACTGAATGA | 500 |
|    | GGCGCTTCCC | GGCGACGCC  | GCAACACCAC | TACCCCGGCC | AGCATGGCCG | 550 |
|    | CGACCCTGCG | CAAGCTGCTG | ACCAGCCAGC | GTCTGAGCGC | CCGTTTCGCA | 600 |
|    | CGGCAGCTGC | TGCAGTGGAT | GGTGGACGAT | CGGGTCGCCG | GACCGTTGAT | 650 |
| 10 | CCGCTCCGTG | CTGCCGCGCG | GCTGGTTTAT | CGCCGATAAG | ACCGGAGCTG | 700 |
|    | GCGAGCGGGG | TGCGCGCGGG | ATTGTCGCCC | TGCTTGGCCC | GAATAACAAA | 750 |
|    | GCAGAGCGCA | TTGTGGTGAT | TTATCTGCGG | GATACCCCGG | CGAGCATGGC | 800 |
|    | CGAGCGAAAT | CAGCAAATCG | CCGGGATCGG | CGCGGCGCTG | ATCGAGCACT | 850 |
|    | GGCAACGCTA | A          |            |            |            | 861 |

## 2) INFORMATION FOR SEQ ID NO: 1902

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 861 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(B) STRAIN: 803

(C) ACCESSION NUMBER: AF164577

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 35 | ATGCGTTATA | TTCGCCTGTG | TATTATCTCC | CTGTTAGCCA | CCCTGCCGCT | 50  |
|    | GGCGGTACAC | GCCAGCCCGC | AGCCGCTTGA | GCAAATTAAA | CAAAGCGAAA | 100 |
|    | GCCAGCTGTC | GGGCCGCGTA | GGCATGATAG | AAATGGATCT | GGCCAGCGGC | 150 |
|    | CGCACGCTGA | CCGCCTGGCG | CGCCGATGAA | CGCTTTCCCA | TGATGAGCAC | 200 |
|    | CTTTAAAGTA | GTGCTCTGCG | GCGCAGTGCT | GGCGCGGGTG | GATGCCGGTG | 250 |
| 40 | ACGAACAGCT | GGAGCGAAAG | ATCCACTATC | GCCAGCAGGA | TCTGGTGGAC | 300 |
|    | TACTCGCCGG | TCAGCGAAAA | ACACCTTGCC | GACGGCATGA | CGGTCGGCGA | 350 |
|    | ACTCTGCGCC | GCCGCCATTA | CCATGAGCGA | TAACAGCGCC | GCCAATCTGC | 400 |
|    | TGCTGGCCAC | CGTCGGCGGC | CCCGCAGGAT | TGACTGCCTT | TTTGCGCCAG | 450 |
|    | ATCGGCGACA | ACGTCACCCG | CCTTGACCGC | TGGGAAACGG | AACTGAATGA | 500 |
| 45 | GGCGCTTCCC | GGCGACGCC  | GCGACACCAC | TACCCCGGCC | AGCATGGCCG | 550 |
|    | CGACCCTGCG | CAAGCTGCTG | ACCAGCCAGC | GTCTGAGCGC | CCGTTTCGCA | 600 |
|    | CGGCAGCTGC | TGCAGTGGAT | GGTGGACGAT | CGGGTCGCCG | GACCGTTGAT | 650 |
|    | CCGCTCCGTG | CTGCCGCGCG | GCTGGTTTAT | CGCCGATAAG | ACCGGAGCTG | 700 |
|    | CCGAGCGGGG | TGCGCGCGGG | ATTGTCGCCC | TGCTTGGCCC | GAATAACAAA | 750 |
| 50 | GCAGAGCGCA | TTGTGGTGAT | TTATCTGCGG | GATACGCCGG | CGAGCATGGC | 800 |
|    | CGAGCGAAAT | CAGCAAATCG | CCGGGATCGG | CGCGGCGCTG | ATCGAGCACT | 850 |
|    | GGCAACGCTA | A          |            |            |            | 861 |

## 2) INFORMATION FOR SEQ ID NO: 1903

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*  
 (B) STRAIN: ATCC 700603  
 (C) ACCESSION NUMBER: AF132290

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGCGTTATT | TTCGCCTGTG | TATTATCTCC | CTGTTAGCCA | CCCTGCCGCT | 50  |
|    | GGCGGTACAC | GCCAGCCCGC | AGCCGCTTGA | GCAAATTAAA | CTAAGCGAAA | 100 |
| 20 | GCCAGCTGTC | GGGCAGCGTA | GGCATGATAG | AAATGGATCT | GGCCAGCGGC | 150 |
|    | CGCACGCTGA | CCGCCTGGCG | CGCCGATGAA | CGCTTTCCCA | TGATGAGCAC | 200 |
|    | CTTTAAAGTA | GTGCTCTGCG | GCGCAGTGCT | GGCGCGGGTG | GATGCCGGTG | 250 |
|    | ACGAACAGCT | GGAGCGAAAG | ATCCACTATC | GCCAGCAGGA | TCTGGTGGAC | 300 |
|    | TACTCGCCGG | TCAGCGAAAA | ACACCTTGCC | GACGGCATGA | CGGTCGGCGA | 350 |
| 25 | ACTCTGTGCC | GCCGCCATTA | CCATGAGCGA | TAACAGCGCC | GCCAATCTGC | 400 |
|    | TGCTGGCCAC | CGTCGGCGGC | CCCGCAGGAT | TGACTGCCTT | TTTGCGCCAG | 450 |
|    | ATCGGCGACA | ACGTCACCCG | CCTTGACCGC | TGGGAAACGG | AACTGAATGA | 500 |
|    | GGCGCTTCCC | GGCGACGCCC | GCGACACCAC | TACCCCGGCC | AGCATGGCCG | 550 |
|    | CGACCCTGCG | CAAGCTGCTG | ACCAGCCAGC | GTCTGAGCGC | CCGTTGCGAA | 600 |
| 30 | CGGCAGCTGC | TGCAGTGGAT | GGTGGACGAT | CGGGTCGCCG | GACCGTTGAT | 650 |
|    | CCGCTCCGTG | CTGCCGGCGG | GCTGGTTTAT | CGCCGATAAG | ACCGGAGCTG | 700 |
|    | CCAAACGGGG | TGCGCGCGGG | ATTGTGCGCC | TGCTTGCCCC | GAATAACAAA | 750 |
|    | GCAGAGCGGA | TTGTGGTGAT | TTATCTGCGG | GATACGCCGG | CGAGCATGGC | 800 |
|    | CGAGCGAAAT | CAGCAAATCG | CCGGGATCGG | CGCGGCGCTG | ATCGAGCACT | 850 |
| 35 | GGCAACGCTA | ACCCGGCGGT | GGCCGCGCGC | GTTATCCGGC | TCGTAG     | 896 |

## 2) INFORMATION FOR SEQ ID NO: 1904

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (B) STRAIN: JC2926  
 (C) ACCESSION NUMBER: AF148851

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGCGTTATA | TTCGCCTGTG | TATTATCTCC | CTGTTAGCCA | CCCTGCCGCT | 50  |
|    | GGCGGTACAC | GCCAGCCCGC | AGCCGCTTGA | GCAAATTAAA | CTAAGCGAAA | 100 |
| 5  | GCCAGCTGTC | GGGCCGCGTA | GGCATGATAG | AAATGGATCT | GGCCAGCGGC | 150 |
|    | CGCACGCTGA | CCGCCTGGCG | CGCCGATGAA | CGCTTTCCCA | TGATGAGCAC | 200 |
|    | CTTTAAAGTA | GTGCTCTGCG | GCGCAGTGCT | GGCGCGGGTG | GATGCCGGTG | 250 |
|    | ACGAACAGCT | GGAGCGAAAG | ATCCACTATC | GCCAGCAGGA | TCTGGTGGAC | 300 |
|    | TACTCGCCGG | TCAGCGAAAA | ACACCTTGCC | GACGGCATGA | CGGTCGGCGA | 350 |
| 10 | ACTCTGCGCC | GCCGCCATTA | CCATGAGCGA | TAACAGCGCC | GCCAATCTGC | 400 |
|    | TACTGGCCAC | CGTCGGCGGC | CCCGCAGGAT | TGACTGCCTT | TTTGCGCCAG | 450 |
|    | ATCGGCGACA | ACGTCACCCG | CCTTGACCGC | TGGGAAACGG | AACTGAATGA | 500 |
|    | GGCGCTTCCC | GGCGACGCC  | GCGACACCAC | TACCCCGGCC | AGCATGGCCG | 550 |
|    | CGACCCTGCG | CAAGCTGCTG | ACCAGCCAGC | GTCTGAGCGC | CCGTTTCGAA | 600 |
| 15 | CGGCAGCTGC | TGCAGTGGAT | GGTGGACGAT | CGGGTCGCCG | GACCGTTGAT | 650 |
|    | CCGCTCCGTG | CTGCCGGCGG | GCTGGTTTAT | CGCCGATAAG | ACCGGAGCTA | 700 |
|    | GCGAGCGGGG | TGCGCGCGGG | ATTGTCGCCC | TGCTTGGCC  | GAATAACAAA | 750 |
|    | GCAGAGCGCA | TTGTGGTGAT | TTATCTGCGG | GATACCCCGG | CGAGCATGGC | 800 |
|    | CGAGCGAAAT | CAGCAAATCG | CCGGGATCGG | CGCGGCGCTG | ATCGAGCACT | 850 |
| 20 | GGCAACGCTA | A          |            |            |            | 861 |

## 2) INFORMATION FOR SEQ ID NO: 1905

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (C) ACCESSION NUMBER: AF096930

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 40 | ATGCGTTATA | TTCGCCTGTG | TATTATCTCC | CTGTTAGCCA | CCCTGCCGCT | 50  |
|    | GGCGGTACAC | GCCAGCCCGC | AGCCGCTTGA | GCAAATTAAA | CTAAGCGAAA | 100 |
|    | GCCAGCTGTC | GGGCCGCGTA | GGCATGATAG | AAATGGATCT | GGCCAGCGGC | 150 |
|    | CGCACGCTGA | CCGCCTGGCG | CGCCGATGAA | CGCTTTCCCA | TGATGAGCAC | 200 |
|    | CTTTAAAGTA | GTGCTCTGCG | GCGCAGTGCT | GGCGCGGGTG | GATGCCGGTG | 250 |
| 45 | ACGAACAGCT | GGAGCGAAAG | ATCCACTATC | GCCAGCAGGA | TCTGGTGGAC | 300 |
|    | TACTCGCCGG | TCAGCGAAAA | ACACCTTGCC | GACGGCATGA | CGGTCGGCGA | 350 |
|    | ACTCTGCGCC | GCCGCCATTA | CCATGAGCGA | TAACAGCGCC | GCCAATCTAC | 400 |
|    | TACTGGCCAC | CGTCGGCGGC | CCCGCAGGAT | TGACTGCCTT | TTTGCGCCAG | 450 |
|    | ATCGGCGACA | ACGTCACCCG | CCTTGACCGC | TGGGAAACGG | AACTGAATGA | 500 |
| 50 | GGCGCTTCCC | GGCGACGCC  | GCGACACCAC | TACCCCGGCC | AGCATGGCCG | 550 |
|    | CGACCCTGCG | CAAGCTGCTG | ACCAGCCAGC | GTCTGAGCGC | CCGTTTCGAA | 600 |
|    | CGGCAGCTGC | TGCAGTGGAT | GGTGGACGAT | CGGGTCGCCG | GACCGTTGAT | 650 |
|    | CCGCTCCGTG | CTGCCGGCGG | GCTGGTTTAT | CGCCGATAAG | ACCGGAGCTA | 700 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GCAAACGGGG | TGCGCGCGGG | ATTGTCGCCC | TGCTTGGCCC | GAATAACAAA | 750 |
| GCAGAGCGCA | TTGTGGTGAT | TTATCTGCGG | GATACGCCGG | CGAGCATGGC | 800 |
| CGAGCGAAAT | CAGCAAATCG | CCGGGATCGG | CGCGGCGCTG | ATCGAGCACT | 850 |
| GGCAACGCTA | A          |            |            |            | 861 |

5

## 2) INFORMATION FOR SEQ ID NO: 1906

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906

20 CCTTATTCCC TTTTGTGCGG

20

## 2) INFORMATION FOR SEQ ID NO: 1907

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907

35

CACCTATCTC AGCGATCTGT CT

22

## 40 2) INFORMATION FOR SEQ ID NO: 1908

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908

50

AACAGCGGTA AGATCCTTGA GAG

23

## 2) INFORMATION FOR SEQ ID NO: 1909

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909

ATGACTTGGT TAAGTACTCA CC

22

## 2) INFORMATION FOR SEQ ID NO: 1910

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910

ATGACTTGGT TGAGTACTCA CC

22

## 2) INFORMATION FOR SEQ ID NO: 1911

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911

CCATAACCAT GGGTGATAAC AC

22

## 2) INFORMATION FOR SEQ ID NO: 1912

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid

1000

(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912

CCATAACCAT GAGTGATAAC AC

22

2) INFORMATION FOR SEQ ID NO: 1913

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913

CGCCTTGATC ATTGGGAACC

20

2) INFORMATION FOR SEQ ID NO: 1914

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914

CGCCTTGATC GTTGGGAACC

20

2) INFORMATION FOR SEQ ID NO: 1915

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915

CGCCTTGATA GTTGGGAACC

20

5

2) INFORMATION FOR SEQ ID NO: 1916

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916

CGTGGGTCTT GCGGTATCAT

20

20

2) INFORMATION FOR SEQ ID NO: 1917

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917

CGTGGGTCTG GCGGTATCAT

20

35

2) INFORMATION FOR SEQ ID NO: 1918

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918

GTGGGTCTCA CGGTATCATT G

21

50



## 2) INFORMATION FOR SEQ ID NO: 1919

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919

CGTGGGTCTC TCGGTATCAT T

21

## 2) INFORMATION FOR SEQ ID NO: 1920

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920

CGTGGNTCTC GCGGTATCAT

20

## 2) INFORMATION FOR SEQ ID NO: 1921

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1921

CGTGGGTCTA GCGGTATCAT T

21

## 2) INFORMATION FOR SEQ ID NO: 1922

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922

GTTTTCCAAT GATTAGCACT TTTA

24

2) INFORMATION FOR SEQ ID NO: 1923

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923

GTTTTCCAAT GATAAGCACT TTTA

24

2) INFORMATION FOR SEQ ID NO: 1924

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924

GTTTTCCAAT GCTGAGCACT TTT

23

2) INFORMATION FOR SEQ ID NO: 1925

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925

CGTTTTCCAA TGATGAGCAC TTT

23

5

2) INFORMATION FOR SEQ ID NO: 1926

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926

GTTTTCCAAT GGTGAGCACT TTT

23

20

2) INFORMATION FOR SEQ ID NO: 1927

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Neisseria meningitidis*  
 (B) STRAIN: MC9690-129  
 (C) ACCESSION NUMBER: AF126482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1927

|    |  |     |
|----|--|-----|
| 40 | ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCTTTT TTGCGGCATT  | 50  |
|    | TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG | 100 |
|    | CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT GGATCTCAAC  | 150 |
|    | AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT | 200 |
|    | GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG | 250 |
| 45 | CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG | 300 |
|    | GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT | 350 |
|    | AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA | 400 |
|    | ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG | 450 |
|    | CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT | 500 |
| 50 | GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA | 550 |
|    | TGGCAACAAC GTTGCGCAAA CTATTAAGT GCGAACTACT TACTCTAGCT  | 600 |
|    | TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC | 650 |
|    | ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG | 700 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GAGCCGGTGA | GCGTGGGTCT | CGCGGTATCA | TTGCAGCACT | GGGGCCAGAT | 750 |
| GGTAAGCCCT | CCCGTATCGT | AGTTATCTAC | ACGACGGGGA | GTCAGGCAAC | 800 |
| TATGGATGAA | CGAAATAGAC | AGATCGCTGA | GATAGGTGCC | TCACTGATTA | 850 |
| AGCATTGGTA | A          |            |            |            | 861 |

5

## 2) INFORMATION FOR SEQ ID NO: 1928

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: HB251
- (C) ACCESSION NUMBER: X57972

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
| 25 | ATGAGTATTC | AACATTTCCG | TGTCGCCCTT | ATTCCCTTTT | TTGCGGCATT | 50  |
|    | TTGCCTTCCT | GTTTTTGCTC | ACCCAGAAAC | GCTGGTGAAA | GTAAAAGATG | 100 |
|    | CTGAAGATCA | GTTGGGTGCA | CGAGTGGGTT | ACATCGAACT | GGATCTCAAC | 150 |
|    | AGCGGTAAGA | TCCTTGAGAG | TTTTCGCCCC | GAAGAACGTT | TTCCAATGAT | 200 |
|    | GAGCACTTTT | AAAGTTCTGC | TATGTGGCGC | GGTATTATCC | CGTGTTGACG | 250 |
| 30 | CCGGGCAAGA | GCAACTCGGT | CGCCGCATAC | ACTATTCTCA | GAATGACTTG | 300 |
|    | GTAAAGTACT | CACCAGTCAC | AGAAAAGCAT | CTTACGGATG | GCATGACAGT | 350 |
|    | AAGAGAATTA | TGCAGTGCTG | CCATAACCAT | GAGTGATAAC | ACTGCGGCCA | 400 |
|    | ACTTACTTCT | GACAACGATC | GGAGGACCGA | AGGAGCTAAC | CGCTTTTTTG | 450 |
|    | CACAACATGG | GGGATCATGT | AACTCGCCTT | GATCATTGGG | AACCGGAGCT | 500 |
| 35 | GAATGAAGCC | ATACCAAACG | ACGAGCGTGA | CACCACGATG | CCTGCAGCAA | 550 |
|    | TGGCAACAAC | GTTGCGCAAA | CTATTAAGTG | GCGAACTACT | TACTCTAGCT | 600 |
|    | TCCCGGCAAC | AATTAATAGA | CTGGATGGAG | GCGGATAAAG | TTGCAGGACC | 650 |
|    | ACTTCTGCGC | TCGGCCCTTC | CGGCTGGCTG | GTTTATTGCT | GATAAATCTG | 700 |
|    | GAGCCGGTGA | GCGTGGGTCT | CGCGGTATCA | TTGCAGCACT | GGGGCCAGAT | 750 |
| 40 | GGTAAGCCCT | CCCGTATCGT | AGTTATCTAC | ACGACGGGGA | GTCAGGCAAC | 800 |
|    | TATGGATGAA | CGAAATAGAC | AGATCGCTGA | GATAGGTGCC | TCACTGATTA | 850 |
|    | AGCATTGGTA | A          |            |            |            | 861 |

45

## 2) INFORMATION FOR SEQ ID NO: 1929

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Klebsiella oxytoca*  
 (B) STRAIN: 26W  
 (C) ACCESSION NUMBER: U09188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929

```

10 ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
   TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
   CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAGCT GGATCTCAAC      150
   AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
   GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
15 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
   GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
   AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
   ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
   CACAACATGG GGGATCATGT AACCCGCCTT GATAGTTGGG AACCGGAGCT      500
20 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
   TGGCAACAAC GTTGCGCAA CTATTAAGT GCGAACTACT TACTCTAGCT      600
   TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
   ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
   GAGCCGGTAA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
25 GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
   TATGGATG                                     808
  
```

30 2) INFORMATION FOR SEQ ID NO: 1930

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (C) ACCESSION NUMBER: AF190692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930

```

45 ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
   TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
   CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT GGATCTCAAC      150
   AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
50 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG      250
   CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
   GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
   AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
  
```

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | ACTTACTTCT | GACAACGATC | GGAGGACCGA | AGGAGCTAAC | CGCTTTTTTTG | 450 |
|    | CACAACATGG | GGGATCATGT | AACTCGCCTT | GATCGTTGGG | AACCGGAGCT  | 500 |
|    | GAATGAAGCC | ATACCAAACG | ACGAGCGTGA | CACCACGATG | CCTGCAGCAA  | 550 |
|    | TGGCAACAAC | GTTGCGCAAA | CTATTAAGT  | GCGAACTACT | TACTCTAGCT  | 600 |
| 5  | TCCCGGCAAC | AATTAATAGA | CTGGATGGAG | GCGGATAAAG | TTGCAGGACC  | 650 |
|    | ACTTCTGCGC | TCGGCCCTTC | CGGCTGGCTG | GTTTATTGCT | GATAAATCTG  | 700 |
|    | GAGCCGGTGA | GCGTGGGTCT | GGCGGTATCA | TTGCAGCACT | GGGGCCAGAT  | 750 |
|    | GGTAAGCCCT | CCCGTATCGT | AGTTATCTAC | ACGACGGGGA | GTCAGGCAAC  | 800 |
|    | TATGGATGAA | CGAAATAGAC | AGATCGCTGA | GATAGGTGCC | TCACTGATTA  | 850 |
| 10 | AGCATTGGTA | A          |            |            |             | 861 |

## 2) INFORMATION FOR SEQ ID NO: 1931

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (B) STRAIN: BM2728  
 (C) ACCESSION NUMBER: AF104442

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1931

30

|    |            |            |            |            |             |     |
|----|------------|------------|------------|------------|-------------|-----|
|    | ATGAGTATTC | AACATTTCCG | TGTCGCCCTT | ATTCCCTTTT | TTGCGGCATT  | 50  |
|    | TTGCCTTCCT | GTTTTTGCTC | ACCCAGAAAC | GCTGGTGAAA | GTAAAAGATG  | 100 |
|    | CTGAAGATCA | GTTGGGTGCA | CGAGTGGGTT | ACATCGAACT | GGATCTCAAC  | 150 |
|    | AGCGGTAAGA | TCCTTGAGAG | TTTTCGCCCC | GAAGAACGTT | TTCCAATGAT  | 200 |
| 35 | GAGCACTTTT | AAAGTTCTGC | TATGTGGCGC | GGTATTATCC | CGTGTTGACG  | 250 |
|    | CCGGGCAAGA | GCAACTCGGT | CGCCGCATAC | ACTATTCTCA | GAATGACTTG  | 300 |
|    | GTTGAGTACT | CACCAGTCAC | AGAAAAGCAT | CTTACGGATG | GATGACAGT   | 350 |
|    | AAGAGAATTA | TGCAGTGCTG | CCATAACCAT | GAGTGATAAC | ACTGCGGCCA  | 400 |
|    | ACTTACTTCT | GACAACGATC | GGAGGACCGA | AGGAGCTAAC | CGCTTTTTTTG | 450 |
| 40 | CACAACATGG | GGGATCATGT | AACTCGCCTT | GATCGTTGGG | AACCGGAGCT  | 500 |
|    | GAATGAAGCC | ATACCAAACG | ACGAGCGTGA | CACCACGATG | CCTGCAGCAA  | 550 |
|    | TGGCAACAAC | GTTGCGCAAA | CTATTAAGT  | GCGAACTACT | TACTCTAGCT  | 600 |
|    | TCCCGGCAAC | AATTAATAGA | CTGGATGGAG | GCGGATAAAG | TTGCAGGACC  | 650 |
|    | ACTTCTGCGC | TCGGCCCTTC | CGGCTGGCTG | GTTTATTGCT | GATAAATCTG  | 700 |
| 45 | GAGCCGGTGA | GCGTGGGTCT | CTCGGTATCA | TTGCAGCACT | GGGGCCAGAT  | 750 |
|    | GGTAAGCCCT | CCCGTATCGT | AGTTATCTAC | ACGACGGGGA | GTCAGGCAAC  | 800 |
|    | TATGGATGAA | CGAAATAGAC | AGATCGCTGA | GATAGGTGCC | TCACTGATTA  | 850 |
|    | AGCATTGGTA | A          |            |            |             | 861 |

50

## 2) INFORMATION FOR SEQ ID NO: 1932

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (C) ACCESSION NUMBER: AF190695

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932

```

15  ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
    TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
    CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
    AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGCT      200
    GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
20  CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
    GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
    AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
    ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
    CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT      500
25  GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
    TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT      600
    TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
    ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
    GAGCCGGTGA GCGTGGGTCT AGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
30  GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
    TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
    AGCATTGGTA A                                     861
  
```

## 2) INFORMATION FOR SEQ ID NO: 1933

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (C) ACCESSION NUMBER: AF190693

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933

```

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
  
```

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CTGAAGATCA | GTTGGGTGCA | CGAGTGGGT  | ACATCGAGCT | GGATCTCAAC | 150 |
|    | AGCGGTAAGA | TCCTTGAGAG | TTTTCGCCCC | GAAGAACGTT | TTCCAATGGT | 200 |
|    | GAGCACTTTT | AAAGTTCTGC | TATGTGGTGC | GGTATTATCC | CGTGTTGACG | 250 |
|    | CCGGGCAAGA | GCAACTCGGT | CGCCGCATAC | ACTATTCTCA | GAATGACTTG | 300 |
| 5  | GTTGAGTACT | CACCAGTCAC | AGAAAAGCAT | CTTACGGATG | GCATGACAGT | 350 |
|    | AAGAGAATTA | TGCAGTGCTG | CCATAACCAT | GAGTGATAAC | ACTGCGGCCA | 400 |
|    | ACTTACTTCT | GACAACGATC | GGAGGACCGA | AGGAGCTAAC | CGCTTTTTTG | 450 |
|    | CACAACATGG | GGGATCATGT | AACCCGCCTT | GATCGTCGGG | AACCGGAGCT | 500 |
|    | GAATGAAGCC | ATACCAAACG | ACGAGCGTGA | CACCACGATG | CCTGCAGCAA | 550 |
| 10 | TGGCAACAAC | GTTGCGCAAA | CTATTAAGT  | GCGAACTACT | TACTCTAGCT | 600 |
|    | TCCCGGCAAC | AATTAATAGA | CTGGATGGAG | GCGGATAAAG | TTGCAGGACC | 650 |
|    | ACTTCTGCGC | TCGGCCCTTC | CGGCTGGCTG | GTTTATTGCT | GATAAATCTG | 700 |
|    | GAGCCGGTGA | GCGTGGATCT | CGCGGTATCA | TTGCAGCACT | GGGGCCAGAT | 750 |
|    | GGTAAGCCCT | CCCGTATCGT | AGTTATCTAC | ACGACGGGGA | GTCAGGCAAC | 800 |
| 15 | TATGGATGAA | CGAGATAGAC | AGATCGCTGA | GATAGGTGCC | TCACTGATTA | 850 |
|    | AGCATTGGTA | A          |            |            |            | 861 |

20 2) INFORMATION FOR SEQ ID NO: 1934

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- 25 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934

GAACGCCAGC GCGAAATTCA AAAAG

25

35

2) INFORMATION FOR SEQ ID NO: 1935

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- 40 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935

AGCTCGGCAT ACTTCGACAG G

21

50

2) INFORMATION FOR SEQ ID NO: 1936



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936

TACCACCCGC ACGGC

## 2) INFORMATION FOR SEQ ID NO: 1937

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937

CGGAGTCGCC GTCGATG

## 2) INFORMATION FOR SEQ ID NO: 1938

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938

CCGCGCACCA TTGCTTCGTA CACTGAGGAG TCTCCGCGCG G

## 2) INFORMATION FOR SEQ ID NO: 1939

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939

5 CGACCCGGAT GGTAGTATCG ATAATGATCC GCCAGCGGCC GGGTCG 46

10 2) INFORMATION FOR SEQ ID NO: 1940

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 19 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940

GTATCGTTGG TGACGTAAT 19

25 2) INFORMATION FOR SEQ ID NO: 1941

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 18 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941

GCAATGGTCC GTTTAAGT 18

40

2) INFORMATION FOR SEQ ID NO: 1942

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 27 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942

GACTGGAACA AAGCCTATAA AAAATCA

27

## 5 2) INFORMATION FOR SEQ ID NO: 1943

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943

GCTGGTGGAC GGCCAG

16

20

## 2) INFORMATION FOR SEQ ID NO: 1944

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

## (ii) MOLECULE TYPE: DNA

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944

TTTCGCCGCC ATGCGTTAC

19

35

## 2) INFORMATION FOR SEQ ID NO: 1945

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

## (ii) MOLECULE TYPE: DNA

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945

CGGCGACTAC GCGGTAT

17

50

## 2) INFORMATION FOR SEQ ID NO: 1946

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946

CGGCGACTTC GCGGTAT

17

## 2) INFORMATION FOR SEQ ID NO: 1947

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947

CGGTATACGG CACCATCGT

19

## 2) INFORMATION FOR SEQ ID NO: 1948

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948

GCGGTATACA ACACCATCG

19

## 2) INFORMATION FOR SEQ ID NO: 1949

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949

CGGTATACGC CACCATCGT

19

10

2) INFORMATION FOR SEQ ID NO: 1950

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 15 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950

GGCGACATCG CCTGC

15

25

2) INFORMATION FOR SEQ ID NO: 1951

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 17 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951

GGCGACAGAG CCTGCTA

17

40

2) INFORMATION FOR SEQ ID NO: 1952

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952

CCTGCTATGG AGCGATGGT

19

5

## 2) INFORMATION FOR SEQ ID NO: 1953

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953

CGCCTGCTAT AAAGCGATGG T

21

20

## 2) INFORMATION FOR SEQ ID NO: 1954

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 589 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
- (B) STRAIN: ATCC 13883
- (C) ACCESSION NUMBER: AF052258

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954

|               |            |            |            |            |     |
|---------------|------------|------------|------------|------------|-----|
| ACACCGGTCA    | ACATTGAGGA | AGAGCTTAAG | AACTCTTATC | TGGATTATGC | 50  |
| 10 GATGTCGGTC | ATTGTTGGCC | GTGCGCTGCC | GGATGTCCGA | GATGGCCTGA | 100 |
| AGCCGGTACA    | CCGTCGCGTA | CTTTACGCCA | TGAACGTATT | GGGCAATGAC | 150 |
| TGGAACAAAG    | CCTATAAAAA | ATCAGCCCGT | GTCGTTGGTG | ACGTAATCGG | 200 |
| TAAATACCAC    | CCGCACGGCG | ACTCCGCGGT | ATACGACACC | ATCGTGCGTA | 250 |
| TGGCGCAGCC    | GTTCTCGCTG | CGTTACATGC | TGGTGGACGG | CCAGGGTAAC | 300 |
| 15 TTTGGTTCCA | TCGACGGCGA | CTCCGCCGCG | GCGATGCGTT | ATACCGAAAT | 350 |
| TCGTCTGGCG    | AAAATCGCTC | ATGAGCTGAT | GGCCGATCTT | GAAAAAGAGA | 400 |
| CGGTTCGATTT   | CGTCGACAAC | TATGACGGTA | CGGAGCGTAT | TCCGGACGTC | 450 |
| ATGCCGACCA    | AAATTCCTAA | CCTGCTGGTG | AACGGCGCCT | CCGGGATCGC | 500 |
| CGTAGGGATG    | GCCACCAACA | TACCGCCACA | TAACCTGACG | GAAGTGATTA | 550 |
| 30 ACGGCTGTCT | GGCGTATGTT | GACGATGAAG | ACATCAGCA  |            | 589 |

## 2) INFORMATION FOR SEQ ID NO: 1955

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955

CGCGCAACCA TTGCTTCGTA CACTGAGGAG TCTGCGCG

38

## 2) INFORMATION FOR SEQ ID NO: 1956

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*  
 (B) STRAIN: ATCC 16783

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956

|            |             |            |            |             |     |
|------------|-------------|------------|------------|-------------|-----|
| CGGTAAAACC | ACTTTAACTG  | CTGCAATCAC | CAAAGTTT   | TCTGAAGAAG  | 50  |
| GTGGTGCAGA | TTTCTTAGAT  | TATTCATCTA | TTGATAAAGC | ACCAGAAGAG  | 100 |
| AGAGCTAGAG | GTATTACCAT  | TTCTACTGCT | CATGTTGAAT | ATGAAACTCC  | 150 |
| AAACAGACAT | TATTCACATG  | TTGATTGTCC | AGGTCATCAA | GATTATATTA  | 200 |
| AGAACATGAT | TACTGGTGCA  | GCTCAAATGG | ATGGTGCTAT | TATTGTTGTT  | 250 |
| GCAGCTACTG | ATGGTCAAAT  | GCCACAAACT | AAGGAACATT | TATTATTAGC  | 300 |
| TAGACAAGTT | GGTGTTC AAC | ATTTAGTTGT | TTTTGTTAAC | AAGTGTGATA  | 350 |
| CCGTTGATGA | TCCAGAAATG  | TTRGAATTAG | TTGAAATGGA | AATGAGAGAA  | 400 |
| TTATTGACCG | AATATGGATT  | YGATGGTGAT | AACACACCAG | TTATTATGGG  | 450 |
| TTCTGCATTA | ATGGCATTAG  | AAGGTAAGAG | ACCAGAAGTT | GGTAAAGAAT  | 500 |
| CTATTGTTAA | GTTAATGGAA  | GCTGTTGATA | CTTGGATTCC | AACTCCACAA  | 550 |
| AGAGACTTAG | AAAAACCAT   | CTTATTACCA | ATTGATGAAG | TTTTCTCTAT  | 600 |
| TTCTGGTAGA | GGTACTGTTG  | TTTCTGGTAC | TGTTGATAGA | GGTACATTAA  | 650 |
| AGAAGGGTGA | AGAAGTTGAA  | ATTGTTGGTG | GTAAAGAAGG | TGTTATTAAG  | 700 |
| ACTACTGTTA | CCGGTATTGA  | AATGTATCAC | AAGGAATTAG | ATCAAGCACA  | 750 |
| AGCTGGTGAT | ACTCCAGGTA  | TTTTGTTAAG | AGGTGTTAAG | AGAGATCAAA  | 800 |
| TTGCAAGAGG | TCAAATTCTT  | GCAAAGCCAG | GWTCTGTTAA | GGCATAACAAG | 850 |
| AAGTTCTTAT | CATCATTATA  | CATTTTAACA | AAGGAAGAAG | GTGGTAGACA  | 900 |
| TACTCCATTT | TCTGAAAATT  | ACAGACCTCA | AATGTACATT | AGAACTTCCA  | 950 |
| ATGTTAATGT | TACTTTGAAG  | TTCCCAGAAA | CTGAAGAAG  |             | 989 |

## 2) INFORMATION FOR SEQ ID NO: 1957

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*  
 (B) STRAIN: ATCC 22023

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957

|            |            |            |             |             |     |
|------------|------------|------------|-------------|-------------|-----|
| GGTAAGACCA | CCCTTACTGC | CGCCATCACC | AAGTGCCTTG  | CTGAGAAGGG  | 50  |
| AGGTGCCTCG | TTCTTGACT  | ACAGTGCCAT | CGACAAGGCG  | CCAGAGGAGA  | 100 |
| GAGCAAGAGG | TATCACCATC | TCCACTGCGC | ACGTTGAGTA  | TGAAACTGCC  | 150 |
| AACAGACACT | ACTCGCACGT | TGACTGTCCA | GGTCACGCTG  | ATTACATCAA  | 200 |
| GAACATGATT | ACCGGTGCTG | CGCAGATGGA | CGGTGCTATC  | ATTGTCTGTTG | 250 |
| CAGCCACTGA | CGGTCAGATG | CCACAGACCA | GAGAACACTT  | GTTGCTTGCC  | 300 |
| AGACAAGTTG | GTGTCCAGCA | CATTGTTGTC | TTCGTCAACA  | AGGTTGACAC  | 350 |
| CATCGACGAC | CCTGAGATGC | TTGAGCTTGT | TGAAATGGAG  | ATGAGAGAGT  | 400 |
| TGCTTACTTC | GTATGGATTT | GACGGTGATA | ACACCCAGT   | TATCATGGGT  | 450 |
| TCTGCTTTGT | GTGCTTTGGA | AGGCCGTGAG | CCAGAGATTG  | GTGCTAAGGC  | 500 |
| CATTGACAAG | TTGATGGAGG | CCATTGATGA | GTACATCCCA  | ACTCCTCAGA  | 550 |
| GAGACCTGGA | AAAGCCATTC | YTGATGGGTG | TTGAAGACGT  | GTTCTCGATC  | 600 |
| TCTGGTAGAG | GTACCGTTGT | CACRGGCCGT | GTTGAGCGTG  | GTAACCTTGAA | 650 |
| GAAAGGTGAT | GAAATTGAAC | TTGTTGGCTA | CAACAAGAAC  | CCAATCAAGA  | 700 |
| CCACCGTCAC | CGGTATCGAA | ATGTTCAAGA | AGGAGTTGGA  | ATCTGCCATG  | 750 |
| GCTGGTGACA | ACTGTGGTAT | CTTGTTGCGT | GGTATCAAGA  | GAGATGACGT  | 800 |
| CAAGAGAGGT | ATGGTTGCTG | CTAAGCCAGG | CTCCGTCTCT  | GCACACACCA  | 850 |
| AGTTCCTCGC | TTCTTGTAC  | ATCCTGACRA | AGGAGGAAGG  | TGGTCGTCAC  | 900 |
| AGTGCCTTTG | CTGAGAACTA | CAGACCACAG | ATGTTTCATCA | GAACCGGAGA  | 950 |
| TGTCACCACC | ATCTTGACAT | GGCCAGAGGA | GCACGCTGAC  | C           | 991 |

## 2) INFORMATION FOR SEQ ID NO: 1958

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*  
 (B) STRAIN: ATCC 7351



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958

|    |            |            |            |             |             |     |
|----|------------|------------|------------|-------------|-------------|-----|
|    | CGGTAAGACC | ACTTTGACCG | CCGCCATCAC | CAAGGTGTTG  | AGCGCCAAAG  | 50  |
|    | GTGGTGCTTC | CTTCTTGAC  | TACGGGTCCA | TCGACAGAGC  | CCCTGAGGAG  | 100 |
| 5  | AGAGCCAGAG | GTATTACTAT | CTCGACTGCC | CACGTTGAGT  | ACGAGACCGA  | 150 |
|    | TAAGAGACAC | TACGCCCACG | TTGATTGCCC | TGGTCACGCT  | GATTACATCA  | 200 |
|    | AGAACATGAT | CACTGGTGCC | GCCCAAATGG | ACGGTGCCAT  | TATTGTCGTT  | 250 |
|    | GCTGCTTCTG | ATGGCCAAAT | GCCGCAGACC | AGAGAGCACT  | TGTTGCTTGC  | 300 |
|    | CAGACAGGTT | GGTGTGCAGA | ACTTGGTTGT | GTTTGTTAAC  | AAGGTGGACA  | 350 |
| 10 | CCATCGACGA | CCCCGAAATG | TTGGAGTTGG | TGGAGATGGA  | AATGAGAGAA  | 400 |
|    | TTGTTGACCC | ACTACGGCTT | TGACGGTGAC | AACACCCCTG  | TCATCATGGG  | 450 |
|    | TTCGGCGTTG | TGTGCCTTGG | AAGACAGGCA | GCCTGAGATT  | GGCGAGCAAG  | 500 |
|    | CCATCATGAA | GTTGTTGGAC | GCTGTCGACG | AGTACATTCC  | CACTCCTCAG  | 550 |
|    | AGAGACTTGG | AGCAACCATT | TTTGATGCCC | GTTGAGGATG  | TTTTCTCCAT  | 600 |
| 15 | CTCTGGCAGA | GGTACTGTTG | TCACCGGTCG | TGTTGAGAGA  | GGCTCATTTGA | 650 |
|    | AGAAGGGTGA | GGAGATTGAG | ATTGTTGGCG | ACTTCCCCAA  | GCCCTTCAAG  | 700 |
|    | ACTACCGTCA | CCGGCATTGA | GATGTTCAAG | AAGGAGTTGG  | ATGCCGCGAT  | 750 |
|    | GGCGGGCGAC | AACGCCGGGA | TCTTGTTGAG | AGGTGTCAAG  | AGAGACGAGG  | 800 |
|    | TCTCGAGAGG | TATGGTTTTG | GCCAAGCCCG | GTACTGTCAC  | TTCGCACACC  | 850 |
| 20 | AAGGTGTTGG | CGTCGCTTTA | CATCTTGACC | AAAGAGGAAG  | GTGGCCGCCA  | 900 |
|    | CTCGCCCTTT | GGTGAGAACT | ACAAGCCACA | GTTATTTCATC | AGAACCTCCG  | 950 |
|    | ATGTCACTGG | TACTTTGAGG | TTCCCCGCCG | GTGAG       |             | 985 |

25

2) INFORMATION FOR SEQ ID NO: 1959

(i) SEQUENCE CHARACTERISTICS:

- |    |     |                      |
|----|-----|----------------------|
|    | (A) | LENGTH: 973 bases    |
| 30 | (B) | TYPE: Nucleic acid   |
|    | (C) | STRANDEDNESS: Double |
|    | (D) | TOPOLOGY: Linear     |

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- |    |     |                                     |
|----|-----|-------------------------------------|
|    | (A) | ORGANISM: <i>Candida catenulata</i> |
|    | (B) | STRAIN: ATCC 10565                  |
| 40 | (C) | ACCESSION NUMBER:                   |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | CGGTAAGACC | ACCTTGACTG | CCGCCATCAC | CAAGGTTCTC | TCCGAGAAGG | 50  |
|    | GTGGTGCCGA | CTTCTTGAC  | TACGGTGCCA | TTGACAGAGC | CCCCGAGGAG | 100 |
| 45 | CGTGCCCGTG | GTATCACCAT | CTCCACTGCC | CACGTTGAGT | ACGAGACTGA | 150 |
|    | CAACCGTCAC | TACGCCCACA | TTGACTGTCC | CGGTCACGCT | GATTACATCA | 200 |
|    | AGAACATGAT | TACCGGTGCC | GCCCAGATGG | ACGGTGCCAT | TATTGTCCTT | 250 |
|    | GCTGCTACTG | ACGGTGCCAT | GCCCCAGACC | CGCGAGCACT | TGCTTCTCGC | 300 |
|    | CCGTCAGGTT | GGTATCCAGG | AATTGGTTGT | GTTTGTGAAC | AAGGTTGACA | 350 |
| 50 | CCATCGACGA | CCCCGAGATG | TTGGAGCTCG | TTGAGATGGA | GATCCGCGAG | 400 |
|    | TTGTTGTCTG | AGTTCGGTTT | TGACGGTGAC | AACACCCCCG | TCATCATGGG | 450 |
|    | TTCCGCTTTG | TGCGCTTTGG | AGGGCAAGCA | GCCCGAGATT | GGTGAGCAGG | 500 |
|    | CTATCACCAA | GTTGATGGCC | GCCGTTGACG | AGCACATCCC | CACCCCCCAG | 550 |

|   |        |        |        |       |        |       |        |       |        |       |     |
|---|--------|--------|--------|-------|--------|-------|--------|-------|--------|-------|-----|
|   | CGTGA  | CTTGG  | AGCAG  | CCCTT | CTTGAT | GCCT  | GTTGAG | GGTG  | TTTTCT | CTAT  | 600 |
|   | CTCTG  | GCCGT  | GGTAC  | CGTGG | TGACT  | GGTAA | GGTTG  | CCCCG | GGTGT  | CCTCA | 650 |
|   | AGAAG  | GGGTGA | GGAGAT | TGAG  | ATTGTT | GGCA  | ACTTTG | GACAA | GCCCTA | CAAG  | 700 |
|   | GTGACT | GTTA   | CTGGT  | ATTGA | GATGTT | CAAG  | AAGGAG | TTGG  | ACCAGG | CCAT  | 750 |
| 5 | GGCTG  | GGTGAC | AACGCC | GGTA  | TCTTGT | TGCG  | TGGTGT | CAAG  | CGTGAC | GAGG  | 800 |
|   | TGTCT  | CGTGG  | TATGG  | TTTTG | GCCAAG | CCCCG | GCACTG | TTGT  | CTCGCA | CAAG  | 850 |
|   | AAGGT  | TTTTGG | CTTCG  | CTTTA | CATCTT | GACC  | CAGGAG | GAGG  | GTGGCC | GTAA  | 900 |
|   | GACCG  | GCTTC  | GGCTC  | CAACT | ACAAGC | CCCCA | GTTGTT | TCTTG | CGCACT | ACCG  | 950 |
|   | ACGTC  | ACTGG  | TACCCT | CACC  | TTC    |       |        |       |        |       | 973 |

10

## 2) INFORMATION FOR SEQ ID NO: 1960

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida krusei*  
 (B) STRAIN: ATCC 28870

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960

|    |         |       |        |        |         |        |        |        |         |     |
|----|---------|-------|--------|--------|---------|--------|--------|--------|---------|-----|
|    | AAGACT  | TGACT | GCTGC  | AATCAC | CAAG    | GTCTTA | GCTG   | ATCAAG | GGTGG   | 50  |
| 30 | TGCTGA  | TTTTC | TTAGAT | TATG   | CATCTA  | TATGA  | CAAGG  | CTCCT  | GAAGAA  | 100 |
|    | CAAGAG  | GTAT  | TACTAT | CTCT   | ACTGCT  | CACG   | TTGAG  | TATGA  | AACCCCA | 150 |
|    | AGACAT  | TATT  | CTCAT  | GTCGA  | TTGTC   | CCTGGC | CATCA  | AAGATT | ATATTA  | 200 |
|    | TATGAT  | TACT  | GGTGCT | GCAC   | AAATGG  | ATGG   | TGCTAT | TATT   | GTTGTT  | 250 |
|    | CTACTG  | ATGG  | TCAAAT | GCCA   | CAAAC   | TAAGG  | AACAT  | TTTATT | ATTAGC  | 300 |
| 35 | CAAGTT  | GGTG  | TTCAAC | ATTT   | AGTTGT  | CTTT   | GTTAAT | AAT    | GTGAC   | 350 |
|    | TGATGA  | CCCA  | GAAATG | TTGG   | AATTAG  | TTGA   | AATGG  | AAATG  | AGAGAA  | 400 |
|    | TGTCTG  | AATA  | TGGT   | TTTTG  | AT      | GGTGA  | TACA   | CTCCAG | TTAT    | 450 |
|    | GCATTG  | ATGG  | CTTTAG | AAGA   | CAAGAG  | ACCT   | GAAGTT | GGTA   | AGGAAT  | 500 |
|    | TTTAA   | AGTTA | ATGGA  | AGCYG  | TTGAC   | ACATG  | GATTCC | CAACC  | CCAGAG  | 550 |
| 40 | ATTTAG  | AAAA  | ACCAT  | TTTTT  | TTACCT  | TATTG  | ATGAAG | TTTT   | CTCAAT  | 600 |
|    | GGTAG   | AGGTA | CTGTC  | GTTT   | TGGT    | ACTG   | TG     | GAAAG  | AGGTA   | 650 |
|    | GGGTG   | AAGAA | GTTGA  | AATTG  | TTGGT   | GGTAA  | GGATG  | GGTTCT | ATTAAA  | 700 |
|    | CTGTCA  | CAGG  | TATTG  | AAATG  | TATCACA | CAAGG  | AATTAG | ACCA   | AGCGCA  | 750 |
|    | GGTGAT  | ACTC  | CAGGT  | ATTTT  | ATTAAG  | AGGT   | GTCAAG | AGAG   | ACCAA   | 800 |
| 45 | GAGAGG  | TCAA  | ATTTT  | AGCAA  | AGCCAG  | ATTC   | CGTTA  | AAGGCA | TACAAG  | 850 |
|    | TCTTGG  | CCTT  | TATATC | TTAAC  | CAAGG   | AAGAAG | GGTGG  | TGG    | TAGACA  | 900 |
|    | CCATTCT | CTG   | AAAAC  | TACAG  | ACCACA  | AAATG  | TACAT  | CAGAA  | CTACCA  | 950 |
|    | TAACGT  | TACT  | TTGAAG | TTCC   | CAGAC   | ACTGA  | AGAAG  |        |         | 985 |

50

## 2) INFORMATION FOR SEQ ID NO: 1961

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961

GCTCAAGGCA GATGGCATTC CC

## 2) INFORMATION FOR SEQ ID NO: 1962

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962

GGACAAGGCG GTTGCGTTTG AT

## 2) INFORMATION FOR SEQ ID NO: 1963

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963

CATTCCCGTC TCGCTGACA GT

## 2) INFORMATION FOR SEQ ID NO: 1964

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964

5 ATCTGCCTGC CCGTCTTGC 19

10 2) INFORMATION FOR SEQ ID NO: 1965

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 816 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmid pGS05  
(C) ACCESSION NUMBER: M36657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965

25  
ATGAATAAAT CGCTCATCAT TTTCGGCATC GTCAACATAA CCTCGGACAG 50  
TTTCTCCGAT GGAGGCCGGT ATCTGGCGCC AGACGCAGCC ATTGCGCAGG 100  
CGCGTAAGCT GATGGCCGAG GGGGCAGATG TGATCGACCT CGGTCCGGCA 150  
TCCAGCAATC CCGACGCCGC GCCTGTTTCG TCCGACACAG AAATCGCGCG 200  
30 TATCGCGCCG GTGCTGGACG CGCTCAAGGC AGATGGCATT CCCGTCTCGC 250  
TCGACAGTTA TCAACCCGCG ACGCAAGCCT ATGCCTTGTC GCGTGGTGTG 300  
GCCTATCTCA ATGATATTCG CGGTTTTCCA GACGCTGCGT TCTATCCGCA 350  
ATTGGCGAAA TCATCTGCCA AACTCGTCGT TATGCATTCTG GTGCAAGACG 400  
GGCAGGCAGA TCGGCGCGAG GCACCCGCTG GCGACATCAT GGATCACATT 450  
35 GCGGCGTTCT TTGACGCGCG CATCGCGGCG CTGACGGGTG CCGGTATCAA 500  
ACGCAACCGC CTTGTCCTTG ATCCCGGCAT GGGGTTTTTT CTGGGGGCTG 550  
CTCCCGAAAC CTCGCTCTCG GTGCTGGCGC GGTTCGATGA ATTGCGGCTG 600  
CGCTTCGATT TGCCGGTGCT TCTGTCTGTT TCGCGCAAAT CCTTTCTGCG 650  
CGCGCTCACA GGCCGTGGTC CGGGGGATGT CGGGGCCGCG AACTCGCTG 700  
40 CAGAGCTTGC CGCCGCCGCA GGTGGAGCTG ACTTCATCCG CACACACGAG 750  
CCGCGCCCCCT TCGCGACGCG GCTGGCGGTA TTGGCGGCGC TGAAAGAAAC 800  
CGCAAGAATT CGTTAA 816

15 2) INFORMATION FOR SEQ ID NO: 1966

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 19 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966

5 CATGCCAGTC TTGCCAACG

19

2) INFORMATION FOR SEQ ID NO: 1967

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967

20

CAGCAATAAG TAATCCAGCG ATG

23

2) INFORMATION FOR SEQ ID NO: 1968

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968

35

GGAGAGATTT CACCGCATAG

20

2) INFORMATION FOR SEQ ID NO: 1969

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969

AGCCAACCAT CATGCTATTC CA

22

## 2) INFORMATION FOR SEQ ID NO: 1970

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Transposon Tn10  
 (C) ACCESSION NUMBER: J01830

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970

|             |            |             |             |            |      |
|-------------|------------|-------------|-------------|------------|------|
| ATGAATAGTT  | CGACAAAGAT | CGCATTGGTA  | ATTACGTTAC  | TCGATGCCAT | 50   |
| GGGGATTGGC  | CTTATCATGC | CAGTCTTGCC  | AACGTTATTA  | CGTGAATTTA | 100  |
| TTGCTTCGGA  | AGATATCGCT | AACCACTTTG  | GCGTATTGCT  | TGCACTTTAT | 150  |
| GCGTTAATGC  | AGGTTATCTT | TGCTCCTTGG  | CTTGGA AAAA | TGTCTGACCG | 200  |
| ATTTGGTCGG  | CGCCCAGTGC | TGTTGTTGTC  | ATTAATAGGC  | GCATCGCTGG | 250  |
| ATTACTTATT  | GCTGGCTTTT | TCAAGTGC GC | TTTGGATGCT  | GTATTTAGGC | 300  |
| CGTTTGCTTT  | CAGGGATCAC | AGGAGCTACT  | GGGGCTGTCG  | CGGCATCGGT | 350  |
| CATTGCCGAT  | ACCACCTCAG | CTTCTCAACG  | CGTGAAGTGG  | TTCGGTTGGT | 400  |
| TAGGGGCAAG  | TTTTGGGCTT | GGTTTAATAG  | CGGGGCCTAT  | TATTGGTGGT | 450  |
| TTTGCAGGAG  | AGATTTCACC | GCATAGTCCC  | TTTTTTATCG  | CTGCGTTGCT | 500  |
| AAATATTGTC  | ACTTTCCTTG | TGGTTATGTT  | TTGGTTCCGT  | GAAACCAAAA | 550  |
| ATACACGTGA  | TAATACAGAT | ACCGAAGTAG  | GGGTTGAGAC  | GCAATCGAAT | 600  |
| TCGGTATACA  | TCACTTTATT | TAAAACGATG  | CCCATTTTGT  | TGATTATTTA | 650  |
| TTTTTTCAGCG | CAATTGATAG | GCCAAATTCC  | CGCAACGGTG  | TGGGTGCTAT | 700  |
| TTACCGAAAA  | TCGTTTTTGA | TGGAATAGCA  | TGATGGTTGG  | CTTTTCATTA | 750  |
| GCGGGTCTTG  | GTCTTTTACA | CTCAGTATTC  | CAAGCCTTTG  | TGGCAGGAAG | 800  |
| AATAGCCACT  | AAATGGGGCG | AAAAAACGGC  | AGTACTGCTC  | GAATTTATTG | 850  |
| CAGATAGTAG  | TGCATTTGCC | TTTTTAGCGT  | TTATATCTGA  | AGGTTGGTTA | 900  |
| GATTTCCCTG  | TTTTAATTTT | ATTGGCTGGT  | GGTGGGATCG  | CTTTACCTGC | 950  |
| ATTACAGGGA  | GTGATGTCTA | TCCAAACAAA  | GAGTCATGAG  | CAAGGTGCTT | 1000 |
| TACAGGGATT  | ATTGGTGAGC | CTTACCAATG  | CAACCGGTGT  | TATTGGCCCA | 1050 |
| TTACTGTTTA  | CTGTTATTTA | TAATCATTCA  | CTACCAATTT  | GGGATGGCTG | 1100 |
| GATTTGGATT  | ATTGGTTTAG | CGTTTTACTG  | TATTATTATC  | CTGCTATCGA | 1150 |
| TGACCTTCAT  | GTTAACCCTT | CAAGCTCAGG  | GGAGTAAACA  | GGAGACAAGT | 1200 |
| GCTTAG      |            |             |             |            | 1206 |

## 2) INFORMATION FOR SEQ ID NO: 1971

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971

5 CYGACTGYGC CATCCTYATC A

21

2) INFORMATION FOR SEQ ID NO: 1972

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972

20 MGICAGCTCA TYITTGCWKS C

21

2) INFORMATION FOR SEQ ID NO: 1973

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973

35 RACACCRGIY TTGGWITCCT T

21

2) INFORMATION FOR SEQ ID NO: 1974

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974

50

ACAAGGGITG GRMSAAGGAG AC

22

## 2) INFORMATION FOR SEQ ID NO: 1975

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975

TGRCCRGGGT GGTTRAGGAC G

21

## 2) INFORMATION FOR SEQ ID NO: 1976

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976

GATGGAYTCY GTYAAITGGG A

21

## 2) INFORMATION FOR SEQ ID NO: 1977

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977

GATGGAYTCY GTYAARTGGG A

21

## 2) INFORMATION FOR SEQ ID NO: 1978

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid



(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978

CATCITGYAA TGGYAATCTY AAT

23

10

2) INFORMATION FOR SEQ ID NO: 1979

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979

CATCYTGYAA TGGYAASCTY AAT

23

25

2) INFORMATION FOR SEQ ID NO: 1980

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980

40 TCRATGGCIT CIAIRAGRGY YT

22

2) INFORMATION FOR SEQ ID NO: 1981

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981

TGGACACCIS CAAGIGGKCY G

21

5

2) INFORMATION FOR SEQ ID NO: 1982

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982

TGGACACYIS CAAGIGGKCY G

21

20

2) INFORMATION FOR SEQ ID NO: 1983

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983

35 CYGAYTGCGC YATICTCATC A

21

2) INFORMATION FOR SEQ ID NO: 1984

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984

50

CYGAYTGYGC YATYCTSATC A

21

## 2) INFORMATION FOR SEQ ID NO: 1985

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*  
 (B) STRAIN: M1-106  
 (C) ACCESSION NUMBER: U81804

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | ATGGGTAAGG | ACAAGCTGCA | CGTCAACGTC | GTTGTTATCG | GTCACGTCGA | 50   |
|    | CTCCGGTAAG | TCGACCACCA | CCGGTCACTT | GATCTACAAG | TGCGGTGGTA | 100  |
| 20 | TCGACAAGCG | AACCATTGAG | AAGTTCGAGA | AGGAGGCTCA | AGAGCTCGGA | 150  |
|    | AAGTCTTCTT | TCAAGTACGC | TTGGGTCTT  | GACAAGCTTA | AGGCCGAGCG | 200  |
|    | AGAGCGAGGT | ATCACCATCG | ACATTGCTCT | TTGGAAGTTC | GAGACCCCTA | 250  |
|    | AGTACCAGGT | TACCGTCATT | GACGCCCCCG | GTCACCGAGA | CTTCATCAAG | 300  |
|    | AACATGATCA | CCGGTACCTC | CCAGGCTGAC | TGTGCCATCC | TCATCATTGC | 350  |
| 25 | CACCGGTATC | GGTGAGTTCG | AGGCTGGTAT | CTCCAAGGAC | GGTCAGACCC | 400  |
|    | GAGAGCACGC | CCTCCTCGCC | TTCACCCTCG | GTGTCAGGCA | GCTCATTGTT | 450  |
|    | GCTTGCAACA | AGATGGACAC | CTGCAAGTGG | TCTGAGGACC | GATTCAACGA | 500  |
|    | AATCGTCAAG | GAGACCAACG | GTTTCATCAA | GAAGGTTGGT | TACAACCCCA | 550  |
|    | AGGCTGTCCC | CTTCGTCCCC | ATCTCTGGTT | GGCACGGTGA | CAACATGTTG | 600  |
| 30 | GAGGAGACCA | CCAACATGCC | CTGGTACAAG | GGATGGACCA | AGGAGACCAA | 650  |
|    | GTCCGGTGTT | TCCAAGGGTA | AGACCCTTCT | CGAGGCCATC | GACGCCAGTA | 700  |
|    | GGCCCCCTAC | CCGACCCACC | GACAAGCCCC | TCCGTCTCCC | TCTCCAGGAC | 750  |
|    | GTCTACAAGA | TCGGTGGTAT | CGGCACAGTC | CCTGTCGGCC | GAGTCGAGAC | 800  |
|    | CGGTGTCATC | AAGGCCGGTA | TGGTCGTCAA | GTTTCGCCCC | ACCAACGTCA | 850  |
| 35 | CCACTGAAGT | CAAGTCCGTT | GAGATGCACC | ACGAGCAGAT | CCCCGAGGGT | 900  |
|    | CTCCCCGGAG | ACAACGTTGG | TTTCAACGTC | AAGAACGTTT | CCATCAAGGA | 950  |
|    | CATCCGACGA | GGTAACGTCT | GTGGTGACTC | CAAGAACGAC | CCCCCTATGG | 1000 |
|    | AGGCTGCTTC | TTTCAACGCC | CAGGTTATCG | TCCTTAACCA | CCCTGGTCAG | 1050 |
|    | ATCGGTGCCG | GTTACACCCC | CGTTCTCGAC | TGTCACACTG | CCCACATTGC | 1100 |
| 10 | TTGCAAGTTC | TCTGAGTTGA | TCGAGAAGAT | TGACCGACGA | ACCGGTAAGG | 1150 |
|    | TCATGGAGGC | CGCCCCCAAG | TTCGTCAAGT | CTGGTGACGC | CGCCATTGTC | 1200 |
|    | AAGCTTGTTT | CCCAGAAGCC | TCTCTGTGTT | GAGACCTACG | CCGACTACCC | 1250 |
|    | CCCTCTTGGT | CGATTGCGCC | TCCGAGACAT | GCGACAGACC | GTTGCCGTTG | 1300 |
|    | GTGTTATTAA | GAGTGTGGAG | AAGTCCGATG | GGAAGAGCGG | CAAGGTTACC | 1350 |
| 15 | AAGGCCGCCG | AGAAGGCTGC | TAAGAAGAAG | TAA        |            | 1383 |

## 2) INFORMATION FOR SEQ ID NO: 1986

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases  
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*  
(B) STRAIN: B3501  
(C) ACCESSION NUMBER: U81803

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | ATGGGTAAGG | ACAAGCTGCA | CGTCAACGTC | GTTGTTATCG | GTCACGTCGA | 50   |
|    | CTCCGGTAAG | TCGACCACCA | CCGGTCACTT | GATCTACAAG | TGCGGTGGTA | 100  |
| 15 | TCGACAAGCG | AACCATTGAG | AAGTTCGAGA | AGGAGGCTCA | AGAGCTCGGA | 150  |
|    | AAGTCTTCTT | TCAAGTACGC | TTGGGTTCCT | GACAAGCTTA | AGGCCGAGCG | 200  |
|    | AGAGCGAGGT | ATCACCATCG | ACATTGCTCT | TTGGAAGTTC | GAGACCCCCA | 250  |
|    | GGTACCAGGT | CACCGTCATT | GACGCCCCCG | GTCACCGAGA | CTTCATCAAG | 300  |
|    | AACATGATCA | CCGGTACCTC | CCAGGCTGAC | TGTGCCATCC | TCATCATTGC | 350  |
| 20 | CACCGGTATC | GGTGAGTTCG | AGGCCGGTAT | CTCCAAGGAC | GGTCAGACCC | 400  |
|    | GAGAGCACGC | CCTCCTCGCC | TTCACCCTCG | GTGTCAGGCA | GCTCATTGTT | 450  |
|    | GCTTGCAACA | AGATGGACAC | CTGCAAGTGG | TCCGAGGACC | GATTCAACGA | 500  |
|    | AATCGTCAAG | GAGACCAACG | GTTTCATCAA | GAAGGTTGGC | TACAACCCCA | 550  |
|    | AGGCTGTCCC | CTTCGTCCCC | ATCTCTGGTT | GGCACGGTGA | CAACATGTTG | 600  |
| 25 | GAGGAGACCA | CCAACATGCC | CTGGTACAAG | GGATGGACCA | AGGAGACCAA | 650  |
|    | GTCTGGTGTT | TCCAGGGGTA | AGACCCTTCT | CGAGGCCATC | AGCGCCAGTA | 700  |
|    | GGCCCCATAC | CCGACCCACC | GACAAGCCCC | TCCGTCTCCC | TCTCCAGGAC | 750  |
|    | GTCTACAAGA | TCGGTGGTAT | CGGCACAGTC | CCTGTCGGCC | GAGTCGAGAC | 800  |
|    | CGGTGTCATC | AAGGCCGGTA | TGGTCGTCAA | GTTCGCCCCC | ACCAACGTCA | 850  |
| 30 | CCACTGAAGT | CAAGTCCGTT | GAGATGCACC | ACGAGCAGAT | CCCCGAGGGT | 900  |
|    | CTTCCCGGAG | ACAACGTTGG | TTTCAACGTC | AAGAACGTTT | CCATCAAGGA | 950  |
|    | CATCCGACGA | GGTAACGTCT | GTGGTGACTC | CAAGAACGAC | CCCCCTATGG | 1000 |
|    | AGGCTGCTTC | TTTCAACGCC | CAGGTTATCG | TCCTTAACCA | CCCTGGTCAG | 1050 |
|    | ATCGGTGCCG | GTTACACCCC | CGTTCTCGAC | TGTCACACTG | CCCACATTGC | 1100 |
| 35 | CTGCAAGTTT | GCTGAGTTGA | TCGAGAAGAT | TGACCGACGA | ACCGGTAAGG | 1150 |
|    | TCATGGAGGC | CGCCCCCAAG | TTCGTCAAGT | CTGGTGACGC | CGCCATTGTC | 1200 |
|    | AAGCTTGTTG | CCCAGAAGCC | CCTCTGTGTT | GAGACCTACG | CCGACTACCC | 1250 |
|    | CCCTCTTGGT | CGATTCGCCG | TCCGAGACAT | GCGACAGACC | GTTGCCGTTG | 1300 |
|    | GTGTTATCAA | GAGCGTGGAC | AAGACCGAGA | AGGGTGGCAA | GGTCACCAAG | 1350 |
| 40 | GCTGCTGAGA | AGGCTGCCAA | GAAGAAGTAA |            |            | 1380 |

2) INFORMATION FOR SEQ ID NO: 1987

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(C) ACCESSION NUMBER: X01638

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987

ATGGGTAAAG AGAAGTCTCA CATTACGTT GTCGTTATCG GTCATGTCGA 50  
TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA 100  
TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT 150  
10 AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG 200  
AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA 250  
AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG 300  
AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC 350  
TGGTGGTGTC GGTGAATTCG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA 400  
15 GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT 450  
GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA 500  
AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA 550  
AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT 600  
GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTGCGGAAA AGGAAACCAA 650  
20 GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG 700  
AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT 750  
GTTTACAAGA TCGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC 800  
CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTGCCCCCA GCTGGTGTGA 850  
CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT 900  
25 GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA 950  
AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG 1000  
GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA 1050  
ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC 1100  
TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA 1150  
30 AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC 1200  
AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC 1250  
ACCATTAGGT AGATTCGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCG 1300  
GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTACCAAG 1350  
GCTGCTCAAA AGGCTGCTAA GAAATAA 1377

35

## 2) INFORMATION FOR SEQ ID NO: 1988

## 40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

50 (C) ACCESSION NUMBER: M10992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988

```

ATGGGGTAAAG AGAAGTCTCA CATTAACGTT GTCGTTATCG GTCATGTCGA      50
TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA      100
TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT      150
AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG      200
5 AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA      250
AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTTCATCAAG      300
AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC      350
TGGTGGTGTC GGTGAATTCG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA      400
GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT      450
10 GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA      500
AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA      550
AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT      600
GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTGAGGAAA AGGAAACCAA      650
GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG      700
15 AACAAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT      750
GTTTACAAGA TTGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC      800
CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTTGCCCCA GCTGGTGTTA      850
CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT      900
GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA      950
20 AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG      1000
GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA      1050
ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC      1100
TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA      1150
AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC      1200
25 AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC      1250
ACCATTAGGT AGATTCGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCTG      1300
GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG      1350
GCTGCTCAAA AGGCTGCTAA GAAATAA      1377

```

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## 2) INFORMATION FOR SEQ ID NO: 1989

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 1377 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Eremothecium gossypii*  
 (B) STRAIN: ATCC 10895  
 45 (C) ACCESSION NUMBER: X73978

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989

```

ATGGGTAAGG AAAAGACTCA CGTTAACGTT GTCGTCATCG GTCACGTCGA      50
50 CTCTGGTAAG TCTACTACCA CCGGTCACTT GATCTACAAG TGTGGTGGTA      100
TTGACAAGAG AACCATCGAG AAGTTCGAGA AGGAGGCTGC CGAGTTGGGT      150
AAGGGTTCTT TCAAGTACGC CTGGGTTTTG GACAAATTGA AGGCTGAGAG      200
AGAGAGAGGT ATCACCATCG ACATTGCGTT GTGGAAGTTC GAGACTCCAA      250

```

|    |            |            |            |            |             |      |
|----|------------|------------|------------|------------|-------------|------|
|    | AGTACCACGT | CACTGTCATT | GACGCCCCAG | GCCACAGAGA | CTTCATCAAG  | 300  |
|    | AACATGATTA | CCGGTACTTC | TCAAGCTGAC | TGTGCCATCT | TGATCATTGC  | 350  |
|    | TGGTGGTGTC | GGTGAGTTCG | AGGCTGGTAT | CTCCAAGGAC | GGTCAGACCA  | 400  |
|    | GAGAGCACGC | TTTGTTGGCT | TACACCTTGG | GTGTCAAGCA | GTTGATCGTT  | 450  |
| 5  | GCCATCAACA | AGATGGACTC | CGTCAAGTGG | GACGAGTCCA | GATACCAGGA  | 500  |
|    | GATTGTCAAG | GAGACCTCCA | ACTTCATCAA | GAAGGTCGGT | TACAACCCTA  | 550  |
|    | AGACTGTTCC | ATTCGTTCCA | ATCTCCGGCT | GGAACGGTGA | CAACATGATT  | 600  |
|    | GAGGCCACCA | CCAACGCCCC | ATGGTACAAG | GGCTGGGAGA | AGGAGACCAA  | 650  |
|    | GGCTGGTGCC | GTCAAGGGTA | AGACCTTGTT | GGAGGCCATT | GACGCCATTG  | 700  |
| 10 | AGCCACCTGT | CAGACCAACT | GACAAGGCAT | TGAGATTGCC | ATTGCAGGAT  | 750  |
|    | GTCTACAAGA | TCGGTGGTAT | TGGTACGGTT | CCAGTCGGCA | GAGTCGAGAC  | 800  |
|    | CGGTGTCATC | AAGCCAGGTA | TGGTTGTTAC | CTTCGCCCCA | TCCGGTGTCA  | 850  |
|    | CCACTGAAGT | CAAGTCCGTC | GAGATGCACC | ACGAGCAATT | GGAGGAGGGT  | 900  |
|    | GTCCCAGGTG | ACAACGTTGG | TTTCAACGTC | AAGAACGTCT | CCGTCAAGGA  | 950  |
| 15 | GATCAGAAGA | GGTAACGTTT | GCGGTGACTC | CAAGAACGAC | CCACCAAAGG  | 1000 |
|    | CTGCTGAGTC | CTTCAACGCT | ACCGTCATTG | TCTTGAACCA | CCCAGGTCAA  | 1050 |
|    | ATCTCTGCCG | GTTACTCTCC | AGTCTTGGAC | TGTCACACTG | CCCACATTGC  | 1100 |
|    | TTGTAAGTTC | GACGAGTTGT | TGGAGAAGAA | CGACAGAAGA | ACCGGTAAGA  | 1150 |
|    | AGTTGGAAGA | CTCTCCAAAG | TTCCTAAAGG | CCGGTGACGC | TGCCATGGTC  | 1200 |
| 20 | AAGTTTGTCC | CATCCAAGCC | AATGTGTGTT | GAGGCTTTCA | CCGACTACCC  | 1250 |
|    | ACCATTGGGT | AGATTCGCTG | TCAGAGACAT | GAGACAGACC | GTTGCTGTCTG | 1300 |
|    | GTGTCATCAA | GTCTGTTGTC | AAGTCCGACA | AGGCTGGTAA | GGTCACCAAG  | 1350 |
|    | GCCGCCCAAA | AGGCTGGTAA | GAAATAG    |            |             | 1377 |

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## 2) INFORMATION FOR SEQ ID NO: 1990

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1377 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

- 35 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eremothecium gossypii*  
 (C) ACCESSION NUMBER: A29820

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | ATGGGTAAGG | AAAAGACTCA | CGTTAACGTT | GTCGTCATCG | GTCACGTCGA | 50  |
|    | CTCTGGTAAG | TCTACTACCA | CCGGTCACTT | GATCTACAAG | TGTGGTGGTA | 100 |
| 15 | TTGACAAGAG | AACCATCGAG | AAGTTCGAGA | AGGAGGCTGC | CGAGTTGGGT | 150 |
|    | AAGGGTTCTT | TCAAGTACGC | CTGGGTTTTG | GACAAATTGA | AGGCTGAGAG | 200 |
|    | AGAGAGAGGT | ATCACCATCG | ACATTGCGTT | GTGGAAGTTC | GAGACTCCAA | 250 |
|    | AGTACCACGT | CACTGTCATT | GACCCCCCAG | GCCACAGAGA | CTTCATCAAG | 300 |
|    | AACATGATTA | CCGGTACTTC | TCAAGCTGAC | TGTGCCATCT | TGATCATTGC | 350 |
| 30 | TGGTGGTGTC | GGTGAGTTCG | AGGCTGGTAT | CTCCAAGGAC | GGTCAGACCA | 400 |
|    | GAGAGCACGC | TTTGTTGGCT | TACACCTTGG | GTGTCAAGCA | GTTGATCGTT | 450 |
|    | GCCATCAACA | AGATGGACTC | CGTCAAGTGG | GACGAGTCCA | GATACCAGGA | 500 |
|    | GATTGTCAAG | GAGACCTCCA | ACTTCATCAA | GAAGGTCGGT | TACAACCCTA | 550 |

|    |            |             |            |            |             |      |
|----|------------|-------------|------------|------------|-------------|------|
|    | AGACTGTTCC | ATTTCGTTCCA | ATCTCCGGCT | GGAACGGTGA | CAACATGATT  | 600  |
|    | GAGGCCACCA | CCAACGCCCC  | ATGGTACAAG | GGCTGGGAGA | AGGAGACCAA  | 650  |
|    | GGCTGGTGCC | GTCAAGGGTA  | AGACCTTGTT | GGAGGCCATT | GACGCCATTG  | 700  |
|    | AGCCACCTGT | CAGACCAACT  | GACAAGGCAT | TGAGATTGCC | ATTGCAGGAT  | 750  |
| 5  | GTCTACAAGA | TCGGTGGTAT  | TGGTACGGTT | CCAGTCGGCA | GAGTCGAGAC  | 800  |
|    | CGGTGTCATC | AAGCCAGGTA  | TGGTTGTTAC | CTTCGCCCCA | TCCGGTGTCA  | 850  |
|    | CCACTGAAGT | CAAGTCCGTC  | GAGATGCACC | ACGAGCAATT | GGAGGAGGGT  | 900  |
|    | GTCCCAGGTG | ACAACGTTGG  | TTTCAACGTC | AAGAACGTCT | CCGTCAAGGA  | 950  |
|    | GATCAGAAGA | GGTAACGTTT  | GCGGTGACTC | CAAGAACGAC | CCACCAAAGG  | 1000 |
| 10 | CTGCTGAGTC | CTTCAACGCT  | ACCGTCATTG | TCTTGAACCA | CCCAGGTCAA  | 1050 |
|    | ATCTCTGCCG | GTTACTCTCC  | AGTCTTGAC  | TGTCACACTG | CCCACATTGC  | 1100 |
|    | TTGTAAGTTC | GACGAGTTGT  | TGGAGAAGAA | CGACAGAAGA | ACCGGTAAGA  | 1150 |
|    | AGTTGGAAGA | CTCTCCAAAG  | TTCCTAAAGG | CCGGTGACGC | TGCCATGGTC  | 1200 |
|    | AAGTTTGTCC | CATCCAAGCC  | AATGTGTGTT | GAGGCTTTCA | CCGACTACCC  | 1250 |
| 15 | ACCATTGGGT | AGATTCGCTG  | TCAGAGACAT | GAGACAGACC | GTTGCTGTCTG | 1300 |
|    | GTGTCATCAA | GTCTGTTGTC  | AAGTCCGACA | AGGCTGGTAA | GGTCACCAAG  | 1350 |
|    | GCCGCCCAA  | AGGCTGGTAA  | GAAATAG    |            |             | 1377 |

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## 2) INFORMATION FOR SEQ ID NO: 1991

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus oryzae*  
 (B) STRAIN: KBN616  
 (C) ACCESSION NUMBER: AB007770

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1991

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | TGGGGTAAGT | TTATCAACCC | GTCGAGTTGT | GTTGCATCTC | AGATCATGGC | 50  |
|    | TGACAAGTAC | TTTCCTCCTT | ACAGTAAGGA | AGACAAGCAG | CACATCAACA | 100 |
| 40 | TCGTGCTTAT | CGGCCACGTC | GATTCCGGCA | AGTCCACCAC | CACTGGTCAC | 150 |
|    | TTGATCTACA | AGTGTGGTGG | TATCGACCAG | CGTACCATCG | AGAAGTTCGA | 200 |
|    | GAAGGAAGCC | GCTGAGCTCG | GTAAGGGTTC | CTTCAAGTAC | GCCTGGGTTC | 250 |
|    | TTGACAAGCT | CAAGTCCGAG | CGTGAGCGTG | GTATCACCAT | CGATATCGCC | 300 |
|    | CTCTGGAAGT | TCCAGACCTC | CAAGTATGAG | GTCACCGTCA | TTGGTAAGCA | 350 |
| 45 | TTTGAGTTCC | AACCTACGTT | GCCCAACATT | TACAGTCATC | TAACAAAGTT | 400 |
|    | CAATAGATGC | CCCCGGTCAC | CGTGACTTCA | TCAAGAACAT | GATCACTGGT | 450 |
|    | ACTTCCCAGG | CTGACTGCGC | TATCCTCATC | ATTGCCTCCG | GTAAGTGGTG | 500 |
|    | ATTTCGAGGT | GGTATCTCCA | AGGATGGTCA | GACCCGTGAG | CACGCTCTGC | 550 |
|    | TCGCTTTCAC | CCTCGGTGTC | CGTCAGCTCA | TCGTTGCCCT | CAACAAGATG | 600 |
| 50 | GACACCTGCA | AGTGGTCTCA | GGATCGTTAC | AACGAAATCG | TTAAGGAGAC | 650 |
|    | TTCCAACCTT | ATCAAGAAGG | TCGGATACAA | CCCCAAGAGC | GTTCTTTTCG | 700 |
|    | TCCCCATCTC | CGGTTTCAAC | GGTGACAACA | TGATTGAGGC | CTCCACCAAC | 750 |
|    | TGCCCCTGGT | ACAAGGGCTG | GGAGAAGGAG | ACCAAGGCTG | GCAAGTCCAC | 800 |



|    |            |             |            |            |             |      |
|----|------------|-------------|------------|------------|-------------|------|
|    | CGGTAAGACC | CTTCTCGAGG  | CCATCGATGC | CATCGAGCCC | CCCGTCCGTC  | 850  |
|    | CCACCGACAA | GCCTCTCCGT  | CTTCCCCTCC | AGGATGTCTA | CAAGATCTCT  | 900  |
|    | GGTATCGGTA | CTGTGCCCCG  | CGGTCGTGTC | GAGACTGGTG | TCATCAAGCC  | 950  |
|    | TGGTATGGTC | GTTACTTTTCG | CTCCTGCCAA | CGTGACCACT | GAAGTCAAGT  | 1000 |
| 5  | CCGTTGAAAT | GCACCACCAG  | CAGCTCCAGG | CCGGTAACCC | CGGTGACAAC  | 1050 |
|    | GTTGGTTTCA | ACGTCAAGAA  | CGTCTCCGTC | AAGGAAGTCC | GCCGTGGTAA  | 1100 |
|    | CGTTGCCGGT | GACTCCAAGA  | ACGACCCCCC | TGCTGGCTGC | GATTCCTTCA  | 1150 |
|    | ACGCCCAGGT | CATCGTCCTT  | AACCACCCCC | GTCAGGTCGG | CAACGGTTAC  | 1200 |
|    | GCTCCCCTCC | TGGACTGCCA  | CACCGCTCAC | ATTGCTTGCA | AGTTCGCTGA  | 1250 |
| 10 | GCTCCTTGAG | AAGATTGACC  | GCCGTACCGG | TAAATCTGTT | GAGGACAAGC  | 1300 |
|    | CCAAGTTCAT | CAAGTCTGGT  | GATGCTGCCA | TCGTCAAGAT | GATTCCTTCC  | 1350 |
|    | AAGCCCATGT | GTGTGGAGTC  | TTTCACTGAC | TTCCCCCCTC | TTGGTCGTTT  | 1400 |
|    | CGCTGTCCGT | GACGTAAGTT  | TTTCCCTCTT | GACTATCTTC | ACAATTTTTTC | 1450 |
|    | ACATATTTTC | ACGCCTCGTC  | CCACTCTTTT | TCCTCCCTTC | CTCTTTGGTT  | 1500 |
| 15 | CCCCTTTTTG | CCTGCAAGTT  | CTCTATAGCT | AACATGATGT | CTAGATGCGT  | 1550 |
|    | CAAACGTGTT | CCGTCGGAGT  | TATCAAGTCG | GTTGAGAAGA | ACACTGGCGG  | 1600 |
|    | TTCTGGCAAG | GTCACCAAGG  | CCGCCCAGAA | GGCTGGCAAG | AAATAA      | 1646 |

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## 2) INFORMATION FOR SEQ ID NO: 1992

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*  
 (B) STRAIN: R106  
 (C) ACCESSION NUMBER: U19723

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992

|    |            |             |             |            |            |     |
|----|------------|-------------|-------------|------------|------------|-----|
|    | ATGGGTAAGG | AAAAGTCCCA  | CATCAACGTC  | GTCGTTATCG | GCCACGTCGA | 50  |
|    | CTCCGGTAAG | TCGACCACCA  | CCGGTCACTT  | GATCTACAAG | TGCGGTGGTA | 100 |
| 40 | TCGACAAGCG | TACCATCGAG  | AAGTTCGAGA  | AGGAAGCCGC | CGAACTCGGC | 150 |
|    | AAGGGTTCCT | TCAAGTACGC  | CTGGGTCCCTC | GACAAGCTGA | AGTCTGAGCG | 200 |
|    | TGAGCGTGGT | ATCACTATCG  | ATATCGCTCT  | GTGGAAGTTC | GAGACCCCCA | 250 |
|    | AGTACATGGT | CACCGTCATC  | GATGCCCCCG  | GTCACCGTGA | TTTCATCAAG | 300 |
|    | AACATGATCA | CTGGTACCTC  | CCAGGCTGAC  | TGCGCCATTC | TCATCATTTG | 350 |
| 45 | CGCCGGTACT | GGTGAGTTCG  | AGGCTGGTAT  | CTCCAAGGAT | GGCCAGACTC | 400 |
|    | GTGAGCACGC | CCTTCTCGCC  | TACACCCCTG  | GTGTCAAGCA | GCTCATCGTC | 450 |
|    | GCTATCAACA | AGATGGACAC  | CACCAAGTGG  | TCTGAGGCC  | GTTACCAGGA | 500 |
|    | GATCATCAAG | GAGACCTCCG  | GTTTCATCAA  | GAAGGTCGGC | TACAACCCCA | 550 |
|    | AGCACGTTCC | CTTTGTCCCC  | ATCTCGGGTT  | TCAACGGTGA | CAACATGATT | 600 |
| 50 | GAGGTTTCTT | CCAAC TGCCC | CTGGTACAAG  | GGTTGGGAGA | AGGAGACCAA | 650 |
|    | GGCCAAGGCC | ACTGGTAAGA  | CTCTCCTCGA  | GGCCATTGAC | GCCATCGACC | 700 |
|    | CTCCTTCGCG | CCCCACCGAC  | AAGCCCCCTC  | GTCTTCCCCT | CCAGGATGTC | 750 |
|    | TACAAGATCG | GTGGTATTGG  | CACGGTGCCC  | GTCGGCCGTG | TCGAGACCGG | 800 |

|    |            |            |            |            |            |      |
|----|------------|------------|------------|------------|------------|------|
|    | TACCATCAAG | GGTGGTATGG | TCGTACCTT  | CGCCCCGCT  | GGTGTACCA  | 850  |
|    | CTGAGGTCAA | GTCCGTCGAG | ATGCACCACG | AGCAGCTCTC | CGAGGGTCTC | 900  |
|    | CCCGGTGACA | ACGTCGGCTT | CAACGTCAAG | AACGTCTCCG | TCAAGGAGAT | 950  |
|    | CCGTCGTGGT | AACGTTGCCG | GTGACTCCAA | GAACGACCCC | CCCAAGGGTT | 1000 |
| 5  | GCGACTCCTT | CAACGCCCAG | GTCATCGTCC | TCAACCACCC | CGGTCAGGTC | 1050 |
|    | GGTGCTGGTT | ACGCACCCGT | CCTCGATTGC | CACACTGCCC | ACATCGCCTG | 1100 |
|    | CAAGTTCTCC | GAGCTTGTTG | AGAAGATTGA | CCGCCGTACC | GGCAAGTCCG | 1150 |
|    | TTGAGGCCGC | CCCCAAGTTC | ATCAAGTCTG | GTGACGCCGC | CATCGTCAAG | 1200 |
|    | ATGGTTCCTT | CCAAGCCTAT | GTGTGTTGAG | GCCTTCACTG | ACTACCCTCC | 1250 |
| 10 | TCTCGGTCGT | TTCGCCGTCC | GTGACATGAG | ACAGACCGTC | GCTGTCGGTG | 1300 |
|    | TCATCAAGTC | CGTCGCCAAG | TCCGACAAGC | AGGGTGCCGG | TAAGGTTACC | 1350 |
|    | AAGGCCGCTG | TCAAGGCTGG | CAAGAAGTAA |            |            | 1380 |

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## 2) INFORMATION FOR SEQ ID NO: 1993

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1383 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
- (B) STRAIN: 186AS
- (C) ACCESSION NUMBER: U14100

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993

|    |            |             |             |             |            |      |
|----|------------|-------------|-------------|-------------|------------|------|
|    | ATGGGTAAGG | AAGACAAGAC  | TCACATTAAC  | CTCGTCGTCA  | TCGGCCACGT | 50   |
|    | CGATTCGGGC | AAATCTACCA  | CCACTGGTCA  | TTTGATCTAC  | AAATGCGGTG | 100  |
| 35 | GTATTGACAG | CCGTACCATT  | GAGAAGTTCG  | AAAAGGAAGC  | CGAAGAGTTG | 150  |
|    | GGCAAGAAAT | CCTTCAAATA  | TGCGTGGGTC  | CTTGACAAAC  | TGAAGTCTGA | 200  |
|    | GCGTGAGCGT | GGTATCACCA  | TCGATATTGC  | CCTCTGGAAA  | TTCGAGACTC | 250  |
|    | CGAAGTACAG | TGTCACTGTC  | ATTGATGCTC  | CCGGCCATCG  | TGACTTCATC | 300  |
|    | AAGAACATGA | TCACTGGTAC  | CTCCCAGGCT  | GA CTGCGCTA | TCCTCATCAT | 350  |
| 40 | TGCTGCCGGT | ACTGGTGAGT  | TCGAGGCTGG  | TATCTCCAAG  | GATGGCCAGA | 400  |
|    | CTCGTGAGCA | CGCTCTGCTT  | GCTTTCACCC  | TTGGTGTGAG  | GCAACTCATC | 450  |
|    | GTTGCCATCA | ACAAGATGGA  | CACCACCAAG  | TGGTCCGAGT  | CCCGTTTCAA | 500  |
|    | CGAAATCATC | AAGGAGGTTT  | CCAAC TTCAT | CAAGAAGGTC  | GGATATAACC | 550  |
|    | CCAAGGCTGT | TCCCTTCGTG  | CCAATCTCTG  | GTTTCGAGGG  | TGACAACATG | 600  |
| 45 | ATTGAACCCT | CCCCCAACTG  | CACATGGTAC  | AAGGGCTGGA  | ACAAGGAGAC | 650  |
|    | TGCCTCTGGC | AAGTCTTCTG  | GTAAAACCCT  | TCTCGATGCC  | ATTGACGCCA | 700  |
|    | TTGAACCCCC | AACCCGTCCT  | ACCGATAAGC  | CCCTCCGTCT  | TCCCCTCCAG | 750  |
|    | GATGTGTACA | AAATCTCTGG  | TATTGGCACT  | GTTCCCGTCG  | GACGTGTTGA | 800  |
|    | GACTGGTGTC | ATCAAGCCCCG | GTATGGTCGT  | GACTTTCGCT  | CCCTCCAACG | 850  |
| 50 | TCACCACTGA | AGTCAAGTCC  | GTGCAAAATGC | ACCACCAACA  | ACTCCAGGCT | 900  |
|    | GGTTACCCTG | GCGACAACGT  | CGGCTTCAAC  | GTCAAGAACG  | TTTCAGTCAA | 950  |
|    | GGAAGTCCGC | CGTGGCAACG  | TTGCTGGCGA  | CTCCAAAAAT  | GATCCCCCTA | 1000 |
|    | AGGGCTGCGA | ATCCTTCAAT  | GCCCAGGTCA  | TCGTCCTTAA  | CCACCCCGGC | 1050 |

|   |            |            |            |            |            |      |
|---|------------|------------|------------|------------|------------|------|
|   | CAGGTTGGCG | CTGGTTATGC | CCCAGTCCTC | GACTGCCACA | CTGCCCACAT | 1100 |
|   | TGCTTGCAAG | TTCTCTGAGC | TTATTGAGAA | GATCGACCGC | CGTACCGGAA | 1150 |
|   | AGTCTGTTGA | GAACAACCCC | AAGTTCATCA | AGTCTGGTGA | TGCTGCTATC | 1200 |
|   | GTCAAGATGG | TTCCCTCCAA | GCCCATGTGC | GTGGAGCCCT | TCACTGACTA | 1250 |
| 5 | TCCCCCTCTT | GGACGTTTCG | CTGTCCGTGA | CATGAGACAA | ACCGTCGCTG | 1300 |
|   | TCGGTGTCAT | CAAGTCCGTC | ATCAAGTCTG | ACAAGACTGC | TGGCAAGGTC | 1350 |
|   | ACCAAGGCCG | CGCAGAAGGC | CACCAAGAAA | TAA        |            | 1383 |

10

## 2) INFORMATION FOR SEQ ID NO: 1994

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1383 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neurospora crassa*
- (C) ACCESSION NUMBER: D45837

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994

|    |             |             |            |            |             |      |
|----|-------------|-------------|------------|------------|-------------|------|
|    | ATGGGCAAGG  | AGGACAAGAC  | TCACATCAAC | GTCGTCGTTA | TCGGCCACGT  | 50   |
|    | CGATTCCGGC  | AAGTCTACCA  | CTACCGGTCA | CTTGATCTAC | AAGTGCGGTG  | 100  |
|    | GTATCGACAA  | GCGTACCATC  | GAGAAGTTCG | AGAAGGAAGC | CGCTGAGCTC  | 150  |
| 30 | GGTAAGGGTT  | CCTTCAAGTA  | TGCCTGGGTT | CTTGACAAGC | TCAAGGCCGA  | 200  |
|    | GCGTGAGCGT  | GGTATCACCA  | TCGATATCGC | CCTCTGGAAG | TTCGAGACTC  | 250  |
|    | CCAAGTACTA  | CGTCACCGTC  | ATCGATGCCC | CCGGTCATCG | TGATTTTCATC | 300  |
|    | AAGAACATGA  | TCACTGGTAC  | CTCCCAGGCT | GATTGCGCTA | TCCTCATCAT  | 350  |
|    | TGCCGCCGGT  | ACTGGTGAGT  | TCGAGGCTGG | TATCTCCAAG | GATGGCCAGA  | 400  |
| 35 | CCCGTGAGCA  | CGCCCTGCTC  | GCCTACACCC | TCGGTGTCAA | GCAGCTCATT  | 450  |
|    | GTTGCCATCA  | ACAAGATGGA  | CACCACCCAG | TGGTCCCAGA | CTCGTTTCGA  | 500  |
|    | GGAGATCATC  | AAGGAGACCA  | AGAACTTCAT | CAAGAAGGTT | GGCTACAACC  | 550  |
|    | CCGCTGGTGT  | CGCTTTCGTC  | CCCATCTCCG | GCTTCAACGG | CGACAACATG  | 600  |
|    | CTTGAGCCCT  | CCACCAACTG  | CCCCTGGTAC | AAGGGTTGGG | AGAAGGAGAC  | 650  |
| 10 | CAAGGCCGGC  | AAGGCCACTG  | GCAAGACCCT | CCTCGAGGCC | ATCGACGCCA  | 700  |
|    | TTGAGCCCCC  | CAAGCGTCCT  | ACCGACAAGC | CCCTCCGTCT | TCCCCTCCAG  | 750  |
|    | GATGTCTACA  | AGATCGGTGG  | TATCGGCACA | GTGCCCCTCG | GCCGTATCGA  | 800  |
|    | GACTGGTGTC  | CTCAAGCCCG  | GTATGGTCGT | TACCTTCGCT | CCTTCCAACG  | 850  |
|    | TCACCACTGA  | AGTCAAGTCC  | GTCGAGATGC | ACCACGAGCA | GCTTGCTCAG  | 900  |
| 15 | GGTGTCCCCG  | GTGACAACGT  | CGGCTTCAAC | GTGAAGAACG | TTTCCGTCAA  | 950  |
|    | GGATATCCGC  | CGTGGTAAACG | TTGCCGGTGA | CTCCAAGAAC | GACCCCCCTG  | 1000 |
|    | CTGGCGCCGC  | CTCTTTCACC  | GCCCAGGTCA | TCGTTCTCAA | CCACCCCGGT  | 1050 |
|    | CAGGTCGGTG  | CCCGCTACGC  | CCCCGTCCTC | GACTGCCACA | CTGCCCACAT  | 1100 |
|    | TGCCTGCAAG  | TTGCGCCGAGC | TCCTCGAGAA | GATCGACCGC | CGTACTGGTA  | 1150 |
| 50 | AGGCTGTTGA  | GGCCTCCCCC  | AAGTTCATCA | AGTCTGGTGA | TGCTGCCATC  | 1200 |
|    | GTCAAGATGA  | TTCCCTCCAA  | GCCCATGTGC | GTTGAGGCTT | TCACCGACTA  | 1250 |
|    | CCCTCCCCCTC | GGCCGTTTCG  | CCGTCCGTGA | CATGCGTCAG | ACCGTCGCCG  | 1300 |
|    | TCGGTGTCAT  | CAAGGCCGTC  | GACAAGTCCA | CCGCTGCCGC | TGGCAAGGTC  | 1350 |

ACCAAGTCCG CTGCCAAGGC CGCCAAGAAG TAA

1383

## 5 2) INFORMATION FOR SEQ ID NO: 1995

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases  
(B) TYPE: Nucleic acid  
10 (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospira anserina*  
(C) ACCESSION NUMBER: X74799

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995

20 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50  
CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG 100  
GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC 150  
GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA 200  
25 GCGTGAGCGT GGTATCACCA TCGATATTGC CCTCTGGAAG TTCGAGACCC 250  
CCAAGTACTA TGTCACCGTC ATTGATGCCC CCGGCCATCG TGATTTTCATC 300  
AAGAACATGA TTACTGGTAC TTCCCAGGCC GATTGCGCCA TTCTCATCAT 350  
TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400  
CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC 450  
30 GTCGCCATCA ACAAGATGGA CACCACCAAG TGGTCCGAGG CCCGCTTCAA 500  
CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC 550  
CCAAGACTGT TGCCTTCGTC CCCATCTCCG GTTTC AACCG CGACAACATG 600  
CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGGT 650  
CAAGGGTGGC AAGGCCACCG GCAAGACCCT CCTTGAGGCC ATCGACTCCA 700  
35 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750  
GATGTCTACA AGATCGGCGG TATCGGCACA GTCCCTGTCTG GCGGTATCGA 800  
GACTGGTATC CTCAAGCCCC GTATGGTCTGT TACCTTCGCT CCTTCCAACG 850  
TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900  
GGTGTTCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA 950  
40 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCCA 1000  
TGGGCGCCGC CTCTTTCGAT GCCCAGGTCA TCGTCCCTCAA CCACCCCGGC 1050  
CAGGTCGGTG CTGGTTACGC CCCCCTCCTC GATTGCCACA CTGCCCACAT 1100  
CGCCTGCAAG TTCTCTGAGC TCCTGCAGAA GATCGACCGC CGTACTGGTA 1150  
AGGCCGTTGA GGAGAGCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200  
45 GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA 1250  
CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300  
TCGGTGTGAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTT 1350  
ACCAAGTCCG CTGCCAAGGC TGGCAAGAAA TAA 1383

50

## 2) INFORMATION FOR SEQ ID NO: 1996

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1386 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Podospira curvicolla*  
(B) STRAIN: VLV  
(C) ACCESSION NUMBER: X96614

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996

15 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50  
CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG 100  
GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC 150  
GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA 200  
20 GCGTGAGCGT GGTATCACCA TTGATATCGC CCTCTGGAAG TTCGAGACCC 250  
CCAAGTACTA TGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTCATC 300  
AAGAACATGA TTAAGGTGAGT TTCCCAGGCC GATTGCGCCA TTCTCATCAT 350  
TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400  
CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC 450  
25 GTCGCCATCA ACAAGATGGA CACCACCAA TGGTCCGAGG CCCGCTTCAA 500  
CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC 550  
CCAAGACTGT TGCTTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG 600  
CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGGT 650  
CAAGGGTGGC AAGGCTACTG GCAAGACCCT CCTCGAGGCC ATCGACTCCA 700  
30 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTTCAG 750  
GACGTTTACA AGATCGGCGG TATCGGCACA GTCCCTGTCG GCCGTATCGA 800  
GACTGGTATC CTCAAGCCCG GTATGGTCGT TACCTTCGCC CCTTCCAACG 850  
TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCTCTGAG 900  
GGTGTCCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA 950  
35 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTC 1000  
TTGGCGCCGC TTCTTTCGAT GCCCAGGTCA TCGTCTCTCA CCACCCCGGC 1050  
CAGGTCGGTG CTGGTTACGC CCCCGTCCTC GATTGCCACA CTGCCACAT 1100  
CGCCTGCAAG TTCGCTGAGC TCCTGCAGAA GATCGATCGC CGTACTGGTA 1150  
AGGCTGTTGA GGAGAGCCCT AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200  
40 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA 1250  
CCCTCCCCTC GGTCGTTTCG CTGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300  
TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTC 1350  
ACCAAGTCCG CTGCCAAGGC TGGTGGCAAG AAATAA 1386

45

## 2) INFORMATION FOR SEQ ID NO: 1997

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1383 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Sordaria macrospora*  
 (B) STRAIN: 000  
 (C) ACCESSION NUMBER: X96615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997

10  
 ATGGGTAAGG AAGACAAGGC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50  
 CGATTCCGGC AAGTCCACCA CTACCGGTCA CCTGATCTAC AAGTGCGGTG 100  
 GTATCGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC CGCTGAGCTC 150  
 GGCAAGGGTT CCTTCAAGTA TGCCTGGGTT CTTGACAAGC TCAAGGCCGA 200  
 15 GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTCGAGACTC 250  
 CCAAGTACTA CGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTCATC 300  
 AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TTCTCATCAT 350  
 TGCCGCTGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400  
 CTCGTGAGCA CGCTCTTCTC GCCTACACCC TCGGTGTCAA GCAGCTCATC 450  
 20 GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCCAGG CTCGTTTCGA 500  
 GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTC GGCTACAACC 550  
 CCGCCACCGT CGCTTTCGTC CCCATCTCCG GCTTCAACGG CGACAACATG 600  
 CTTGAGGCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC 650  
 CAAGGCCGGC AAGTCCACTG GCAAGACCCT CCTCGAGGCC ATCGACGCCA 700  
 25 TTGAGCAGCC CAAGCGCCCG ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750  
 GATGTCTACA AGATCGGCGG TATCGGCACA GTGCCCGTCG GCCGTATCGA 800  
 GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG 850  
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG 900  
 GGTGTTCCCG GTGACAACGT CGGCTTCAAC GTGAAGAACG TTTCCGTCAA 950  
 30 GGATATCCGT CGTGGTAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTG 1000  
 TCGGCGCTGC CTCTTTCACC GCCCAGGTCA TCGTCCTTAA CCACCCCGGT 1050  
 CAGGTCGGTG CCGGCTACGC TCCCGTCCTC GATTGCCACA CTGCCCACAT 1100  
 TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGATCGC CGTACTGGTA 1150  
 AGGCTGTTGA GACTTCTCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200  
 35 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTCGAGGCTT TCACCGACTA 1250  
 CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300  
 TCGGTGTCAT CAAGGCCGTC GACAAGACCC AGGCTGTCGC TGGCAAGGTC 1350  
 ACCAAGTCTG CTGCCAAGGC TGCCAAGAAG TAA 1383

10

2) INFORMATION FOR SEQ ID NO: 1998

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1383 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichoderma reesei*

(B) STRAIN: QM9414

(C) ACCESSION NUMBER: Z23012

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998

5  
 ATGGGTAAGG AGGACAAGAC TCACATCAAC GTGGTCGTCA TCGGCCACGT 50  
 CGACTCCGGC AAGTCTACCA CCACTGGTCA CTTGATCTAC CAGTGCGGTG 100  
 GTATCGACAA GCGTACCATT GAGAAGTTCG AGAAGGAAGC CGCCGAAGTC 150  
 GGCAAGGGTT CCTTCAAGTA CGCGTGGGTT CTTGACAAGC TCAAGGCCGA 200  
 10 GCGTGAGCGT GGTATCACCA TCGACATTGC CCTCTGGAAG TTCGAGACTC 250  
 CCAAGTACTA TGTCACCGTC ATTGACGCTC CCGGCCACCG TGAATTCATC 300  
 AAGAACATGA TCACTGGTAC TTCCCAGGCC GACTGCGCTA TCCTCATCAT 350  
 CGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400  
 CCCGTGAGCA CGCTCTGCTC GCCTACACCC TGGGTGTCAA GCAGCTCATC 450  
 15 GTCGCCATCA ACAAGATGGA CACTGCCAAC TGGGCCGAGG CTCGTTACCA 500  
 GGAAATCATC AAGGAGACTT CCAACTTCAT CAAGAAGGTC GGCTTCAACC 550  
 CCAAGGCCGT TGCTTTCGTC CCCATCTCCG GCTTCAACGG TGACAACATG 600  
 CTCACCCCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGAC 650  
 CAAGGCTGGC AAGTTCACCG GCAAGACCCT CCTTGAGGCC ATCGACTCCA 700  
 20 TCGAGCCCCC CAAGCGTCCC ACGGACAAGC CCCTGCGTCT TCCCCTCCAG 750  
 GACGTCTACA AGATCGGTGG TATCGGAACA GTTCCCGTCG GCCGTATCGA 800  
 GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCCTCCAACG 850  
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900  
 GGCCAGCCTG GTGACAACGT TGGTTTCAAC GTGAAGAACG TTTCCGTCAA 950  
 25 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCCA 1000  
 TGGGCGCCGC TTCTTTCACC GCCCAGGTCA TCGTCATGAA CCACCCCGGC 1050  
 CAGGTCGGTG CCGGCTACGC CCCCGTCCTC GACTGCCACA CTGCCCACAT 1100  
 TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACCGGTA 1150  
 AGGCTACCGA GTCTGCCCCC AAGTTCATCA AGTCTGGTGA CTCCGCCATC 1200  
 30 GTCAAGATGA TCCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA 1250  
 CCCTCCCCTG GGTCGTTTCG CCGTCCGTGA CATGCGCCAG ACCGTCGCTG 1300  
 TCGGTGTCAT CAAGGCCGTC GAGAAGTCCT CTGCCGCCGC CGCCAAGGTC 1350  
 ACCAAGTCCG CTGCCAAGGC CGCCAAGAAA TAA 1383

35

## 2) INFORMATION FOR SEQ ID NO: 1999

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 29 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999

CATGTCAAYA TTGGTACTAT TGGTCATGT

29

50

## 2) INFORMATION FOR SEQ ID NO: 2000

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000

CCACCYTCIC TCAMGTTGAA RCGTT

## 2) INFORMATION FOR SEQ ID NO: 2001

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001

ACYACITTRA CIGCYGCIAT YAC

## 2) INFORMATION FOR SEQ ID NO: 2002

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002

CCIGARGARA GAGCIMGWGG T

## 2) INFORMATION FOR SEQ ID NO: 2003

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single



(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003

CATYTCRAIR TTGTCACCTG G

21

## 2) INFORMATION FOR SEQ ID NO: 2004

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: SC5314
- (C) ACCESSION NUMBER: Genome project

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004

|             |             |            |            |            |      |
|-------------|-------------|------------|------------|------------|------|
| GCTGCCTTCG  | ACCGTTCTAA  | ACCTCATGTC | AACATTGGTA | CTATTGGTCA | 50   |
| TGTTGATCAT  | GGTAAACTA   | CATTGACTGC | TGCTATCACC | AAAGTTTTAG | 100  |
| CCGAACAAGG  | TGGTGCCAAC  | TTCTTGGATT | ATGGTTCTAT | TGATAGAGCT | 150  |
| CCAGAAGAAA  | GAGCTAGAGG  | TATCACTATT | TCCACTGCCC | ACGTTGAATA | 200  |
| CGAAACCAAG  | AACAGACACT  | ATGCCCACGT | TGATTGTCCA | GGACACGCTG | 250  |
| ATTATATCAA  | AAATATGATT  | ACTGGTGCCG | CTCAAATGGA | TGGTGCTATC | 300  |
| ATTGTTGTTG  | CTGCCACTGA  | TGGTCAAATG | CCTCAAACCA | GAGAACATTT | 350  |
| GTTATTGGCC  | AGACAAGTTG  | GTGTTCAAGA | CTTGGTTGTG | TTTGTCAACA | 400  |
| AAGTCGATAC  | TATTGATGAC  | CCTGAAATGT | TGGAATTAGT | CGAAATGGAA | 450  |
| ATGAGAGAAT  | TGTTATCCAC  | CTACGGTTTT | GATGGTGACA | ACACTCCAGT | 500  |
| TATTATGGGA  | TCTGCTTTAA  | TGGCTTTGGA | AGACAAGAAA | CCAGAAATTG | 550  |
| GTAAGGAAGC  | TATCTTGAAA  | TTGTTAGATG | CTGTCGATGA | ACACATTCCA | 600  |
| ACTCCATCAA  | GAGACTTGGA  | ACAACCATTT | TTGTTACCAG | TTGAAGACGT | 650  |
| GTTCTCCATC  | TCCGGTAGAG  | GAAGTGTGT  | CACTGGTAGA | GTTGAAAGAG | 700  |
| GTGTTTTGAA  | GAAGGGTGAA  | GAAATCGAAA | TTGTTGGTGG | TTTTGACAAA | 750  |
| CCTTACAAGA  | CTACTGTTAC  | CGGTATTGAA | ATGTTCAAAA | AAGAATTAGA | 800  |
| CTCTGCTATG  | GCTGGTGACA  | ACTGTGGTGT | TTTGTTAAGA | GGTGTTAAAA | 850  |
| GAGATGAAAT  | CAAGAGAGGT  | ATGGTTTTGG | CCAAACCAGG | TACTGCTACT | 900  |
| TCTCACAAAG  | AGTTCTTGGC  | TTCCTTGTAT | ATTTTGACTT | CCGAAGAAGG | 950  |
| TGGTCGTTCC  | ACTCCATTTG  | GTGAAGGTTA | CAAGCCTCAA | TGCTTCTTCA | 1000 |
| GAACATAACGA | TGTCCTACC   | ACATTTTCAT | TCCCAGAAGG | AGAAGGTGTT | 1050 |
| GATCATTCTC  | AAATGATCAT  | GCCAGGTGAC | AACATTGAAA | TGGTTGGTGA | 1100 |
| ATTGATCAAA  | TCTTGTTCCAT | TAGAAGTCAA | CCAACGTTTC | AACTTGAGAG | 1150 |
| AAGGTGGTAA  | AACTGTTGGT  | ACTGGTTTGA | TTACCAGAAT | CATCGAATAA | 1200 |
| ACAGAATGTG  | CACTGTGAAT  | AATAAAAAGA | AAAGAGGTAT | ATATAGGTGA | 1250 |
| CTTTGTATTT  | TGTATTGAAC  | AATAAAATTC | TGTAAATAGT | AAGGGCCTCA | 1300 |
| GAAGTTTTGA  | TTTGATTTAT  | GCCATGTGGA | CTTGTAGAGA | TATCCTTCTC | 1350 |
| AAACTTCTTG  |             |            |            |            | 1360 |

## 2) INFORMATION FOR SEQ ID NO: 2005

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005

|             |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------|
| AAGCCGCATG  | TCAATATTGG | TACTATTGGT | CATGTTGACC | ACGGTAAAAC | 50   |
| GACGTTGACG  | GCTGCTATTA | CTAAATGCCT | TTCTGATCTT | GGTCAAGCTA | 100  |
| GTTTTATGGA  | TTATAGTCAA | ATTGACAAGG | CCCCCGAGGA | AAAGGCACGT | 150  |
| GGTATTACCA  | TTTCATCTGC | CCATGTTGAA | TACGAAACTG | CTAATCGTCA | 200  |
| CTATGCCCAT  | GTGGATTGTC | CTGGTCACGC | CGATTACATT | AAGAATATGA | 250  |
| TTACTGGTGC  | TGCTACAATG | GATGGCGCTA | TCATTGTTGT | TTCTGCTACC | 300  |
| GATGGTCAAA  | TGCCTCAAAC | TCGTGAACAT | TTGCTTCTGG | CTCGTCAAGT | 350  |
| CGGTGTAAAG  | CAAATTGTTG | TATACATCAA | TAAAGTCGAT | ATGGTCGAGC | 400  |
| CTGATATGAT  | CGAGCTTGTC | GAAATGGAAA | TGCGTGAGCT | ACTCTCCGAA | 450  |
| TACGGATTTG  | ATGGTGACAA | TACTCCAATT | GTTAGCGGCA | GTGCTTTATG | 500  |
| TGCCTTAGAG  | GGTCGTGAGC | CTGAGATTGG | TCTCAATAGT | ATTACTAAAT | 550  |
| TGATGGAAGC  | TGTTGATAGT | TATATTACTC | TTCCTGAAAG | AAAAACGGAT | 600  |
| GTCCCTTTCT  | TGATGGCCAT | CGAGGACGTT | TTTTCAATTT | CAGGTCGCGG | 650  |
| AACTGTAGTC  | ACTGGCCGTG | TCGAGCGCGG | TACTTTAAAG | AAGGGTGCTG | 700  |
| AAATCGAAAT  | CGTCGGTTAT | GGTAGCCATT | TAAAGACTAC | CGTTACTGGA | 750  |
| ATTGAAATGT  | TCAAAAAGCA | GCTTGATGCC | GCCGTTGCCG | GTGACAATTG | 800  |
| TGGCCTTTTA  | CTTCGTTCTA | TCAAGCGAGA | GCAATTAAAA | CGTGGAATGA | 850  |
| TTGTCGCTCA  | ACCAGGAACC | GTTGCTCCTC | ATCAGAAATT | CAAGGCATCA | 900  |
| TTCTATATTT  | TGACAAAAGA | GGAAGGAGGT | CGTCGTACCG | GTTTCGTTGA | 950  |
| CAAGTATCGT  | CCCCAACTGT | ACAGTCGTAC | TTCCGACGTT | ACTGTCGAAC | 1000 |
| TTACCCACCC  | TGATCCTAAC | GACTCAGACA | AAATGGTTAT | GCCTGGAGAC | 1050 |
| AATGTCGAGA  | TGATCTGTAC | GCTTATTCAC | CCCATTGTCA | TCGAAAAAGG | 1100 |
| ACAACGCTTC  | ACAGTTCGTG | AGGGTGGAAG | CACTGTAGGC | ACAGCTTTGG | 1150 |
| TTACTGAACT  | TTTGGATTAG | TGCATTTATG | AACTTATTGG | CTTTAAAAAT | 1200 |
| TTTGTCATGCT | GAATACCAAT | ATTATGTCCC | TTCTCAGAAT | TCTATAACTA | 1250 |
| CAGTGTCATT  | ATTGTAATAA | GACTTTTGCA | TCCATTGACA | ATGGTATTTG | 1300 |
| ATACTTTTAT  | AGTTTCTACT | ATTGTTAGCC | AAAGTTATAA | AA         | 1342 |

2) INFORMATION FOR SEQ ID NO: 2006

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006

TGGAGCCGGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2007

1045

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007

TGGAGCCAGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2008

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008

TCTGGAGCCG ATGAGCGTG

19

2) INFORMATION FOR SEQ ID NO: 2009

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009

CTGGAGCCAG TAAGCGTGG

19

2) INFORMATION FOR SEQ ID NO: 2010

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 861 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*  
 (B) STRAIN: KMK107  
 (C) ACCESSION NUMBER: AF027199

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGAGTATTC | AACATTTTCG | TGTCGCCCTT | ATTCCCTTTT | TTGCGGCATT | 50  |
| TTGCCTTCCT | GTTTTTGCTC | ACCCAGAAAC | GCTGGTGAAA | GTAAAAGATG | 100 |
| CTGAAGATCA | GTTGGGTGCA | CGAGTGGGT  | ACATCGAACT | GGATCTCAAC | 150 |
| AGCGGTAAGA | TCCTTGAGAG | TTTTCGCCCC | GAAGAACGTT | TTCCAATGAT | 200 |
| GAGCACTTTT | AAAGTTCTGC | TATGTGGTGC | GGTATTATCC | CGTGTTGACG | 250 |
| CCGGGCAAGA | GCAACTCGGT | CGCCGCATAC | ACTATTCTCA | GAATGACTTG | 300 |
| GTTAAGTACT | CACCAGTCAC | AGAAAAGCAT | CTTACGGATG | GCATGACAGT | 350 |
| AAGAGAATTA | TGCAGTGCTG | CCATAACCAT | GAGTGATAAC | ACTGCTGCCA | 400 |
| ACTTACTTCT | GACAACGATC | GGAGGACCGA | AGGAGCTAAC | CGCTTTTTTG | 450 |
| CACAACATGG | GGGATCATGT | AACTCGCCTT | GATCGTTGGG | AACCGGAGCT | 500 |
| GAATGAAGCC | ATACCAAACG | ACGAGCGTGA | CACCACGACG | CCTGCAGCAA | 550 |
| TGGCAACAAC | GTTGCGCAAA | CTATTAAGTG | GCGAACTACT | TACTCTAGCT | 600 |
| TCCCGGCAAC | AATTAATAGA | CTGGATGGAG | GCGGATAAAG | TTGCAGGACC | 650 |
| ACTTCTGCGC | TCGGCCCTTC | CGGCTGGCTG | GTTTATTGCT | GATAAATCTG | 700 |
| GAGCCAGTGA | GCGTGGGTCT | CGCGGTATCA | TTGCAGCACT | GGGGCCAGAT | 750 |
| GGTAAGCCCT | CCCGTATCGT | AGTTATCTAC | ACGACGGGGA | GTCAGGCAAC | 800 |
| TATGGATGAA | CGAAATAGAC | AGATCGCTGA | GATAGGTGCC | TCACTGATTA | 850 |
| AGCATTGGTA | A          |            |            |            | 861 |

## 2) INFORMATION FOR SEQ ID NO: 2011

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*  
 (B) STRAIN: CLSiS L-491  
 (C) ACCESSION NUMBER:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGAGTATTC | AACATTTCCG | TGTCGCCCTT | ATTCCCTTTT | TTGCGGCATT | 50  |
| TTGCTTTCCT | GTTTTTGCTC | ACCCAGAAAC | GCTGGTGAAA | GTAAAAGATG | 100 |
| CTGAAGATCA | GTTGGGTGCA | CGAGTGGGT  | ACATCGAGCT | GGATCTCAAC | 150 |
| AGCGGTAAGA | TCCTTGAGAG | TTTTCGCCCC | GAAGAACGTT | TTCCAATGAT | 200 |
| GAGCACTTTT | AAAGTTCTGC | TATGTGGTGC | GGTATTATCC | CGTGTTGACG | 250 |
| CCGGGCAAGA | GCAACTCGGT | CGCCGCATAC | ACTATTCTCA | GAATGACTTG | 300 |
| GTTGAGTACT | CACCAGTCAC | AGAAAAGCAT | CTTACGGATG | GCATGACAGT | 350 |
| AAGAGAATTA | TGCAGTGCTG | CCATAACCAT | GAGTGATAAC | ACTGCGGCCA | 400 |
| ACTTACTTCT | GACAACGATC | GGAGGACCGA | AGGAGCTAAC | CGCTTTTTTG | 450 |
| CACAACATGG | GGGATCATGT | AACCCGCCTT | GATCGTTGGG | AACCGGAGCT | 500 |
| GAATGAAGCC | ATACCAAACG | ACGAGCGTGA | CACCACGATG | CCTGCAGCAA | 550 |
| TGGCAACAAC | GTTGCGCAAA | CTATTAAGTG | GCGAACTACT | TACTCTAGCT | 600 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TCCCGGCAAC | AATTAATAGA | CTGGATGGAG | GCGGATAAAG | TTGCAGGACC | 650 |
| ACTTCTGCGC | TCGGCCCTTC | CGGCTGGCTG | GTTTATTGCT | GATAAATCTG | 700 |
| GAGCCAGTAA | GCGTGGATCT | CGCGGTATCA | TTGCAGCACT | GGGGCCAGAT | 750 |
| GGTAAGCCCT | CCCGTATCGT | AGTTATCTAC | ATGACGGGGA | GTCAGGCAAC | 800 |
| TATGGATGAA | CGAAATAGAC | AGATCGCTGA | GATAGGTGCC | TCACTGATTA | 850 |
| AGCATTGGTA | A          |            |            |            | 861 |

## 2) INFORMATION FOR SEQ ID NO: 2012

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012

CCGCGGATTA TTAAACCGCC CTTCCGCGG-MR-HEG-ATGTCAGAGG GATAGATCCA 49

## 2) INFORMATION FOR SEQ ID NO: 2013

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
- (B) STRAIN: ATCC 33433

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| AGCTTAAGAA | CTCTTATCTG | GATTACGCGA | TGTCGGTCAT | TGTTGGCCGT | 50  |
| GCGCTGCCGG | ATGTCCGAGA | TGGCCTGAAG | CCGGTACACC | GTCGCGTACT | 100 |
| TTACGCCATG | AACGTATTGG | GCAATGACTG | GAACAAAGCC | TACAAAAAAT | 150 |
| CAGCCCGTGT | CGTGGGTGAC | GTGATCGGTA | AATATCACCC | GCATGGTGAT | 200 |
| ACTGCCGTCT | ATGACACTAT | CGTCCGTATG | GCACAGCCAT | TCTCACTGCG | 250 |
| ATACATGCTG | GTAGATGGTC | AAGGTAACCT | CGGTTCTGTC | GATGGCGACT | 300 |
| CCGCCGCAGC | GATGCGTTAT | ACGGAAATCC | GTATGTCGAA | AATCGCCCAT | 350 |
| GAG        |            |            |            |            | 353 |

## 2) INFORMATION FOR SEQ ID NO: 2014

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 bases
- (B) TYPE: Nucleic acid

1048

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
- (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| AGCTCCTATC | TGGATTATGC | GATGTCGGTC | ATTGTTGGCC | GTGCGCTGCC | 50  |
| AGATGTCCGA | GATGGCCTGA | AGCCGGTACA | CCGTCGCGTA | CTTTACGCCA | 100 |
| TGAACGTACT | AGGCAATGAC | TGGAACAAAG | CCTATAAAAA | ATCTGCCCGT | 150 |
| GTCGTTGGTG | ACGTAATCGG | TAAATACCAT | CCCCATGGTG | ACTCGGCGGT | 200 |
| CTATGACACG | ATCGTCCGCA | TGGCGCAGCC | ATTCTCGCTG | CGTTATATGC | 250 |
| TGGTAGACGG | TCAGGGTAAC | TTCGGTTCTA | TCGACGGCGA | CTCTGCGGCG | 300 |
| GCAATGCGTT | ATACGGAAAT | CCGTCTGGCG | AAAATTGCCC | ATGAACTGAT | 350 |
| GGCCG      |            |            |            |            | 355 |

## 2) INFORMATION FOR SEQ ID NO: 2015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015

CCAAGAAGCT CAAAACATC TG

22

## 2) INFORMATION FOR SEQ ID NO: 2016

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016

TADCCTGTCC AWACAGCCAT

20

## 2) INFORMATION FOR SEQ ID NO: 2017

(i) SEQUENCE CHARACTERISTICS:

1049

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017

ACTTTGAATA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2018

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018

ACACTAAACA AGGTTGGTTT AG

22

2) INFORMATION FOR SEQ ID NO: 2019

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019

ACACTAAACA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2020

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020



GTAGCTCCAG ATGAAATGTT TG

22

## 2) INFORMATION FOR SEQ ID NO: 2021

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021

GTAGCTCCAG ACGAAATGTT TG

22

## 2) INFORMATION FOR SEQ ID NO: 2022

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022

GTAGCTCCAG ATGAAACGTT TG

22

## 2) INFORMATION FOR SEQ ID NO: 2023

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023

GTAAGTCCAG ATGAAATGTT TG

22

## 2) INFORMATION FOR SEQ ID NO: 2024

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

1051

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024

AGTGAAAAGA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2025

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025

AGTGAGAAAA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2026

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026

TCCAAGCATG CATTATGCAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2027

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027

TCGGTCTAGA TAGAGCTAAA ACG

23

## 2) INFORMATION FOR SEQ ID NO: 2028

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028

TATGCTCTTC AACAATCACG

20

## 2) INFORMATION FOR SEQ ID NO: 2029

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029

AGCCGTTGAG ACTTTGAATA AG

22

## 2) INFORMATION FOR SEQ ID NO: 2030

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030

CTTAATGGTC TTGGTATCG

19

## 2) INFORMATION FOR SEQ ID NO: 2031

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single

1053

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031

CGTGACTGGG GTTCTGCTAT GA

22

2) INFORMATION FOR SEQ ID NO:2032

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032

CGTGACTGGG GATCATCAAT GA

22

2) INFORMATION FOR SEQ ID NO: 2033

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033

CGTGACTGGG GTTCTGCCAT GA

22

2) INFORMATION FOR SEQ ID NO: 2034

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034

ATCAAGAACA CTGGCTATGT AG

22

## 2) INFORMATION FOR SEQ ID NO: 2035

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035

ATCAAGAACA CTGGCTACGT AG

22

## 2) INFORMATION FOR SEQ ID NO: 2036

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036

ATCAAGAACA CTGGTTACGT AG

22

## 2) INFORMATION FOR SEQ ID NO: 2037

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037

ATCAAAAATA CTGGTTATGT AG

22

## 2) INFORMATION FOR SEQ ID NO: 2038

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single

1055

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038

ATCAAGAATA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2039

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039

ATCAAAAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2040

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040

TGTGACCCCA GACAAACCC

19

2) INFORMATION FOR SEQ ID NO: 2041

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041

GTTGAGCGGC AGCACTATCT

20

2) INFORMATION FOR SEQ ID NO: 2042

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042

CACGGGGATT TCTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2043

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043

CACGGGGATT ACTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2044

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044

ACCGTAAGTC GGCCAAGTCA

20

2) INFORMATION FOR SEQ ID NO: 2045

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045

1057

GTTCTTTCTC CGTATCGTC

19

## 2) INFORMATION FOR SEQ ID NO: 2046

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046

ACGGGGATTT TTCTATCTAT

20

## 2) INFORMATION FOR SEQ ID NO: 2047

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: CS109
- (C) ACCESSION NUMBER: Z49094

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGAACAAAC | CAACGATTCT | GCGCCTAATC | AAGTATCTGA | GCATTAGCTT | 50  |
| CTTAAGCTTG | GTTATCGCAG | CCATTGTCTT | AGGCGGAGGA | GTTTTTTTCT | 100 |
| ACTATGTTAG | CAAGGCTCCT | AGCCTATCCG | AGAGTAAACT | AGTTGCAACA | 150 |
| ACCTCTAGTA | AAATCTACGA | CAATAAAAAT | CAACTCATTG | CTGACTTGGG | 200 |
| TTCTGAACGC | CGCGTCAATG | CCCAAGCTAA | TGATATTCCC | ACAGATTTGG | 250 |
| TTAAGGCAAT | CGTTTCTATC | GAAGACCATC | GCTTCTTCGA | CCACAGGGGG | 300 |
| ATTGATACCA | TCCGTATCCT | GGGAGCTTTC | TTGCGCAATC | TGCAAAGCAA | 350 |
| TTCCCTCCAA | GGTGGATCAA | CTCTCACCCA | ACAGTTGATT | AAATTGACTT | 400 |
| ACTTTTCAAC | CTCGACTTCC | GACCAGACTA | TTTCTCGTAA | GGCTCAGGAA | 450 |
| GCTTGGTTAG | CGATTCAAGT | AGAACAAAAA | GCAACCAAAC | AGGAAATCTT | 500 |
| GACCTACTAT | ATAAATAAGG | TCTACATGTC | TAATGGCAAC | TATGGAATGC | 550 |
| AGACAGCAGC | TCAAAACTAC | TATGGTAAAG | ACCTCAATAA | TTTAAGTTTA | 600 |
| CCTCAGTTAG | CCTTGCTGGC | TGGAATGCCT | CAGGCACCAA | ACCAATATGA | 650 |
| CCCCTATTCA | CATCCAGAAG | CAGCCCAAGA | CCGCCGAAAC | TTGGTCTTAT | 700 |
| CTGAAATGAA | AAATCAAGGT | TACATCTCTG | CTGAACAGTA | TGAGAAAGCA | 750 |
| GTCAATACAC | CAATTACTGA | TGGACTACAA | AGTCTCAAAT | CAGCAAGTAA | 800 |
| TTACCCTGCT | TACATGGATA | ATTACCTCAA | GGAAGTCATC | AATCAAGTTG | 850 |
| AAGAAGAAAC | TGGCTATAAC | CTTCTAACTA | CTGGGATGGA | TGTTTACACA | 900 |

1058



|            |            |            |             |            |      |
|------------|------------|------------|-------------|------------|------|
| AATGTAGACC | AAGAAGCTCA | AAAACATCTG | TGGGATATCT  | ACAACTCCGA | 950  |
| TCAATACGTC | TCTTACCCTG | ACGATGATTT | GCAAGTCGCA  | TCTACGGTCG | 1000 |
| TAGATGTTTC | AAATGGTAAA | GTCATCGCAC | AAC TTGGTGC | TCGTCATCAA | 1050 |
| GCAAGTAATG | TTTCATTTCG | TACCAACCAG | GCCGTAGAAA  | CCAATCGTGA | 1100 |
| CTGGGGATCA | TCAATGAAAC | CAATCACTGA | CTATGCTCCC  | GCTTTAGAAT | 1150 |
| ATGGAGTCTA | TGACTCTACT | GCTTCTATTG | TACATGATGT  | CCCTTATAAC | 1200 |
| TATCCTGGCA | CTGATACTCC | ACTCTACAAC | TGGGATCATG  | TCTACTTTGG | 1250 |
| AAACATTACA | ATCCAGTATG | CTCTTCAACA | ATCACGAAAT  | GTCACAGCCG | 1300 |
| TTGAGACTTT | GAATAAGGTC | GGTCTAGATA | GAGCTAAAAC  | CTTCCTTAAT | 1350 |
| GGTCTTGGTA | TCGACTATCC | AAGCATGCAT | TATGCAAACG  | CCATTTCAAG | 1400 |
| TAACACAAC  | GAATCCAACA | AAAAATATGG | TGCAAGTAGT  | GAAAAAATGG | 1450 |
| CTGCTGCCTA | CGCTGCTTTT | GCTAATGGTG | GTATTTATCA  | CAAACCAATG | 1500 |
| TATATCAATA | AAATCGTCTT | TAGTGATGGT | AGCGAAAAAG  | AATTTTCTGA | 1550 |
| TGCTGGTACA | CGAGCTATGA | AAGAGACTAC | TGCCTATATG  | ATGACTGAAA | 1600 |
| TGATGAAAAC | TGTTTTAACT | TACGGAACAG | GACGTGGAGC  | CTACCTACCA | 1650 |
| TGGCTTCCAC | AAGCAGGTAA | GACAGGTACT | TCTAACTATA  | CTGACGAAGA | 1700 |
| AATTGAAAAG | TATATCAAGA | ACACTGGTTA | CGTAGCTCCA  | GATGAAATGT | 1750 |
| TTGTAGGGTA | TACCCGTAAA | TATGCAATGG | CTGTTTGGAC  | AGGATACTCA | 1800 |
| AATCGTCTAA | CTCCAATCAT | CGGAGATGGT | TTCCTTGTTG  | CTGGTAAAGT | 1850 |
| CTATCGTTCA | ATGATAACTT | ACCTTTCTGA | AGATGACCAA  | CCTGGAGATT | 1900 |
| GGACAATGCC | AGATGGCTTG | TATAGAAATG | GAGAATTTCGT | ATTTAAAAAT | 1950 |
| GGTGCTCGTT | CTACGTGGAG | CTCACCTGCT | CCACAACAAC  | CCCCATCAAC | 2000 |
| TGAAAGTTCA | AGCTCATCAT | CAGATAGTTC | AACTTCACAG  | TCTAACTCAA | 2050 |
| CCACTCCAAG | CACAAATAAT | AGTACGACTA | CCAATCCTAA  | CAATAATACG | 2100 |
| CAACAATCAA | ATACAACCCC | TGATCAACAA | AATCAGAATC  | CTCAACCAGC | 2150 |
| ACAACCATAA |            |            |             |            | 2160 |

## 2) INFORMATION FOR SEQ ID NO: 2048

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: R6
- (C) ACCESSION NUMBER: M90527

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGAACAAAC | CAACGATTCT | GCGCCTAATC | AAGTATCTGA | GCATTAGCTT | 50  |
| CTTAAGCTTG | GTTATCGCAG | CCATTGTCTT | AGGCGGAGGA | GTTTTTTTCT | 100 |
| ACTACGTTAG | CAAGGCTCCT | AGCCTATCCG | AGAGTAAACT | AGTTGCAACA | 150 |
| ACTTCTAGTA | AAATCTACGA | CAATAAAAAT | CAACTCATTG | CTGACTTGGG | 200 |
| TTCTGAACGC | CGCGTCAATG | CCCAAGCTAA | TGATATTCCC | ACAGATTTGG | 250 |
| TTAAGGCAAT | CGTTTCTATC | GAAGACCATC | GCTTCTTCGA | CCACAGGGGG | 300 |
| ATTGATACCA | TCCGTATCCT | GGGAGCTTTC | TTGCGCAATC | TGCAAAGCAA | 350 |
| TTCCCTCCAA | GGTGGATCAG | CTCTCACTCA | ACAGTTGATT | AAGTTGACTT | 400 |
| ACTTTTCAAC | TTCGACTTCC | GACCAGACTA | TTTCTCGTAA | GGCTCAGGAA | 450 |
| GCTTGGTTAG | CGATTTCAGT | AGAACAACAA | GCAACCAAGC | AAGAAATCTT | 500 |
| GACCTACTAT | ATAAATAAGG | TCTACATGTC | TAATGGGAAC | TATGGAATGC | 550 |

|            |            |            |             |            |      |
|------------|------------|------------|-------------|------------|------|
| AGACAGCAGC | TCAAAACTAC | TATGGTAAAG | ACCTCAATAA  | TTTAAGTTTA | 600  |
| CCTCAGTTAG | CCTTGCTGGC | TGGAATGCCT | CAGGCACCAA  | ACCAATATGA | 650  |
| CCCCTATTCA | CATCCAGAAG | CAGCCCAAGA | CCGCCGAAAC  | TTGGTCTTAT | 700  |
| CTGAAATGAA | AAATCAAGGC | TACATCTCTG | CTGAACAGTA  | TGAGAAAGCA | 750  |
| GTCAATACAC | CAATTACTGA | TGGGCTACAA | AGTCTCAAAT  | CAGCAAGTAA | 800  |
| TTACCCTGCT | TACATGGATA | ATTACCTCAA | GGAAGTCATC  | AATCAAGTTG | 850  |
| AAGAAGAAAC | AGGCTATAAC | CTACTCACAA | CTGGGATGGA  | TGTCTACACA | 900  |
| AATGTAGACC | AAGAAGCTCA | AAAACATCTG | TGGGATATTT  | ACAATACAGA | 950  |
| CGAATACGTT | GCCTATCCAG | ACGATGAATT | GCAAGTCGCT  | TCTACCATTG | 1000 |
| TTGATGTTTC | TAACGGTAAA | GTCATTGCC  | AGCTAGGAGC  | ACGCCATCAG | 1050 |
| TCAAGTAATG | TTTCCTTCGG | AATTAACCAA | GCAGTAGAAA  | CAAACCGCGA | 1100 |
| CTGGGGATCA | ACTATGAAAC | CGATCACAGA | CTATGCTCCT  | GCCTTGAGGT | 1150 |
| ACGGTGTCTA | CGAGTCAACT | GCCACTATCG | TTCACGATGA  | GCCCTATAAC | 1200 |
| TACCCTGGGA | CAAATACCCC | TGTTTATAAC | TGGGATAGGG  | GCTACTTTGG | 1250 |
| CAACATCACC | TTGCAATACG | CCCTGCAACA | ATCGCGAAAC  | GTCCCAGCCG | 1300 |
| TGGAAACTCT | AAACAAGGTC | GGACTCAACC | GCGCCAAGAC  | TTTCCTAAAT | 1350 |
| GGTCTCGGAA | TCGACTACCC | AAGTATTCAC | TACTCAAATG  | CCATTTCAAG | 1400 |
| TAACACAACC | GAATCAGACA | AAAAATATGG | AGCAAGTAGT  | GAAAAGATGG | 1450 |
| CTGCTGCTTA | CGCTGCCTTT | GCAAATGGTG | GAACCTACTA  | TAAACCAATG | 1500 |
| TATATCCATA | AAGTCGTCTT | TAGTGATGGG | AGTGAAAAAG  | AGTTCTCTAA | 1550 |
| TGTCGGAAC  | CGTGCCATGA | AAGAAACGAC | AGCCTATATG  | ATGACCGACA | 1600 |
| TGATGAAAAC | AGTCTTGAGT | TATGGAAGT  | GACGAAATGC  | CTATCTTGCT | 1650 |
| TGGCTCCCTC | AGGCTGGTAA | AACAGGAACC | TCTAACTATA  | CAGACGAGGA | 1700 |
| AATTGAAAAC | CACATCAAGA | CCTCTCAATT | TGTAGCACCT  | GATGAACAT  | 1750 |
| TTGCTGGCTA | TACGCGTAAA | TATTCAATGG | CTGTATGGAC  | AGGCTATTCT | 1800 |
| AACCGTCTGA | CACCACTTGT | AGGCAATGGC | CTTACGGTCG  | CTGCCAAAGT | 1850 |
| TTACCGCTCT | ATGATGACCT | ACCTGTCTGA | AGGAAGCAAT  | CCAGAGGATT | 1900 |
| GGAATATACC | AGAGGGGCTC | TACAGAAATG | GAGAATTTCG  | ATTTAAAAAT | 1950 |
| GGTGCTCGTT | CTACGTGGAG | CTCACCTGCT | CCACAACAAC  | CCCCATCAAC | 2000 |
| TGAAAGTTCA | AGCTCATCAT | CAGATAGTTC | AACCTTCACAG | TCTAGCTCAA | 2050 |
| CCACTCCAAG | CACAAATAAT | AGTACGACTA | CCAATCCTAA  | CAATAATACG | 2100 |
| CAACAATCAA | ATACAACCCC | TGATCAACAA | AATCAGAATC  | CTCAACCAGC | 2150 |
| ACAACCATAA |            |            |             |            | 2160 |

## 2) INFORMATION FOR SEQ ID NO: 2049

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: URU-E159
- (C) ACCESSION NUMBER: AF139890

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ATGAACAAAC | CAACGATTCT | GCGCCTAATC | AAGTATCTGA | GCATTAGCTT | 50  |
| CTTAAGCTTG | GTTATCGCAG | CCATTGTCTT | AGGCGGAGGA | GTTTTTTTCT | 100 |
| ACTACGTTAG | CAAGGCTCCT | AGCCTATCCG | AGAGTAAACT | AGTTGCAACA | 150 |
| ACTTCTAGTA | AAATCTACGA | CAATAAAAAA | CAACTCATTG | CTGACTTGGG | 200 |

|            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------|
| TTCTGAACGC | CGCGTCAATG | CCCAAGCTAA | TGATATTCCC | ACAGATTTGG | 250  |
| TTAAGGCAAT | CGTTTCTATC | GAAGACCATC | GCTTCTTCGA | CCACAGGGGG | 300  |
| ATTGATTCCA | TCCGTATCCT | GGGAGCTTTC | TTGCGCAATC | TGCAAAGTAA | 350  |
| TTCCCTCCAA | GGTGGATCAA | CTCTCACCCA | ACAGTTGATT | AAGTTGACTT | 400  |
| ACTTTTCAAC | CTCGACTTCC | GACCAGACTA | TTTCTCGTAA | GGCTCAGGAA | 450  |
| GCTTGGTTAG | CGATTCAAGT | AGAACAAAAA | GCAACCAAAC | AGGAAATCTT | 500  |
| GACCTACTAT | ATAAATAAGG | TCTACATGTC | TAATGGCAAC | TATGGAATGC | 550  |
| AGACAGCAGC | TCAAAACTAC | TATGGTAAAG | ACCTCAATAA | TTTAAGTTTA | 600  |
| CCTCAGTTAG | CCTTGCTGGC | TGGAATGCCT | CAGGCACCAA | ACCAATATGA | 650  |
| CCCCTATTCA | CATCCAGAAG | CAGCCCAAGA | CCGCCGAAAC | TTGGTCTTAT | 700  |
| CTGAAATGAA | AAATCAAGGT | TACATCTCTG | CTGAACAGTA | TGAGAAAGCA | 750  |
| GTCAATACAC | CAATTACTGA | TGGACTACAA | AGTCTCAAAT | CAGCAAGTAA | 800  |
| TTACCCTGCT | TACATGGATA | ATTACCTCAA | GGAGGTCATC | AATCAAGTAG | 850  |
| AACAAGAAAC | TGGCTATAAC | CTTCTAACTA | CTGGGATGGA | TGTTTACACA | 900  |
| AATGTAGACC | AAGAAGCTCA | AAAACATCTG | TGGGATATCT | ACAACTCCGA | 950  |
| TCAATACGTC | TCTTACCCTG | ACGATGATTT | GCAAGTCGCA | TCTACGGTCG | 1000 |
| TAGATGTTTC | AAATGGTAAA | GTCATCGCCC | AACTTGGAGC | TCGTCAACCA | 1050 |
| GCAAGTAAAC | TTTCATTGGG | TACCAACCAA | GCTGTGGAAA | CCAATCGTGA | 1100 |
| CTGGGGTTCT | GCTATGAAAC | CAATCACCGA | TTATGCACCT | GCCATAGAAT | 1150 |
| ACGGTGTTTA | TGATTCCACT | GCAACTATGG | TTAATGATAT | TCCTTATAAC | 1200 |
| TATCCGGGAA | CAAGCACACC | TGTCTACAAC | TGGGATAGAG | CATATTTCCG | 1250 |
| TAATATTACT | CTGCAATATG | CTCTTCAACA | ATCACGAAAT | GTCACAGCCG | 1300 |
| TTGAGACTTT | GAATAAGGTC | GGTCTAGATA | GAGCTAAAAC | CTTCCTTAAT | 1350 |
| GGTCTTGCTA | TCGACTATCC | AAGCATGCAT | TATGCAAACG | CCATTTCAAG | 1400 |
| TAATACAACA | GAATCTAATA | AACAATACGG | AGCAAGTAGT | GAAAAAATGG | 1450 |
| CTGCTGCTTA | TGCTGCCTTT | GCAAATGGTG | GCACTTACTA | TAAACCAATG | 1500 |
| TATATCCATA | AAGTCGTCTT | CAGTGATGGA | AGTAAAAAAG | AGTTCTCTAA | 1550 |
| TGTCGGAAC  | CGTGCCATGA | AGGAAACGAC | AGCCTATATG | ATGACCGACA | 1600 |
| TGATGAAAAC | AGTCTTGACT | TATGGAAC   | GGCGTGGAGC | CTATCTTCCT | 1650 |
| TGGCTTCCTC | AAGCTGGTAA | AACAGGAACC | TCTAACTATA | CAGATGAGGA | 1700 |
| AGTTGAAAAC | CACATCAAGA | ACACTGGCTA | TGTAGCTCCA | GATGAAATGT | 1750 |
| TTGTTGGTTA | TACTCGTAAG | TATTCTATGG | CTGTATGGAC | AGGTTATTCG | 1800 |
| AATCGTTTAA | CTCCTATCGT | TGGAGATGGT | TTCCTAGTTG | CAGCTAAAGT | 1850 |
| TTATCGCTCA | ATGATAACGT | ATCTATCAGA | AGATACTCAT | CCAGAAGACT | 1900 |
| GGACGATGCC | AGACGGACTT | TTCAGAAATG | GAGAATTCGT | ATTTAAAAAT | 1950 |
| GGTGCTCGTT | CTACGTGGAA | CTCACCTGCT | CCACAACAAC | CCCCATCAAC | 2000 |
| TGAAAGTTCA | AGCTCATCAT | CAGATAGTTC | AACTTCACAG | TCTAGCTCAA | 2050 |
| CCACTCCAAG | CACAAATAAT | AGTACGACTA | CCAATCCTAA | CAATAATACG | 2100 |
| CAACAATCAA | ATACAACCCC | TGATCAACAA | AATCAGAATC | CTCAACCAGC | 2150 |
| ACAACCATAA |            |            |            |            | 2160 |

## 2) INFORMATION FOR SEQ ID NO: 2050

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 8303; 35193
- (C) ACCESSION NUMBER: AF046230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050

|            |             |            |            |             |     |
|------------|-------------|------------|------------|-------------|-----|
| CTGTGGGATA | TCTACAACCTC | CGATCAATAC | GTCTCTTACC | CTGACGATGA  | 50  |
| TTTGCAAGTC | GCATCTACGG  | TCGTAGATGT | TTCAAATGGT | AAAGTCATCG  | 100 |
| CCCAACTTGG | AGCTCGTCAC  | CAAGCAAGTA | ACGTTTCATT | TGGTACCAAC  | 150 |
| CAAGCTGTGG | AAACCAATCG  | TGACTGGGGT | TCTGCTATGA | AACCAATCAC  | 200 |
| CGATTATGCA | CCTGCCATAG  | AATACGGTGT | TTATGATTCC | ACTGCAACTA  | 250 |
| TGGTTAATGA | TATTCCTTAT  | AACTATCCGG | GAACAAGCAC | ACCTGTCTAC  | 300 |
| AACTGGGATA | GAGCATATTT  | CGGTAATATT | ACTCTGCAAT | ATGCTCTTCA  | 350 |
| ACAATCACGA | AATGTCACAG  | CCGTTGAGAC | TTTGAATAAG | GTCGGTCTAG  | 400 |
| ATAGAGCTAA | AACCTTCCTT  | AATGGTCTTG | GTATCGACTA | TCCAAGCATG  | 450 |
| CATTATGCAA | ACGCCATTTT  | AAGTAATACA | ACAGAATCTA | ATAAACAAATA | 500 |
| CGGAGCAAGT | AGTGAAGAAA  | TGGCTGCTGC | TTATGCTGCC | TTTGCAAATG  | 550 |
| GTGGCACTTA | CTATAAACCA  | ATGTATATCC | ATAAAGTCGT | CTTCAGTGAT  | 600 |
| GGAAGTAAAA | AAGAGTTCTC  | TAATGTCGGA | ACTCGTGCCA | TGAAGGAAAC  | 650 |
| GACAGCCTAT | ATGATGACCG  | ACATGATGAA | AACAGTCTTG | ACTTATGGAA  | 700 |
| CTGGGCGTGG | AGCCTATCTT  | CCTTGGCTTC | CTCAAGCTGG | TAAACAGGA   | 750 |
| ACCTCTAACT | ATACAGATGA  | GGAAGTTGAA | AACCACATCA | AGAACACTGG  | 800 |
| CTATGTAGCT | CCAGATGAAA  | TGTTTGTGTT | TTATACTCGT | AAGTATTCTA  | 850 |
| TGGCTGTATG | GACAGGTTAT  | TCGAATCGTT | TAACCTCTAT | CGTTGGAGAT  | 900 |
| GTTTTCCTAG | TTGCAGCTAA  | AGTTTATCGC |            |             | 930 |

## 2) INFORMATION FOR SEQ ID NO: 2051

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 63509; M11
- (C) ACCESSION NUMBER: AF046238

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051

|            |             |            |            |            |     |
|------------|-------------|------------|------------|------------|-----|
| CTGTGGGATA | TTTACAATAC  | AGACGAATAC | GTTGCCTATC | CAGATGATGA | 50  |
| CATGCAAGTA | GCTTCGACTA  | TTGTAGATGT | ATCTAATGGT | AACGTTATTG | 100 |
| CACAACTTGG | TGCTCGTCAT  | CAAGCAAGTA | ATGTTTCATT | CGGCACCAAC | 150 |
| CAGGCTGTGG | AGACCAATCG  | TGACTGGGGT | TCTTCTATGA | AACCAATCAC | 200 |
| TGACTATGCT | CCCGCTTTAG  | AATATGGAGT | CTATGACTCT | ACTGCTTCTA | 250 |
| TTGTACATGA | TGTTCCCTTAT | AACTATCCTG | GCACTGATAC | TCCAGTCTAC | 300 |
| AACTGGGATC | ATGTCTACTT  | TGGAAACATT | ACAATCCAGT | ATGCTCTTCA | 350 |
| ACAATCACGA | AATGTCACAG  | CCGTTGAGAC | TTTGAATAAG | GTCGGTCTAG | 400 |
| ATAGAGCTAA | AACCTTCCTT  | AATGGTCTTG | GTATCGACTA | TCCAAGCATG | 450 |
| CATTATGCAA | ACGCCATTTT  | AAGTAACACA | ACTGAATCCA | ACAAACAGTA | 500 |
| CGGTGCAAGT | AGTGAAGAAA  | TGGCTGCTGC | TTATGCCGCC | TTTTCTAATG | 550 |
| GTGGTATTTA | CCACAAACCA  | ATGTATATCA | ATAAAATCGT | CTTCAGTGAT | 600 |
| GGTAGTGAAA | AAGAATTTTC  | TGATGCTGGT | ACACGAGCTA | TGAAAGAAAC | 650 |
| TACTGCCTAT | ATGATGACCG  | AAATGATGAA | AACTGTTTTA | GCTTACGGAA | 700 |
| CCGGACGTGG | TGCTTACCTA  | CCATGGCTTC | CACAAGCAGG | TAAGACAGGT | 750 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| ACTTCTAACT | ATACTGACGA | CGAAATTGAA | AAGTATATCA | AGAACACTGG | 800 |
| CTACGTAGCT | CCAGATGAAA | TGTTTGTGG  | TTATACTCGT | AAGTATTCTA | 850 |
| TGGCTGTATG | GACTGGTTAC | TCAAATCGTT | TAAGTCCAAT | CGTAGGAGAT | 900 |
| GGTTTCCTAG | TTGCTGCTAA | GGTTTATCGC |            |            | 930 |

## 2) INFORMATION FOR SEQ ID NO: 2052

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: #22/HA5
- (C) ACCESSION NUMBER: AB006877

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052

|            |            |             |            |            |      |
|------------|------------|-------------|------------|------------|------|
| GTCTCTTACC | CTGACGATGA | TTTGCAAGTC  | GCATCTACGG | TCGTAGATGT | 50   |
| TTCCAATGGT | AAAGTCATCG | CCCAACTTGG  | AGCTCGTCAC | CAAGCAAGTA | 100  |
| ACGTTTCATT | TGGTACCAAC | CAAGCTGTGG  | AAACCAATCG | TGACTGGGGT | 150  |
| TCAACAATGA | AACCAATCAC | CGATTATGCA  | CCTGCCATAG | AATACGGTGT | 200  |
| ATATGATTCC | ACTGCAACTA | TGGTTAATGA  | TATTCCTTAT | AACTATCCGG | 250  |
| GAACAAGCAC | ACCTGTCTAC | AACTGGGATC  | GAGCATATTT | TGGTAATATT | 300  |
| ACTCTGCAAT | ATGCCCTTCA | ACAATCACGT  | AATGTTACAG | CAGTTGAAAC | 350  |
| ATTAAACAAG | GTTGGTTTAT | ATCGAGCCAA  | AACTTTCCTA | AATGGCTTAG | 400  |
| GTATCGATTA | CCCAAGCATA | CACATATGCTA | ACGCCATTTT | AAGTAATACA | 450  |
| ACAGAATCTA | ACAAACATTA | CGGTGCAAGT  | AGTGAAAAAA | TGGCTGCTGC | 500  |
| TTATGCCGCC | TTTGCTAATG | GTGGTATTTA  | CCACAAACCA | ATGTATATCA | 550  |
| ATAAAATCGT | CTTTAGTGAT | GGTAGTGAGA  | AAGAATTTTC | TGATGCTGGT | 600  |
| ACACGAGCTA | TGAAAGAAAC | TACTGCCTAT  | ATGATGACCG | AAATGATGAA | 650  |
| AACTGTTTTA | GCTTACGGAA | CCGGACGTGG  | TGCTTACCTA | CCATGGCTTC | 700  |
| CACAAGCAGG | TAAGACAGGT | ACTTCTAACT  | ATACTGATGA | CGAAATCGAA | 750  |
| AAACATATCA | AGAATACTGG | CTACGTAGCT  | CCAGATGAAA | TGTTTGTAGG | 800  |
| CTATACTCGT | AAGTATTCTA | TGGCTGTATG  | GACTGGTTAC | TCAAATCGTT | 850  |
| TAAGTCCAAT | TGTTGGAGAT | GGTTTCCTAG  | TTGCTGCTAA | GGTTTATCGC | 900  |
| TCAATGATAT | CGTATCTATC | AGAAGATGAC  | CAACCTGGAG | ATTGGACGAT | 950  |
| GCCAGACGGC | CTGTTCCGAA | ATGGAGAATT  | CGTATTTAAA | AATGGTGCTC | 1000 |
| GTTCTACGTG | GAACACACCT | GCTCCACAAC  | AACCCCATC  | AACTGAAAGT | 1050 |
| TCAAGCTCAT | CATCAGATAG | TTCAACTTCA  | CAGTCTAGCT | CAACCACTCC | 1100 |
| AAGCACAAAT | AATAGTACGA | CTACCAATCC  | TAACAATAAT | ACGCAACAAT | 1150 |
| CAAATACAAC | CCCTGATCAA | CAAAATCAGA  | ATCCTCAACC | AGCAC      | 1195 |

## 2) INFORMATION FOR SEQ ID NO: 2053

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: 17619

(C) ACCESSION NUMBER: AF046237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CTGTGGGATA | TTTACAATAC | AGACGAATAC | GTTGCCTATC | CAGACGATGA | 50  |
| ATTGCAAGTC | GCTTCTACCA | TTGTTGATGT | TTCTAACGGT | AAAGTCATTG | 100 |
| CCCAGCTAGG | AGCACGCCAT | CAGTCAAGTA | ATGTTTCCTT | CGGAATTAAC | 150 |
| CAAGCAGTAG | AAACAAACCG | CGACTGGGGA | TCAACTATGA | AACCGATCAC | 200 |
| AGACTATGCT | CCTGCCTTGG | AGTACGGTGT | CTACGATTCA | ACTGCTACTA | 250 |
| TCGTTACGA  | TGAGCCCTAT | AACTACCCTG | GGACAAATAC | TCCTGTTTAT | 300 |
| AACTGGGATA | GGGGCTACTT | TGGCAACATC | ACCTTGCAAT | ACGCCCTGCA | 350 |
| ACAATCGCGA | AACGTCCCAG | CCGTGGAAAC | TCTAAACAAG | GTCGGACTCA | 400 |
| ACCGCGCCAA | GACTTTCCTA | AATGGTCTCG | GAATCGACTA | CCCAAGTATT | 450 |
| CACTACTCAA | ATGCCATTTT | AAGTAACACA | ACCGAATCAG | ACAAAAAATA | 500 |
| TGGAGCAAGT | AGTGAAAAGA | TGGCTGCTGC | TTACGCTGCC | TTTGCAAATG | 550 |
| GTGGAACCTA | CTATAAACCA | ATGTATATCC | ATAAAGTCGT | CTTTAGTGAT | 600 |
| GGGAGTGAAA | AAGAGTTCTC | TAATGTCGGA | ACTCGTGCCA | TGAAGGAAAC | 650 |
| GACAGCCTAT | ATGATGACCG | AAATGATGAA | AACAGTCTTG | AGTTATGGAA | 700 |
| CTGGACGAAA | TGCCTATCTT | GCTTGGCTTC | CTCAAGCTGG | TAAAACAGGT | 750 |
| ACCTCTAACT | ATACAGATGA | AGAAATTGAA | AAACACATCA | AAAACACTGG | 800 |
| CTATGTAGCT | CCAGATGAAA | CGTTTGTTGG | TTATACTCGT | AAGTATTCTA | 850 |
| TGGCTGTATG | GACAGGTTAC | ACAAACCGTC | TCACACCAAT | TGTGGGGGAT | 900 |
| GGCTTCACAG | TTGCTGCCAA | AGTTTACCGC |            |            | 930 |

2) INFORMATION FOR SEQ ID NO: 2054

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: R6

(C) ACCESSION NUMBER: Y07845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CGTCGCATTC | TCTACGGAAT | GAATGAATTG | GGTGTGACCC | CAGACAAACC | 50  |
| CCATAAAAAA | TCTGCTCGTA | TTACAGGGGA | TGTCATGGGT | AAATACCACC | 100 |
| CACACGGGGA | TTCCTCTATT | TATGAAGCCA | TGGTCCGTAT | GGCTCAATGG | 150 |
| TGGAGCTACC | GTTACATGCT | TGTAGATGGT | CATGGGAATT | TTGGTTCCAT | 200 |
| GGATGGAGAT | AGTGCTGCCG | CTCAACGTTA | TACCGAGGCA | CGTATGAGCA | 250 |
| AGATTGCTCT | GGAAATGCTT | CGTGATATCA | ACAAAAATAC | AGTTGATTTC | 300 |
| GTTGAT     |            |            |            |            | 306 |

## 2) INFORMATION FOR SEQ ID NO: 2055

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 7785
- (C) ACCESSION NUMBER: Z67739

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055

|             |             |            |            |            |      |
|-------------|-------------|------------|------------|------------|------|
| ATGTCTAACA  | TTCAAAACAT  | GTCCCTGGAG | GACATCATGG | GAGAGCGCTT | 50   |
| TGGTCGCTAC  | TCCAAGTACA  | TTATTCAAGA | CCGGGCTTTG | CCAGATATTC | 100  |
| GTGATGGGTT  | GAAGCCGGTT  | CAGCGCCGTA | TTCTTTATTC | TATGAATAAG | 150  |
| GATAGCAATA  | CTTTTGACAA  | GAGCTACCGT | AAGTCGGCCA | AGTCAGTCGG | 200  |
| GAACATCATG  | GGAATTTC    | ACCCACACGG | GGATTCTTCT | ATCTATGATG | 250  |
| CCATGGTTTCG | TATGTCACAG  | AACTGGAAAA | ATCGTGAGAT | TCTAGTTGAA | 300  |
| ATGCACGGTA  | ATAACGGTTC  | TATGGACGGA | GATCCTCCTG | CGGCTATGCG | 350  |
| TTATACTGAG  | GCACGTTTGT  | CTGAAATTGC | AGGCTACCTT | CTTCAGGATA | 400  |
| TCGAGAAAAA  | GACAGTTCCT  | TTTGCATGGA | ACTTTGACGA | TACGGAGAAA | 450  |
| GAACCAACGG  | TCTTGCCAGC  | AGCCTTTCCA | AACCTCTTGG | TCAATGGTTC | 500  |
| GACTGGGATT  | TCGGCTGGTT  | ATGCCACAGA | CATTCTCCC  | CATAATTTAG | 550  |
| CTGAGGTCAT  | AGATGCTGCA  | GTTTACATGA | TTGACCACCC | AACTGCAAAG | 600  |
| ATTGATAAAC  | TCATGGAATT  | CTTACCTGGA | CCAGACTTCC | CTACAGGGGC | 650  |
| TATTATTCAG  | GGTCGTGATG  | AAATCAAGAA | AGCTTATGAG | ACTGGGAAAG | 700  |
| GGCGCGTGGT  | TGTTTCGTTCC | AAGACTGAAA | TTGAAAAGCT | AAAAGGTGGT | 750  |
| AAGGAACAAA  | TCGTTATTAC  | TGAGATTCCT | TATGAAATCA | ATAAGGCCAA | 800  |
| TCTAGTCAAG  | AAAATCGATG  | ATGTTCTGTG | TAATAACAAG | GTAGCTGGGA | 850  |
| TTGCTGAGGT  | TCGTGATGAG  | TCTGACCGTG | ATGGTCTTCG | TATCGCTATC | 900  |
| GAACCTAAGA  | AAGACGCTAA  | TACTGAGCTT | GTTCTCAACT | ACTTATTTAA | 950  |
| GTACACCGAC  | CTACAAATCA  | ACTACAACCT | TAATATGGTG | GCGATTGACA | 1000 |
| ATTTACACACC | TCGTCAGGTT  | GGGATTGTTT | CAATCCTGTC | TAGCTACATC | 1050 |
| GCTCACCGTC  | GAGAAGTGAT  | TTTGGCGCGT | TCACGCTTTG | ACAAAGAAAA | 1100 |
| GGCTGAGAAA  | CGTCTCCATA  | TCGTGGAAGG | TTTGATTTCG | GTGATTTCGA | 1150 |
| TTTTTGATGA  | AGTCATTGCT  | CTTATCCGTG | CTTCTGAGAA | TAAGGCGGAC | 1200 |
| GCCAAGGAAA  | ACCTCAAAGT  | TAGCTATGAT | TTTACGGAAG | AACAGGCTGA | 1250 |
| GGCTATCGTA  | ACTTTGCAAC  | TGTACCGTTT | GACCAATACC | GATGTGGTTG | 1300 |
| TCTTGACAGGA | AGAAGAAGCA  | GAGCTTCGTG | AGAAGATTGC | TATGCTGGCG | 1350 |
| GCTATTATCG  | GTGATGAAAG  | GACTATGTAC | AATCTCATGA | AGAAAGAACT | 1400 |
| TCGTGAGGTC  | AAGAAGAAAT  | TTGCAACTCC | TCGTTTGAGT | TCTTTAGAAG | 1450 |
| AACTGCGAA   | AGCAATTGAG  | ATTGATACAG | CTAGTCTTAT | CGCTGAGGAA | 1500 |
| GATACCTACG  | TCAGCGTGAC  | CAAGGCAGGT | TACATCAAGC | GTACCAGTCC | 1550 |
| ACGTTTCCTTT | GCGGCTTCCA  | CCTTGGAAGA | AATTGGCAAG | CGTGATGATG | 1600 |
| ACCGTTTGAT  | TTTTGTTCAA  | TCTGCCAAGA | CAACCCAGCA | CCTCTTGATG | 1650 |
| TTCAACAAGTC | TTGGAAATGT  | CATCTACAGA | CCAATCCATG | AGTTGGCAGA | 1700 |
| TATTCGTTGG  | AAGGACATCG  | GAGAGCATCT | GAGCCAAACC | ATCACAAACT | 1750 |
| TTGAAACGAA  | TGAAGAAATC  | CTTTATGTGG | AAGTACTGGA | TCAGTTTGAC | 1800 |
| GATGCGACAA  | CCTACTTTGC  | AGTGACTCGC | CTTGGTCAAA | TCAAACGGGT | 1850 |

|            |             |            |             |            |      |
|------------|-------------|------------|-------------|------------|------|
| AGAGCGAAAA | GAATTCACCTC | CATGGCGGAC | CTATAGATCT  | AAGTCTGTCA | 1900 |
| AGTATGCTAA | GCTCAAAGAC  | GATACAGATC | AGATTGTAGC  | AGTGGCTCCG | 1950 |
| ATTAAACTAG | ATGATGTTGT  | CTTGGTTAGT | CAAAATGGTT  | ATGCCCTGCG | 2000 |
| TTTCAATATC | GAAGAGGTTT  | CGGTTGTCGG | TGCTAAGGCA  | GCAGGTGTCA | 2050 |
| AGGCTATGAA | TTTGAAAGAA  | GATGATGTCC | TCCAATCTGG  | CTTTATCTGT | 2100 |
| AATACTTCGT | CCTTCTACCT  | CTTGACCCAG | CGTGGGAAGCT | TGAAACGTGT | 2150 |
| TTCTATTGAG | GAAATTCTAG  | CAACCAGCCG | TGCCAAACGA  | GGATTACAAG | 2200 |
| TCTTGCGTGA | GTTGAAAAAC  | AAACCGCATC | GTGTCTTCTT  | GGCAGGAGCA | 2250 |
| GTTGCAGAGC | AAGGATTTGT  | TGGCGATTTT | TTCAGTACGG  | AAGTGGATGT | 2300 |
| GAACGACCAA | ACTCTGCTTG  | TCCAATCCAA | TAAAGGAACA  | ATCTATGAAA | 2350 |
| GCCGATTGCA | AGACTTGAAC  | TTGTCAGAAC | GCACTAGCAA  | TGGAAGCTTC | 2400 |
| ATTTCTGACA | CGATTTCAAG  | TGAAGAAGTT | TTTGACGCTT  | ATCTTCAGGA | 2450 |
| AGTAGTTACT | GAAGATAAAT  | AA         |             |            | 2472 |

## 2) INFORMATION FOR SEQ ID NO: 2056

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056

|            |            |            |            |             |      |
|------------|------------|------------|------------|-------------|------|
| AAGCTCAAAA | ACATCTGTGG | GATATCTACA | ACTCCGATCA | ATACGTCTCT  | 50   |
| TACCCTGACG | ATGATTTGCA | AGTCGCATCT | ACGGTCGTAG | ATGTTTCAAA  | 100  |
| TGGTAAAGTC | ATTGCCCAAC | TTGGAGCTCG | TCACCAAGCA | AGTAACGTTT  | 150  |
| CATTTGGCAC | CAACCAAGCT | GTGGAAACCA | ATCGTGAAGT | GGGTTCAACA  | 200  |
| ATGAAACCAA | TCACAGACTA | TGCTCCTGCC | TTGGAATACG | GTGTCTACGA  | 250  |
| TTCAACTGCT | ACTATCGTTC | ACGATGAGCC | CTATAACTAT | CCTGGGACAG  | 300  |
| ATACCCCTGT | CTATAACTGG | GATAGGGGCT | ACTTTGGCAA | TATCACCTTG  | 350  |
| CAATACGCC  | TGCAACAATC | GCGAAACGTC | CCAGCCGTGG | AAACACTAAA  | 400  |
| CAAGGTCGGG | CTCAACCGCG | CCAAGACTTT | TCTAAATGGT | CTCGGAATCG  | 450  |
| ACTACCCAAG | TATTCACCTA | TCAAATGCCA | TTTCAAGTAA | CACAACCGAG  | 500  |
| TCAGACAAAA | AATATGGAGC | AAGTAGTGAA | AAGATGGCTG | CTGCTTACGC  | 550  |
| TGCCTTTGCA | AATGGTGGAA | CTTACTATAA | ACCAATGTAT | ATCCATAAAG  | 600  |
| TCGTCTTTAG | TGATGGAAGT | GAAAAAGAGT | TCTCTAATGT | CGGAACCTCG  | 650  |
| GCCATGAAAG | AAACGACTGC | TTACATGATG | ACAGAAATGA | TGAAAACAGT  | 700  |
| CTTGACGTAC | GGAATTGGTC | GTGGTGCCTA | CCTGCCTTGG | CTTCCTCAAG  | 750  |
| CTGGTAAAC  | AGGTACTTCT | AACTATACTG | ACGAAGAAAT | TGAAAAGTAT  | 800  |
| ATCAAGAACA | CTGGTTACGT | AACTCCAGAT | GAAATGTTTG | TAGGGTATAC  | 850  |
| CCGTAAATAT | GCAATGGCTG | TATGGACAGG | CTATTCTAAC | CGTCTGACAC  | 900  |
| CACCTGTAGG | CGATGGCCTT | ACGGTCGCTG | CCAAGGTTTA | CCGCTCTATG  | 950  |
| ATGACCTACC | TGTCTGAAGG | AAGCAATCCA | GAGGATTGGA | ATATAACCAGA | 1000 |
| GGGGCTCTAC | AGAAATGGAG | AATTCGTATT | TAAAAATGGT | GCTCGTTCTA  | 1050 |
| CGTGGAGCTC | ACCTGCTCCA | CAACAACCCC | CATCAACTGA | AAGTTCAAGC  | 1100 |
| TCATCATCAG | ATAGTTCAAC | TTACAGTCTT | AGCTCAACCA | CTCCAAGCAC  | 1150 |
| AAATAATAGT | ACGACTACCA | ATCCTAACAA | TAATACGCAA | CAATCAAATA  | 1200 |
| CAACCCCTGA | TC         |            |            |             | 1212 |



## 2) INFORMATION FOR SEQ ID NO: 2057

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057

|            |            |            |             |            |      |
|------------|------------|------------|-------------|------------|------|
| ATGTAGACCA | AGAAGCTCAA | AAACATCTGT | GGGATATTTA  | CAATACAGAC | 50   |
| GAATACGTTG | CCTATCCAGA | CGATGAATTG | CAAGTCGCTT  | CTACCATTGT | 100  |
| TGATGTTTCT | AACGGGAAAG | TTATTGCTCA | GTTAGGTTCT  | CGTCACCAAT | 150  |
| CAAGCAATGT | TTCCTTCGGA | ATCAACCAAG | CTGTTGAAAC  | CAACCGTGAC | 200  |
| TGGGGTTCTG | CCATGAAGCC | AATCACAGAC | TATGCTCCTG  | CCTTAGAGTA | 250  |
| TGACATCTAC | GACTCAACTG | CTTCGATTGT | ACATGATGTT  | CCTTATAACT | 300  |
| ATCCAGGTAC | TGATACTCCC | CTCTACAACT | GGGATAAAGT  | CTACTTTGGA | 350  |
| AATATTACAA | TCCAGTATGC | ACTTCAACAG | TCACGTAATG  | TCACAGCCGT | 400  |
| TGAGACTTTG | AATAAGGTCG | GTCTAGATAG | AGCTAAAACC  | TTTCTTAATG | 450  |
| GTCTTGGTAT | CGACTATCCA | AGCATGCATT | ATGCAAACGC  | CATTTCAAGT | 500  |
| AATACGACTG | AGTCAAACAA | AAAGTACGGA | GCAAGTAGTG  | AGAAAATGGC | 550  |
| TGCTGCTTAC | GCTGCTTTTG | CTAACGGTGG | TATCTACCAT  | AAACCAATGT | 600  |
| ATATCAACAA | AATCGTCTTT | AGCGATGGTA | GCTCAAAAGA  | ATACGCTGAT | 650  |
| CCTGGTACTC | GTGCCATGAA | AGAGACGACC | GCCTATATGA  | TGACAGAAAT | 700  |
| GATGAAGACT | GTCTTGGCAT | ACGGAACGGG | TCGTGGTGCT  | TATCTCCCTT | 750  |
| GGCTACCTCA | AGCTGGTAAG | ACTGGTACAT | CAAACATATAC | AGATGATGAA | 800  |
| ATTGAAAAC  | ACATCAAAAA | TACTGGTTAT | GTAGCTCCAG  | ACGAAATGTT | 850  |
| TGTTGGTTAT | ACTCGCAAAT | ATTCAATGGC | GGTATGGACA  | GGTTACTCAA | 900  |
| ACCGCCTGAC | TCCTATCGTT | GGTGATGGCT | TCTATGTTGC  | AGCTAAGGTT | 950  |
| TACCGTTCAA | TGATGACTTA | TCTGTCTGAG | GATAACAACC  | CTGGCGACTG | 1000 |
| GACTATGCCA | GAAGGTCTCT | ATCGAAGTGG | TGAGTTCGTC  | TTTAAAAAAG | 1050 |
| GTGCTCGTTC | TGCATGGACT | GCTCCTGCTC | CGCAACAGGC  | CCCAACACCA | 1100 |
| GAAAGTTCGA | GCTCGACATC | AGAAAGTTCA | ACTTCACAGT  | CAAGCTCAAC | 1150 |
| TACTCCAAGC | ACGAATAATA | GTGCAAACAA | TAATACCAAT  | AACCAGCAAC | 1200 |
| CAAATACAAC | GCCTGGTCAA | CAAAACCAGA | ACCAAAATCA  | GA         | 1242 |

## 2) INFORMATION FOR SEQ ID NO: 2058

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: StrR-18

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058

|            |            |            |            |             |      |
|------------|------------|------------|------------|-------------|------|
| GAAGCTCAAA | AACATCTGTG | GGATATTTAC | AATACAGACG | AATACGTTGC  | 50   |
| CTATCCAGAC | GATGAATTGC | AAGTCGCTTC | TACCATTGTT | GATGTTTCTA  | 100  |
| ACGGGAAAGT | TATTGCTCAG | TTAGGTTCTC | GTCACCAATC | AAGCAATGTT  | 150  |
| TCCTTCGGAA | TCAACCAAGC | TGTTGAAACC | AACCGTGACT | GGGGTTCTGC  | 200  |
| CATGAAGCCA | ATCACAGACT | ATGCTCCTGC | CTTAGAGTAT | GACATCTACG  | 250  |
| ACTCAACTGC | TTCGATTGTA | CATGATGTTT | CTTATAACTA | TCCAGGTACT  | 300  |
| GATACTCCCC | TCTACAACTG | GGATAAAGTC | TACTTTGGAA | ATATTACAAT  | 350  |
| CCAGTATGCA | CTTCAACAGT | CACGTAATGT | CACAGCCGTT | GAGACTTTGA  | 400  |
| ATAAGGTCGG | TCTAGATAGA | GCTAAAACCT | TTCTTAATGG | TCTTGGTATC  | 450  |
| GACTATCCAA | GCATGCATTA | TGCAAACGCC | ATTTCAAGTA | ATACGACTGA  | 500  |
| GTCAAACAAA | AAGTACGGAG | CAAGTAGTGA | GAAAATGGCT | GCTGCTTACG  | 550  |
| CTGCTTTTGC | TAACGGTGGT | ATCTACCATA | AACCAATGTA | TATCAACAAA  | 600  |
| ATCGTCTTTA | GCGATGGTAG | CTCAAAAGAA | TACGCTGATC | CTGGTACTCG  | 650  |
| TGCCATGAAA | GAGACGACCG | CCTATATGAT | GACAGAAATG | ATGAAGACTG  | 700  |
| TCTTGGCATA | CGGAACGGGT | CGTGGTGCTT | ATCTCCCTTG | GCTACCTCAA  | 750  |
| GCTGGTAAGA | CTGGTACATC | AAACTATACA | GATGATGAAA | TTGAAAACATA | 800  |
| CATCAAAAAT | ACTGGTTATG | TAGCTCCAGA | CGAAATGTTT | GTTGGTTATA  | 850  |
| CTCGCAAATA | TTCAATGGCG | GTATGGACAG | GTTACTCAAA | CCGCCTGACT  | 900  |
| CCTATCGTTG | GTGATGGCTT | CTATGTTGCA | GCTAAGGTTT | ACCGTTCAAT  | 950  |
| GATGACTTAT | CTGTCTGAGG | ATAACAACCC | TGGCGACTGG | ACTATGCCAG  | 1000 |
| AAGGTCTCTA | TCGAAGTGGT | GAGTTCGTCT | TTAAAAAAGG | TGCTCGTTCT  | 1050 |
| GCATGGACTG | CTCCTGCTCC | GCAACAGGCC | CCAACACCAG | AAAGTTCGAG  | 1100 |
| CTCGACATCA | GAAAGTTCAA | CTTCACAGTC | AAGCTCAACT | ACTCCAAGCA  | 1150 |
| CGAATAATAG | TGCAAACAAT | AATACCAATA | ACCAGCAACC | AAATACAACG  | 1200 |
| CCTGGTCAAC | AAAACCAGAA | CCAAA      |            |             | 1225 |

## 2) INFORMATION FOR SEQ ID NO: 2059

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: StrR-38

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TGGCTACTTT | GGAAACATTA | CAGTCCAGTA | TGCTCTTCAA | CAATCACGAA | 50  |
| ATGTCACAGC | CGTTGAGACT | TTGAATAAGG | TCGGTCTAGA | TAGAGCTAAA | 100 |
| ACCTTCCTCA | ATGGACTTGG | TATCGATTAT | CCAAGCATGC | TTTATGCAAA | 150 |
| CGCCATTTCA | AGTAACACAA | CTGAATCCAA | CAAAAAGTAC | GGAGCAAGTA | 200 |
| GTGAAAAAAT | GGCCGCTGCC | TACGCAGCTT | TTGCTAATGG | TGGTACTTAC | 250 |
| CACAAACCAA | TGTATATCAA | TAAAATCGTC | TTTAGTGATG | GTAGTGAAAA | 300 |
| AGAATTTTCT | GATGCCGGTA | CTCGGGCTAT | GAAAGAACT  | ACTGCCTATA | 350 |

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TGATGACCGA | AATGATGAAA | ACTGTCTTAT | TATACGGAAC | CGGACGTGGA | 400 |
| GCCTACCTAC | CTTGGCTTCC | ACAAGCAGGT | AAGACAGGTA | CTTCTAACTA | 450 |
| TACTGACGAA | GAAATTGAAA | AGTATATCAA | GAATGCTGGT | TACGTAGCTC | 500 |
| CAGATGAAAT | GTTTGTTGGT | TATACCCGCA | AATATGCAAT | GGCTGTTTGG | 550 |
| ACAG       |            |            |            |            | 554 |

## 2) INFORMATION FOR SEQ ID NO: 2060

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-57

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060

|            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------|
| CAACTGGGAT | GGATGTCTAC | ACAAATGTAG | ACCAAGAAGC | TCAAAAACAT | 50   |
| CTGTGGGATA | TTTACAATAC | AGACGAATAC | GTTGCCTATC | CAGACGATGA | 100  |
| ATTGCAAGTC | GCTTCTACCA | TTGTTGATGT | TTCTAACGGT | AAAGTCATTG | 150  |
| CCCAGCTAGG | AGCACGCCAT | CAGTCAAGTA | ATGTTTCCTT | CGGAATTAAC | 200  |
| CAAGCAGTAG | AAACAAACCG | CGACTGGGGA | TCAACTATGA | AACCGATCAC | 250  |
| AGACTATGCT | CCTGCCTTGG | AGTACGGTGT | CTACGATTCA | ACTGCTACTA | 300  |
| TCGTTACGGA | TGAGCCCTAT | AACTACCCTG | GGACAAATAC | TCCTGTTTAT | 350  |
| AACTGGGATA | GGGGCTACTT | TGGCAACATC | ACCTTGCAAT | ACGCCCTGCA | 400  |
| ACAATCGCGA | AACGTCCCAG | CCGTGGAAAC | TCTAAACAAG | GTCGGACTCA | 450  |
| ACCGCGCCAA | GACTTTCCTA | AATGGTCTAG | GAATCGACTA | CCCAAGTATT | 500  |
| CACTACTCAA | ATGCCATTTC | AAGTAACACA | ACCGAATCAG | ACAAAAAATA | 550  |
| TGGAGCAAGT | AGTGAAAAGA | TGGCTGCTGC | TTACGCTGCC | TTTGCAAATG | 600  |
| GTGGAACCTA | CTATAAACCA | ATGTATATCC | ATAAAGTCGT | CTTTAGTGAT | 650  |
| GGGAGTGAAA | AAGAGTTCCT | TAATGTCGGA | ACTCGTGCCA | TGAAGGAAAC | 700  |
| GACAGCCTAT | ATGATGACCG | ACATGATGAA | AACAGTCTTG | ACTTATGGAA | 750  |
| CTGGACGAAA | TGCCTATCTT | GCTTGGCTCC | CTCAGGCTGG | TAAAACAGGA | 800  |
| ACCTCTAACT | ATACAGACGA | GGAAATTGAA | AACCACATCA | AGACCTCTCA | 850  |
| ATTTGTAGCA | CCTGATGAAC | TATTTGCTGG | CTATACGCGT | AAATATTCAA | 900  |
| TGGCTGTATG | GACAGGCTAT | TCTAACCGTC | TGACACCACT | TGTAGGCAAT | 950  |
| GGCCTTACGG | TCGCTGCCAA | AGTTTACCGC | TCTATGATGA | CCTACCTGTC | 1000 |
| TGAAGGAAGC | AATCCAGAAG | ATTGGAATAT | ACCAGAGGGG | CTCTACAGAA | 1050 |
| ATGGAGAATT | CGTATTTAAA | AATGGTGCTC | GTTCTACGTG | GAGCTCACCT | 1100 |
| GCTCCACAAC | AACCCCCATC | AACTGAAAGT | TCAAGCTCAT | CATCAGATAG | 1150 |
| TTCAACTTCA | CAGTCTAGCT | CAACCACTCC | AAGCACAAAT | AATAGTACGA | 1200 |
| CTACCAATCC | TAACAATAAT | ACGCAACAAT | CAAATACAAC | CCCTGATCA  | 1249 |

## 2) INFORMATION FOR SEQ ID NO: 2061

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 bases
- (B) TYPE: Nucleic acid

1069

- (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
(B) STRAIN: StrR-60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GAAGTTGAAC | AGACTGGTCA | CCAAGCTCCT | TCATATCCGC | CAACACTGCA | 50  |
| ATTTTCCTTG | CACCTTCATT | GGCTGGAATG | GCAGAGAAAG | TCTCTAAAAT | 100 |
| CAGTTTCATA | GCAGTTGGAT | TGGCATTATA | AACATCTGAC | AGGATATCTG | 150 |
| CTCCATTGGC | TGCTTTCTTC | CACTCGGTAC | GGTTACGCGT | CAATTCAAGA | 200 |
| TGTTGGAAGG | CCAAACGAAT | TTGCTCCTCT | GAAACTCCTT | CTTGCAAGGC | 250 |
| AACATAGGAT | GCAATCATAG | CATTTGTGCG | ATTGTACTTG | CCAGTTACTG | 300 |
| GCAAATCAAG | GGCTTGCTCT | AAGAAATTGA | CCTTGAAGGT | CAGACTATCT | 350 |
| TTGCGCTCAA | CCAAGTCGGT | AATTCCCAGC | TCTGCTCCTT | GACCAAAACG | 400 |
| AACCACCTTT | TTATCAGTTG | GCAAATAGTC | CTCTACGATA | GGGTCAGCCG | 450 |
| GCGCTAAAAG | CAAGGAACCT | GAAGCCATTC | CGTCTGCAAT | TTGCATTTTT | 500 |
| CCTTTAGCAA | TCTCAGAACG | GTCTTTGAAA | AAGGCCAAAT | GAGCTTCTCC | 550 |
| AACCAAGGTC | ACGATGGCTG | TATGGACAG  |            |            | 579 |

## 2) INFORMATION FOR SEQ ID NO: 2062

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
(B) STRAIN: StrR-63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062

|             |             |            |            |            |     |
|-------------|-------------|------------|------------|------------|-----|
| AAGCTCAAAA  | ACATCTGTGG  | GATATCTACA | ACTCCGATCA | ATACGTCTCT | 50  |
| TACCCTGACG  | ATGATTTGCA  | AGTCGCATCT | ACGGTCGTAG | ATGTTTCAAA | 100 |
| TGGTAAAGTC  | ATCGCACAAAC | TTGGTGCTCG | TCATCAAGCA | AGTAATGTTT | 150 |
| CATTTCGGTAC | CAACCAGGCC  | GTAGAAACCA | ATCGTGACTG | GGGATCATCA | 200 |
| ATGAAACCAA  | TCACTGACTA  | TGCTCCCGCT | TTAGAATATG | GAGTCTATGA | 250 |
| CTCTACTGCT  | TCTATTGTAC  | ATGATGTCCC | TTATAACTAT | CCTGGCACTG | 300 |
| ATACTCCACT  | CTACAACTGG  | GATCATGTCT | ACTTTGGAAA | CATTACAATC | 350 |
| CAGTATGCTC  | TTCAACAATC  | ACGAAATGTC | ACAGCCGTTG | AGACTTTGAA | 400 |
| TAAGGTCGGT  | CTAGATAGAG  | CTAAAACCTT | CCTTAATGGT | CTTGGTATCG | 450 |
| ACTATCCAAG  | CATGCATTAT  | GCAAACGCCA | TTTCAAGTAA | CACAACTGAA | 500 |
| TCCAACAAAA  | AATATGGTGC  | AAGTAGTGAA | AAAATGGCTG | CTGCCTACGC | 550 |
| TGCTTTTTCG  | AATGGTGGTA  | TTTATCACAA | ACCAATGTAT | ATCAATAAAA | 600 |
| TCGTCTTTAG  | TGATGGTAGC  | GAAAAAGAAT | TTTCTGATGC | TGGTACACGA | 650 |
| GCTATGAAAG  | AGACTACTGC  | CTATATGATG | ACTGAAATGA | TGAAAACTGT | 700 |
| TTTAACTTAC  | GGAACAGGAC  | GTGGAGCCTA | CCTACCATGG | CTTCCACAAG | 750 |

|            |            |             |            |            |      |
|------------|------------|-------------|------------|------------|------|
| CAGGTAAGAC | AGGTACTTCT | AACTATACTG  | ACGAAGAAAT | TGAAAAGTAT | 800  |
| ATCAAGAACA | CTGGTTACGT | AGCTCCAGAT  | GAAATGTTTG | TAGGGTATAC | 850  |
| CCGTAAATAT | GCAATGGCTG | TTTGGACAGG  | ATACTCAAAT | CGTCTAACTC | 900  |
| CAATCATCGG | AGATGGTTTC | CTTGTTGCTG  | GTAAAGTCTA | TCGTTCAATG | 950  |
| ATAACTTACC | TTTCTGAAGA | TGACCAACCT  | GGAGATTGGA | CAATGCCAGA | 1000 |
| TGGCTTGTAT | AGAAATGGAG | AATTTCGTATT | TAAAAATGGT | GCTCGTTCTA | 1050 |
| CGTGGAGCTC | ACCTGCTCCA | CAACAACCCC  | CATCAACTGA | AAGTTCAAGC | 1100 |
| TCATCATCAG | ATAGTTCAAC | TTACAGTCT   | AGCTCAACCA | CTCCAAGCAC | 1150 |
| AAATAATAGT | ACGACTACCA | ATCCTAACAA  | TAATACGCAA | CAATCAAATA | 1200 |
| CAACCCCTGA | TCAACA     |             |            |            | 1216 |

## 2) INFORMATION FOR SEQ ID NO: 2063

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: ATCC 700673

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063

|            |             |            |             |            |     |
|------------|-------------|------------|-------------|------------|-----|
| AATACGTCTC | TTACCCTGAC  | GATGATTTGC | AAGTCGCATC  | CACGGTCGTA | 50  |
| GATGTTTCAA | ATGGTAAAGT  | CATCGCCCAA | CTTGGAGCTC  | GTCACCAAGC | 100 |
| AAGTAACGTT | TCATTTGGTA  | CCAACCAAGC | TGTGGAAACC  | AATCGTGACT | 150 |
| GGGGTTCAAC | AATGAAACCC  | ATCACCGATT | ATGCACCTGC  | CATAGAATAC | 200 |
| GGTGTATATG | ATTCCACTGC  | AACTATGGTT | AATGATATTC  | CTTATAACTA | 250 |
| TCCGGGAACA | AGCACACCTG  | TCTACAACTG | GGATCGAGCA  | TATTTTGGTA | 300 |
| ATATTACTCT | GCAATATGCC  | CTTCAACAAT | CTCGTAACGT  | ACCCGCCGTT | 350 |
| GAGACACTAA | ACAAGGTTGG  | TTTAGATAGA | GCTAAAAGTT  | TCCTAAATGG | 400 |
| TTTAGGAATC | GA CTATCCTG | TAATGCACTA | TTCAAATGCT  | ATTTCAAGTA | 450 |
| ATACTACCGA | ATCTAGTAAA  | CAGTACGGGG | CAAGTAGTGA  | AAAAATGGCC | 500 |
| ACTGCCTATG | CCGCATTTCG  | AAACGGCGGT | ATTTACCACA  | AACCAATGTA | 550 |
| CATCAATAAG | GTTGTCTTTA  | GCGATGGTAG | CGAAAAAGAA  | TTTTCTGACC | 600 |
| CTGGCACAAG | AGCCATGAAA  | GAAACGACTG | CTTACATGAT  | GACAGAGATG | 650 |
| ATGAAAACAG | TCTGGACTTA  | CGGAACTGGT | CGCGGTGCCT  | ACCTACCTTG | 700 |
| GCTTCCACAA | GCAGGTAAAA  | CAGGTACTTC | TA ACTATACT | GACGAAGAAA | 750 |
| TTGAAAAGTA | TATCAAGAAC  | ACTGGTTACG | TAGCTCCAGA  | TGAAATGTTT | 800 |
| GTAGGGTATA |             |            |             |            | 810 |

## 2) INFORMATION FOR SEQ ID NO: 2064

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: ATCC 700678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TCTTACCCTG | ACGATGATTT | GCAAGTCGCA | TCTACGGTCG | TAGATGTTTC | 50  |
| AAATGGTAAA | GTCATCGCCC | AACTTGGAGC | TCGTCACCAA | GCAAGTAACG | 100 |
| TTTCATTTGG | TACCAACCAA | GCTGTGGAAA | CCAATCGTGA | CTGGGGATCA | 150 |
| ACTATGAAAC | CAATCACAGA | CTATGCTCCT | GCCTTGGAGT | ACGGTGTCTA | 200 |
| CGATTCAACT | GCTACTATCG | TTCACGATGA | GCCCTATAAC | TACCCTGGGA | 250 |
| CAGATATCCC | TCTCTATAAC | TGGGATCGAG | CATATTTCCG | TAATATTACT | 300 |
| CTGCAATATG | CCCTTCAACA | ATCTCGTAAC | GTACCTGCCG | TTGAAACACT | 350 |
| AAACAAGGTC | GGTCTAGATA | AGGCTAAAAC | CTTCCTTAAT | GGTCTTGGTA | 400 |
| TCGACTATCC | AAGCATGCAT | TATGCAAACG | CCATTTCAAG | TAATACAACT | 450 |
| GAATCCAACA | AAAAATATGG | TGCAAGTAGT | GAAAAAATAG | CTACCGCCTA | 500 |
| TGCCGCATTC | GCAAATGGTG | GTATTTACCA | CAAACCAATG | TACATCAATA | 550 |
| AAGTTGTCTT | TAGCGATGGT | AGCGAAAAAG | AATTTTCTGA | CCCTGGCACA | 600 |
| AGAGCCATGA | AAGAAACGAC | TGCTTACATG | ATGACAGAAA | TGATGAAAAC | 650 |
| AGTCTGGACG | TACGGAACGT | GTCGTGGTGC | CTACCTGCCT | TGGCTTCCTC | 700 |
| AAGCTGGTAA | AACAGGTACC | TCTAACTATA | CTGACGAAGA | AATTGAAAAG | 750 |
| TATATCAAGA | ACACTGGTTA | CGTAGCTCCA | GA         |            | 782 |

2) INFORMATION FOR SEQ ID NO: 2065

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2065

CCAGGACGTG GAGGCGATCA CA

22

2) INFORMATION FOR SEQ ID NO: 2066

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066

CACCGACAGC GAGCCGATCA GA

22

## 2) INFORMATION FOR SEQ ID NO: 2067

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067

AGCTGAGCCA ATTCATGG

18

## 2) INFORMATION FOR SEQ ID NO: 2068

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

ATTCATGGAC CAGAACAAC

19

## 2) INFORMATION FOR SEQ ID NO: 2069

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069

CGCTGTCGGG GTTGACCC

18

## 2) INFORMATION FOR SEQ ID NO: 2070

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1073

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070

GTTGACCCAC AAGCGCCG

18

## 2) INFORMATION FOR SEQ ID NO: 2071

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071

CGACTGTCGG CGCTGGGG

18

## 2) INFORMATION FOR SEQ ID NO: 2072

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: Rv
- (C) ACCESSION NUMBER: L27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072

|            |            |            |            |             |     |
|------------|------------|------------|------------|-------------|-----|
| GTGCTGGAAG | GATGCATCTT | GGCAGATTCC | CGCCAGAGCA | AAACAGCCGC  | 50  |
| TAGTCCTAGT | CCGAGTCGCC | CGCAAAGTTC | CTCGAATAAC | TCCGTACCCG  | 100 |
| GAGCGCCAAA | CCGGGTCTCC | TTCGCTAAGC | TGCGCGAACC | ACTTGAGGTT  | 150 |
| CCGGGACTCC | TTGACGTCCA | GACCGATTCC | TTCGAGTGGC | TGATCGGTTC  | 200 |
| GCCGCGCTGG | CGCGAATCCG | CCGCCGAGCG | GGGTGATGTC | AACCCAGTGG  | 250 |
| GTGGCCTGGA | AGAGGTGCTC | TACGAGCTGT | CTCCGATCGA | GGACTTCTCC  | 300 |
| GGGTCGATGT | CGTTGTCTGT | CTCTGACCTT | CGTTTCGACG | ATGTCAAGGC  | 350 |
| ACCCGTCGAC | GAGTGCAAAG | ACAAGGACAT | GACGTACGCG | GCTCCACTGT  | 400 |
| TCGTCAACGC | CGAGTTCATC | AACAACAACA | CCGGTGAGAT | CAAGAGTCAG  | 450 |
| ACGGTGTTCA | TGGGTGACTT | CCCGATGATG | ACCGAGAAGG | GCACGTTTCAT | 500 |
| CATCAACGGG | ACCGAGCGTG | TGGTGGTCAG | CCAGCTGGTG | CGGTCGCCCCG | 550 |
| GGGTGTACTT | CGACGAGACC | ATTGACAAGT | CCACCGACAA | GACGCTGCAC  | 600 |
| AGCGTCAAGG | TGATCCCGAG | CCGCGGCGCG | TGGCTCGAGT | TTGACGTCGA  | 650 |
| CAAGCGCGAC | ACCGTCGGCG | TGCGCATCGA | CCGCAAACGC | CGGCAACCCG  | 700 |



|             |            |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|------|
| TCACCGTGCT  | GCTCAAGGCG | CTGGGCTGGA  | CCAGCGAGCA  | GATTGTGCGAG | 750  |
| CGGTTCCGGT  | TCTCCGAGAT | CATGCGATCG  | ACGCTGGAGA  | AGGACAACAC  | 800  |
| CGTCGGCACC  | GACGAGGCGC | TGTTGGACAT  | CTACCGCAAG  | CTGCGTCCGG  | 850  |
| GCGAGCCCCC  | GACCAAAGAG | TCAGCGCAGA  | CGCTGTTGGA  | AAACTTGTTT  | 900  |
| TTCAAGGAGA  | AGCGCTACGA | CCTGGCCCCG  | GTCGGTCGCT  | ATAAGGTCAA  | 950  |
| CAAGAAGCTC  | GGGCTGCATG | TCGGCGAGCC  | CATCACGTCG  | TCGACGCTGA  | 1000 |
| CCGAAGAAGA  | CGTCGTGGCC | ACCATCGAAT  | ATCTGGTCCG  | CTTGACGAG   | 1050 |
| GGTCAGACCA  | CGATGACCGT | TCCGGGCGGC  | GTCGAGGTGC  | CGGTGGAAC   | 1100 |
| CGACGACATC  | GACCACTTCG | GCAACCGCCG  | CCTGCGTACG  | GTCGGCGAGC  | 1150 |
| TGATCCAAAA  | CCAGATCCGG | GTCGGCATGT  | CGCGGATGGA  | GCGGGTGGTC  | 1200 |
| CGGGAGCGGA  | TGACCACCCA | GGACGTGGAG  | GCGATCACAC  | CGCAGACGTT  | 1250 |
| GATCAACATC  | CGGCCGGTGG | TCGCCGCGAT  | CAAGGAGTTC  | TTCGGCACCA  | 1300 |
| GCCAGCTGAG  | CCAATTCATG | GACCAGAACA  | ACCCGCTGTC  | GGGGTTGACC  | 1350 |
| CACAAGCGCC  | GACTGTGCGC | GCTGGGGCCC  | GGCGGTCTGT  | CACGTGAGCG  | 1400 |
| TGCCGGGCTG  | GAGGTCCGCG | ACGTGCACCC  | GTCGCACTAC  | GGCCGGATGT  | 1450 |
| GCCCCGATCGA | AACCCCTGAG | GGGCCCAACA  | TCGGTCTGAT  | CGGCTCGCTG  | 1500 |
| TCGGTGTACG  | CGCGGGTCAA | CCCGTTCCGG  | TTCATCGAAA  | CGCCGTACCG  | 1550 |
| CAAGGTGGTC  | GACGGCGTGG | TTAGCGACGA  | GATCGTGTAC  | CTGACCGCCG  | 1600 |
| ACGAGGAGGA  | CCGCCACGTG | GTGGCACAGG  | CCAATTCCGC  | GATCGATGCG  | 1650 |
| GACGGTCGCT  | TCGTGAGGCC | GCGCGTGCTG  | GTCCGCCGCA  | AGGCGGGCGA  | 1700 |
| GGTGGAGTAC  | GTGCCCTCGT | CTGAGGTGGA  | CTACATGGAC  | GTCTCGCCCC  | 1750 |
| GCCAGATGGT  | GTCGGTGGCC | ACCGCGATGA  | TTCCCTTCCT  | GGAGCACGAC  | 1800 |
| GACGCCAACC  | GTGCCCTCAT | GGGGGCAAAC  | ATGCAGCGCC  | AGGCGGTGCC  | 1850 |
| GCTGGTCCGT  | AGCGAGGCC  | CGCTGGTGGG  | CACCGGGATG  | GAGCTGCGCG  | 1900 |
| CGGCGATCGA  | CGCGGCGACG | TCGTGCTCGC  | AAGAAAGCGG  | CGTCATCGAG  | 1950 |
| GAGGTGTCGG  | CCGACTACAT | CACTGTGATG  | CACGACAACG  | GCACCCGGCG  | 2000 |
| TACCTACCGG  | ATGCGCAAGT | TTGCCCGGTC  | CAACCACGGC  | ACTTGCGCCA  | 2050 |
| ACCAAGTCCC  | CATCGTGGAC | GCGGGCGACC  | GAGTCGAGGC  | CGGTGAGGTG  | 2100 |
| ATCGCCGACG  | GTCCCTGTAC | TGAGGACGGC  | GAGATGGCGC  | TGGGCAAGAA  | 2150 |
| CCTGCTGGTG  | GCCATCATGC | CGTGGGAGGG  | CCACAACCTAC | GAGGACGCGA  | 2200 |
| TCATCCTGTC  | CAACCGCCTG | GTCGAAGAGG  | ACGTGCTCAC  | CTCGATCCAC  | 2250 |
| ATCGAGGAGC  | ATGAGATCGA | TGCTCGCGAC  | ACCAAGCTGG  | GTGCGGAGGA  | 2300 |
| GATCACCCGC  | GACATCCCGA | ACATCTCCGA  | CGAGGTGCTC  | GCCGACCTGG  | 2350 |
| ATGAGCGGGG  | CATCGTGC   | ATCGGTGCCG  | AGGTTCGCGA  | CGGGGACATC  | 2400 |
| CTGGTCCGCA  | AGGTCACCCC | GAAGGGTGAG  | ACCGAGCTGA  | CGCCGGAGGA  | 2450 |
| GCGGCTGCTG  | CGTGCCATCT | TCGGTGAGAA  | GGCCCGCGAG  | GTGCGCGACA  | 2500 |
| CTTCGCTGAA  | GGTGCCGCAC | GGCGAATCCG  | GCAAGGTGAT  | CGGCATTCCG  | 2550 |
| GTGTTTTTCCC | GCGAGGACGA | GGACGAGTTG  | CCGGCCGGTG  | TCAACGAGCT  | 2600 |
| GGTGCGTGTG  | TATGTGGCTC | AGAAACGCAA  | GATCTCCGAC  | GGTGACAAGC  | 2650 |
| TGGCCGGCCG  | GCACGGCAAC | AAGGGCGTGA  | TCGGCAAGAT  | CCTGCCGGTT  | 2700 |
| GAGGACATGC  | CGTTCCCTTG | CGACGGCACC  | CCGGTGGACA  | TTATTTTGA   | 2750 |
| CACCCACGGC  | GTGCCGCGAC | GGATGAACAT  | CGGCCAGATT  | TTGGAGACCC  | 2800 |
| ACCTGGGTTG  | GTGTGCCCCA | AGCGGCTGGA  | AGGTGACGCG  | CGCCAAGGGG  | 2850 |
| GTTCCGGACT  | GGGCCGCCAG | GCTGCCCCGAC | GAAGTGTCTG  | AGGCGCATGC  | 2900 |
| GAACGCCATT  | GTGTCGACGC | CGGTGTTTGA  | CGGCGCCAG   | GAGGCCGAGC  | 2950 |
| TGCAGGGCCT  | GTTGTGCTGC | ACGCTGCCCCA | ACCGCGACGG  | TGACGTGCTG  | 3000 |
| GTCGACGCCG  | ACGGCAAGGC | CATGCTCTTC  | GACGGGCGCA  | GCGGCGAGCC  | 3050 |
| GTTCCCGTAC  | CCGGTCACGG | TTGGCTACAT  | GTACATCATG  | AAGCTGCACC  | 3100 |
| ACCTGGTGGA  | CGACAAGATC | CACGCCCCGCT | CCACCGGGCC  | GTACTCGATG  | 3150 |
| ATCACCCAGC  | AGCCGCTGGG | CGGTAAGGCG  | CAGTTCGGTG  | GCCAGCGGTT  | 3200 |
| CGGGGAGATG  | GAGTGCTGGG | CCATGCAGGC  | CTACGGTGCT  | GCCTACACCC  | 3250 |
| TGCAGGAGCT  | GTTGACCATC | AAGTCCGATG  | ACACCGTCGG  | CCGCGTCAAG  | 3300 |
| GTGTACGAGG  | CGATCGTCAA | GGGTGAGAAC  | ATCCCGGAGC  | CGGGCATCCC  | 3350 |
| CGAGTCGTTC  | AAGGTGCTGC | TCAAAGAACT  | GCAGTCGCTG  | TGCCTCAACG  | 3400 |
| TCGAGGTGCT  | ATCGAGTGAC | GGTGCGGCGA  | TCGAACTGCG  | CGAAGGTGAG  | 3450 |
| GACGAGGACC  | TGGAGCGGGC | CGCGGCCAAC  | CTGGGAATCA  | ATCTGTCCCG  | 3500 |
| CAACGAATCC  | GCAAGTTTCG | AGGATCTTGC  | GTAA        |             | 3534 |

## 2) INFORMATION FOR SEQ ID NO: 2073

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073

CCGAGCAACA TGATTGAACC ATCCACCAAC TGGCTCGG

38

## 2) INFORMATION FOR SEQ ID NO: 2074

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074

CCGAGCAACA TGATTGAAGC TTCCACCAAC TGGCTCGG

38

## 2) INFORMATION FOR SEQ ID NO: 2075

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075

CCGAGCCAGG TTCTGAAGTC TCTGCATTAT TAGGTGCTCG G

41

## 2) INFORMATION FOR SEQ ID NO: 2076

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single

1076

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076

CCGAGCYGAY AACATTTTCA GATTCACCCA RCGCTCGG

39

2) INFORMATION FOR SEQ ID NO: 2077

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077

CCGAGCAACC GATCCAGCTC CAGCTACGCT CGG

33

2) INFORMATION FOR SEQ ID NO: 2078

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078

CCGAGCCTTG GTCTTCGGCC AAATGAACGC TCGG

34

2) INFORMATION FOR SEQ ID NO: 2079

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079

CCGAGCGTTC AGTTACTTCA GTCCAAGCCG GCTCGG

36

## 2) INFORMATION FOR SEQ ID NO: 2080

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080

CCGAGCCGAA GAGGGCCAAG ATGTCGCTCG G

31

## 2) INFORMATION FOR SEQ ID NO: 2081

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081

GRATYRTYAA AGTTGGTGAG GAAG

24

## 2) INFORMATION FOR SEQ ID NO: 2082

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082

CMACTTCATC YCGCTTCGTA CC

22

## 2) INFORMATION FOR SEQ ID NO: 2083

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single

1078

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083

CCGCCGATGT TCCGTAAATT ACTTGAIGAA GGTCGAGCCG GCGG

44

2) INFORMATION FOR SEQ ID NO: 2084

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084

CACGCGTCAA CACCCGTACA AGTCGTCTTT TGCGCGTG

38

2) INFORMATION FOR SEQ ID NO: 2085

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085

CAAACCTAAAG AACATATCTT GCTA

24

2) INFORMATION FOR SEQ ID NO: 2086

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086

ATATAATTTG CATCACCTTC AAG

23

## 2) INFORMATION FOR SEQ ID NO: 2087

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087

TCAGCTCGTG GGATTAGGAG AG

22

## 2) INFORMATION FOR SEQ ID NO: 2088

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088

AGGCTTCACG CTGTTAGGCT GA

22

## 2) INFORMATION FOR SEQ ID NO: 2089

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089

ATGCTGAACT TATTGACCTT

20

## 2) INFORMATION FOR SEQ ID NO: 2090

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single

1080

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090

CGTTACTGGA GTCGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2091

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091

CGCGACTTGA GATGGAAGTT AGTGAGCTTC TTGGTCGCG

39

2) INFORMATION FOR SEQ ID NO: 2092

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092

CGCGACGAAA GAACTTCCTG AAGGTCGTGC AGGTCCAG

38

2) INFORMATION FOR SEQ ID NO: 2093

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093

TGTTGGCAAT CGAAGACACC

20

## 2) INFORMATION FOR SEQ ID NO: 2094

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094

TTCAATTTCT TGACCTACTT TCAA

24

## 2) INFORMATION FOR SEQ ID NO: 2095

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095

CGGTCGGGTT GAACGTGG

18

## 2) INFORMATION FOR SEQ ID NO: 2096

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096

CGCGACCGGT ACCACGGCCA GTAATCGTGT CGCG

34

## 2) INFORMATION FOR SEQ ID NO: 2097

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1185 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

1082



(A) ORGANISM: *Mycoplasma pneumoniae*  
 (B) STRAIN: ATCC 29342  
 (C) ACCESSION NUMBER: AE000019

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097

|            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------|
| ATGGCAAGAG | AGAAATTTGA | CCGATCTAAA | CCCCACGTTA | ATGTAGGTAC | 50   |
| TATTGGCCAC | ATTGACCACG | GTAAAACAAC | TTTAACAGCA | GCTATTTGTA | 100  |
| CTGTATTAGC | AAAAGAAGGT | AAATCAGCTG | CTACTCGTTA | CGACCAAATC | 150  |
| GATAAGGCTC | CGGAAGAAAA | AGCACGGGGA | ATTACGATTA | ACTCCGCTCA | 200  |
| CGTGAGGTAC | TCCTCTGACA | AGCGTCACTA | TGCTCACGTT | GACTGTCCAG | 250  |
| GACACGCTGA | CTACATTAAG | AACATGATTA | CTGGTGCTGC | ACAAATGGAT | 300  |
| GGTGCCATTC | TAGTAGTTTC | AGCAACTGAC | AGTGTTATGC | CCCAAACCCG | 350  |
| TGAACACATT | TTGTTGGCCC | GCCAAGTGGG | TGTGCCACGC | ATGGTAGTGT | 400  |
| TCCTAAACAA | GTGTGACATT | GCAACTGATG | AAGAAGTGCA | AGAGTTAGTA | 450  |
| GCAGAAGAGG | TACGTGACTT | ATTAACTTCT | TACGGCTTTG | ATGGCAAGAA | 500  |
| CACCCCTATT | ATTTATGGTT | CTGCACTTAA | AGCGCTTGAA | GGTGATCCTA | 550  |
| AGTGGAAGC  | TAAGATCCAT | GATTTAATGA | ATGCAGTTGA | TGAATGGATT | 600  |
| CCAACTCCTG | AACGTGAAGT | GGACAAACCC | TTCTTGTTGG | CAATCGAAGA | 650  |
| CACCATGACG | ATTACTGGCC | GTGGTACCGT | GGTTACCGGT | CGGGTTGAAC | 700  |
| GTGGTGAATT | GAAAGTAGGT | CAAGAAATTG | AAATCGTTGG | TTTACGTCCA | 750  |
| ATCCGTAAAG | CAGTTGTTAC | CGGAATCGAA | ATGTTCAAAA | AGGAACTTGA | 800  |
| TTCAGCAATG | GCTGGGGACA | ACGCTGGGGT | ATTACTCCGT | GGTGTGGACC | 850  |
| GTAAAGAAGT | GGAACGTGGT | CAAGTGTTAG | CTAAACCAGG | TTCGATTAAA | 900  |
| CCGCACAAGA | AATTTAAAGC | GGAAATCTAT | GCTTTAAAGA | AGGAAGAAGG | 950  |
| TGGTCGTCAC | ACCGGTTTCT | TAAACGGTTA | CCGTCCCCAA | TTCTACTTCC | 1000 |
| GTACTACAGA | CGTTACTGGT | TCGATTTCCT | TACCAGAAAA | CACCGAAATG | 1050 |
| GTGCTACCAG | GTGACAATAC | CTCGATTACA | GTTGAATAA  | TTGCACCAAT | 1100 |
| TGCTTGTAAG | AAAGGTAGTA | AGTTCTCCAT | CCGTGAAGGT | GGTCGAACGG | 1150 |
| TTGGTGCTGG | TTCAGTCACG | GAAGTGCTTG | AATAG      |            | 1185 |

## 2) INFORMATION FOR SEQ ID NO: 2098

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098

CTGAGTCACA CCGACAAACG TC

22

## 2) INFORMATION FOR SEQ ID NO: 2099

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099

CCAGGACTGA ACGGGATACG AA

22

## 2) INFORMATION FOR SEQ ID NO: 2100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100

GCGAGACGAT AGGTTGTC

18

## 2) INFORMATION FOR SEQ ID NO: 2101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv
- (C) ACCESSION NUMBER: Z79701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CAGCCCGCGA | GCGTAACCTG | GCTGCGATTT | CCGGCGCGGA | TTTTCGCAGT | 50  |
| GCGGTTACGC | TCGGAAAGCG | CGGGCCTCGC | CCACGCGGCG | GATGATGTCA | 100 |
| GCGGGGTGGT | CCTCGGCGAC | GACCCGAC   | ACGATCCACC | CGTAGCGGTG | 150 |
| CTGGACTTTC | TCGTGCCGGA | GGATGTCTTT | CCGGTAGTGG | TAGCGACTGG | 200 |
| TCAGATGGTG | GTCGCCGTCA | TACTCGGCCG | CGACCTTGAT | GTCTTGCCAG | 250 |
| CCCATATCCA | AATGGGCTTC | CGCCCAGCCC | CATTCGTTGC | GCACCGCGAT | 300 |
| CTGCGTCTGG | GGGCGCGGAA | AGCCGGCGCG | GATCAACAAC | AAGCGCAGCC | 350 |
| AGGTTTCCTT | GGGGGACTGG | GCACCGCCGT | CGACGAGGTC | CAGAGCGGCT | 400 |
| CTTGCGGCCT | TCATGCCACG | GCGGCCCGGA | TAGCGCTCGA | TCAGCGGCTC | 450 |
| GACGTCGGCC | ACCTTCAAAT | CGGTGGCCTG | TATCAGGGCG | TCGACGGCCG | 500 |
| CGACGGCGGG | GTCCAATGGA | AATCGACTGG | TCAGGTCGAG | CGCCGTTTCG | 550 |
| TCCGGTGTGG | TCACGCGCAT | GCCCTCGATG | ACGCAGATCT | CGTCGGGCTC | 600 |
| GATGCGCTCT | TCCCAGACTT | GCAGCCCCGG | GGCACGGCGG | CGGTTGGTGT | 650 |
| CGATGATCGC | GGCGGGAAGA | TCCGCGTCGA | TCCACTTGGC | GCCATGGAAG | 700 |
| GCAGAAGCCG | AGTAGCCGGC | CAGCACGCCG | CGGCGGCGCG | AGCGCAGCCA | 750 |
| CAGCGCTTTT | GCACGCAATT | GCGCGGTCAG | TTCCACACCC | TGCGGCACGT | 800 |

1084

|             |            |            |             |            |      |
|-------------|------------|------------|-------------|------------|------|
| ACACGTCTTT  | ATGTAGCGCG | ACATACCTGC | TGCGCAATTC  | GTAGGGCGTC | 850  |
| AATACACCCG  | CAGCCAGGGC | CTCGCTGCCC | AGAAAGGGAT  | CCGTCATGGT | 900  |
| CGAAGTGTGC  | TGAGTCACAC | CGACAAACGT | CACGAGCGTA  | ACCCAGTGC  | 950  |
| GAAAGTTCCC  | GCCGGAAATC | GCAGCCACGT | TACGCTCGTG  | GACATACCGA | 1000 |
| TTTCGGCCCC  | GCCGCGGCGA | GACGATAGGT | TGTCGGGGTG  | ACTGCCACAG | 1050 |
| CCACTGAAGG  | GGCCAAACCC | CCATTCGTAT | CCCGTTCACT  | CCTGGTTACC | 1100 |
| GGAGGAAACC  | GGGGGATCGG | GCTGGCGATC | GCACAGCGGC  | TGGCTGCCGA | 1150 |
| CGGCCACAAG  | GTGGCCGTCA | CCCACCGTGG | ATCCGGAGCG  | CCAAAGGGGC | 1200 |
| TGTTTGGCGT  | CGAATGTGAC | GTCACCGACA | GCGACGCCGT  | CGATCGCGCC | 1250 |
| TTCACGGCGG  | TAGAAGAGCA | CCAGGGTCCG | GTCGAGGTGC  | TGGTGTCCAA | 1300 |
| CGCCGGCCTA  | TCCGCGGACG | CATTCCTCAT | GCGGATGACC  | GAGGAAAAGT | 1350 |
| TCGAGAAGGT  | CATCAACGCC | AACCTCACCG | GGGCGTTCCG  | GGTGGCTCAA | 1400 |
| CGGGCATCGC  | GCAGCATGCA | GCGCAACAAA | TTCGGTTCGAA | TGATATTCAT | 1450 |
| AGGTTTCGGTC | TCCGGCAGCT | GGGGCATCGG | CAACCAGGCC  | AACTACGCAG | 1500 |
| CCTCCAAGGC  | CGGAGTGATT | GGCATGGCCC | GCTCGATCGC  | CCGCGAGCTG | 1550 |
| TCGAAGGCAA  | ACGTGACCGC | GAATGTGGTG | GCCCCGGGCT  | ACATCGACAC | 1600 |
| CGATATGACC  | CGCGCGCTGG | ATGAGCGGAT | TCAGCAGGGG  | GCGCTGCAAT | 1650 |
| TTATCCCAGC  | GAAGCGGGTC | GGCACCCCCG | CCGAGGTCGC  | CGGGGTGGTC | 1700 |
| AGCTTCCTGG  | CTTCCGAGGA | TGCGAGCTAT | ATCTCCGGTG  | CGGTCATCCC | 1750 |
| GGTCGACGGC  | GGCATGGGTA | TGGGCCACTG | ACACAACACA  | AGGACGCACA | 1800 |
| TGACAGGACT  | GCTGGACGGC | AAACGGATTC | TGGTTAGCGG  | AATCATCACC | 1850 |
| GACTCGTCGA  | TCGCGTTTCA | CATCGCACGG | GTAGCCCAGG  | AGCAGGGCGC | 1900 |
| CCAGCTGGTG  | CTCACCGGGT | TCGACCGGCT | GCGGCTGATT  | CAGCGCATCA | 1950 |
| CCGACCGGCT  | GCCGGCAAAG | GCCCCGCTGC | TCGAACTCGA  | CGTGCAAAAC | 2000 |
| GAGGAGCACC  | TGGCCAGCTT | GGCCGGCCGG | GTGACCGAGG  | CGATCGGGGC | 2050 |
| GGGCAACAAG  | CTCGACGGGG | TGGTGCATTC | GATTGGGTTC  | ATGCCGCAGA | 2100 |
| CCGGGATGGG  | CATCAACCCG | TTCTTCGACG | CGCCCTACGC  | GGATGTGTCC | 2150 |
| AAGGGCATCC  | ACATCTCGGC | GTATTCGTAT | GCTTCGATGG  | CCAAGGCGCT | 2200 |
| GCTGCCGATC  | ATGAACCCCG | GAGGTTCCAT | CGTCGGCATG  | GACTTCGACC | 2250 |
| CGAGCCGGGC  | GATGCCGGCC | TACAACCTGA | TGACGGTCGC  | CAAGAGCGCG | 2300 |
| TTGGAGTCGG  | TCAACAGGTT | CGTGCGCGCG | GAGGCCGGCA  | AGTACGGTGT | 2350 |
| GCGTTTCAAT  | CTCGTTGCCG | CAGGCCCTAT | CCGGACGCTG  | GCGATGAGTG | 2400 |
| CGATCGTCGG  | CGGTGCGCTC | GGCGAGGAGG | CCGGCGCCCA  | GATCCAGCTG | 2450 |
| CTCGAGGAGG  | GCTGGGATCA | GCGCGCTCCG | ATCGGCTGGA  | ACATGAAGGA | 2500 |
| TGCGACGCCG  | GTCGCCAAGA | CGGTGTGCGC | GCTGCTGTCT  | GACTGGCTGC | 2550 |
| CGGCGACCAC  | GGGTGACATC | ATCTACGCCG | ACGGCGGCGC  | GCACACCCAA | 2600 |
| TTGCTCTAG   |            |            |             |            | 2609 |

## 2) INFORMATION FOR SEQ ID NO: 2102

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102

CACCTTCACC CTGACCGACG

20

## 2) INFORMATION FOR SEQ ID NO: 2103

1085

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103

CGAACCAGCG GAAATAGTTG GAC

23

## 2) INFORMATION FOR SEQ ID NO: 2104

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104

CTGGGCATGG CICGAGTC

18

## 2) INFORMATION FOR SEQ ID NO: 2105

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37rv
- (C) ACCESSION NUMBER: U68480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105

|            |            |            |             |            |     |
|------------|------------|------------|-------------|------------|-----|
| ATGACACAGT | GCGCGAGCAG | ACGCAAAGC  | ACCCCAAATC  | GGGCGATTTT | 50  |
| GGGGGCTTTT | GCGTCTGCTC | GCGGGACGCG | CTGGGTGGCC  | ACCATCGCCG | 100 |
| GGCTGATTGG | CTTTGTGTTG | TCGGTGGCGA | CGCCGCTGCT  | GCCCGTCGTG | 150 |
| CAGACCACCG | CGATGCTCGA | CTGGCCACAG | CGGGGGCAAC  | TGGGCAGCGT | 200 |
| GACCGCCCCG | CTGATCTCGC | TGACGCCGGT | CGACTTTACC  | GCCACCGTGC | 250 |
| CGTGCGACGT | GGTGCGCGCC | ATGCCACCCG | CGGGCGGGGT  | GGTGCTGGGC | 300 |
| ACCGCACCCA | AGCAAGGCAA | GGACGCCAAT | TTGCAGGCGT  | TGTTTCGTCT | 350 |
| CGTCAGCGCC | CAGCGCGTGG | ACGTCACCGA | CCGCAACGTG  | GTGATCTTGT | 400 |
| CCGTGCCGCG | CGAGCAGGTG | ACGTCCCCGC | AGTGTC AACG | CATCGAGGTC | 450 |

1086

|             |             |            |             |             |      |
|-------------|-------------|------------|-------------|-------------|------|
| ACCTCTACCC  | ACGCCGGCAC  | CTTCGCCAAC | TTCGTCGGGC  | TCAAGGACCC  | 500  |
| GTCGGGCGCG  | CCGCTGCGCA  | GCGGCTTCCC | CGACCCCAAC  | CTGCGCCCCG  | 550  |
| AGATTGTCGG  | GGTGTTTACC  | GACCTGACCG | GGCCCCGCGC  | GCCCCGGGCTG | 600  |
| GCGGTCTCGG  | CGACCATCGA  | CACCCGGTTC | TCCACCCGGC  | CGACCACGCT  | 650  |
| GAAACTGCTG  | GCGATCATCG  | GGGCGATCGT | GGCCACCGTC  | GTCGCACTGA  | 700  |
| TCGCGTTGTG  | GCGCCTGGAC  | CAGTTGGACG | GGCGGGGCTC  | AATTGCCCCAG | 750  |
| CTCCTCCTCA  | GGCCGTTCCG  | GCCTGCATCG | TCGCCGGGCG  | GCATGCGCCG  | 800  |
| GCTGATTCCG  | GCAAGCTGGC  | GCACCTTCAC | CCTGACCGAC  | GCCGTGGTGA  | 850  |
| TATTCGGCTT  | CCTGCTCTGG  | CATGTCATCG | GCGCGAATTC  | GTCGGACGAC  | 900  |
| GGCTACATCC  | TGGGCATGGC  | CCGAGTCGCC | GACCACGCCG  | GCTACATGTC  | 950  |
| CAACTATTTT  | CGCTGGTTCG  | GCAGCCCCGA | GGATCCCTTC  | GGCTGGTATT  | 1000 |
| ACAACCTGCT  | GGCGCTGATG  | ACCCATGTCA | GCGACGCCAG  | TCTGTGGATG  | 1050 |
| CGCCTGCCAG  | ACCTGGCCCG  | CGGGCTAGTG | TGCTGGCTGC  | TGCTGTGCGG  | 1100 |
| TGAGGTGCTG  | CCCCGCCTCG  | GGCCGGCGGT | GGAGGCCAGC  | AAACCCGCCT  | 1150 |
| ACTGGGCGGC  | GGCCATGGTC  | TTGCTGACCG | CGTGGATGCC  | GTTCAACAAC  | 1200 |
| GGCCTGCGGC  | CGGAGGGCAT  | CATCGCGCTC | GGCTCGCTGG  | TCACCTATGT  | 1250 |
| GCTGATCGAG  | CGGTCCATGC  | GGTACAGCCG | GCTCACACCG  | GCGGCGCTGG  | 1300 |
| CCGTCGTTAC  | CGCCGCATTC  | ACACTGGGTG | TGCAGCCAC   | CGGCCTGATC  | 1350 |
| GCGGTGGCCG  | CGCTGGTGGC  | CGGCGGCCGC | CCGATGCTGC  | GGATCTTGGT  | 1400 |
| GCGCCGYCAT  | CGCCTGGTCG  | GCACGTTGCC | GTTGGTGTCTG | CCGATGCTGG  | 1450 |
| CCGCCGGCAC  | CGTCATCCTG  | ACCGTGGTGT | TCGCCGACCA  | GACCCTGTCA  | 1500 |
| ACGGTGTTGG  | AAGCCACCAG  | GGTTCGCGCC | AAAATCGGGC  | CGAGCCAGGC  | 1550 |
| GTGGTATACC  | GAGAACCTGC  | GTTACTACTA | CCTCATCCTG  | CCCACCGTCG  | 1600 |
| ACGGTTCGCT  | GTCGCGGCGC  | TTCGGCTTTT | TGATCACCGC  | GCTATGCCTG  | 1650 |
| TTCACCGCGG  | TGTTTCATCAT | GTTGCGGCGC | AAGCGAATTC  | CCAGCGTGGC  | 1700 |
| CCGCGGACCG  | GCGTGCGGCG  | TGATGGGCGT | CATCTTCGGC  | ACCATGTTCT  | 1750 |
| TCCTGATGTT  | CACGCCACC   | AAGTGGGTGC | ACCACTTCGG  | GCTGTTCCGC  | 1800 |
| GCCGTAGGGG  | CGGCGATGGC  | CGCGCTGACG | ACGGTGTTGG  | TATCCCCATC  | 1850 |
| GGTGCTGCGC  | TGGTCGCGCA  | ACCGGATGGC | GTTCTTGCGG  | GCGTTATTCT  | 1900 |
| TCCTGCTGGC  | GTTGTGTTGG  | GCCACCACCA | ACGGCTGGTG  | GTATGTCTCC  | 1950 |
| AGCTACGGTG  | TGCCGTTCAA  | CAGCGCGATG | CCGAAGATCG  | ACGGGATCAC  | 2000 |
| AGTCAGCACA  | ATCTTTTTTCG | CCCTGTTTGC | GATCGCCGCC  | GGCTATGCGG  | 2050 |
| CCTGGCTGCA  | CTTCGCGCCC  | CGCGGCGCCG | GCGAAGGGCG  | GCTGATCCGC  | 2100 |
| GCGCTGACGA  | CAGCCCCGGT  | ACCGATCGTG | GCCGGTTTCA  | TGGCGGCGGT  | 2150 |
| GTTTCGTGCG  | TCCATGGTGG  | CCGGGATCGT | GCGACAGTAC  | CCGACCTACT  | 2200 |
| CCAACGGCTG  | GTCCAACGTG  | CGGGCGTTTG | TCGGCGGCTG  | CGGACTGGCC  | 2250 |
| GACGACGTAC  | TCGTGAGGCC  | TGATACCAAT | GCGGGTTTCA  | TGAAGCCGCT  | 2300 |
| GGACGGCGAT  | TCGGGTTCCT  | GGGGCCCCCT | GGGCCCGCTG  | GGTGGAGTCA  | 2350 |
| ACCCGGTCGG  | CTTCACGCCC  | AACGGCGTAC | CGGAACACAC  | GGTGGCCGAG  | 2400 |
| GCGATCGTGA  | TGAAACCCAA  | CCAGCCCCGC | ACCGACTACG  | ACTGGGATGC  | 2450 |
| GCCGACCAAG  | CTGACGAGTC  | CTGGCATCAA | TGGTTCTACG  | GTGCCGCTGC  | 2500 |
| CCTATGGGCT  | CGATCCCGCC  | CGGGTACCGT | TGGCAGGCAC  | CTACACCACC  | 2550 |
| GGCGCACAGC  | AACAGAGCAC  | ACTCGTCTCG | GCGTGGTATC  | TCCTGCCTAA  | 2600 |
| GCCGGACGAC  | GGGCATCCGC  | TGGTCGTGGT | GACCGCCGCG  | GGCAAGATCG  | 2650 |
| CCGGCAACAG  | CGTGCTGCAC  | GGGTACACCC | CCGGGCAGAC  | TGTGGTGCTC  | 2700 |
| GAATACGCCA  | TGCCGGGACC  | CGGAGCGCTG | GTACCCGCCG  | GGCGGATGGT  | 2750 |
| GCCCCGACGAC | CTATACGGAG  | AGCAGCCCAA | GGCGTGCGCG  | AACCTGCGCT  | 2800 |
| TCGCCCCGAGC | AAAGATGCCC  | GCCGATGCCG | TCGCGGTCCG  | GGTGGTGGCC  | 2850 |
| GAGGATCTGT  | CGCTGACACC  | GGAGGACTGG | ATCGCGGTGA  | CCCCGCCGCG  | 2900 |
| GGTACCGGAC  | CTGCGCTCAC  | TGCAGGAATA | TGTGGGCTCG  | ACGCAGCCGG  | 2950 |
| TGCTGCTGGA  | CTGGGCGGTC  | GGTTTGGCCT | TCCCGTGCCA  | GCAGCCGATG  | 3000 |
| CTGCACGCCA  | ATGGCATCGC  | CGAAATCCCG | AAGTTCCGCA  | TCACACCGGA  | 3050 |
| CTACTCGGCT  | AAGAAGCTGG  | ACACCGACAC | GTGGGAAGAC  | GGCACTAACG  | 3100 |
| GCGGCCTGCT  | CGGGATCACC  | GACCTGTTGC | TGCGGGCCCA  | CGTCATGGCC  | 3150 |
| ACCTACCTGT  | CCCGCGACTG  | GGCCCGCGAT | TGGGGTTCCC  | TGCGCAAGTT  | 3200 |
| CGACACCCTG  | GTCGATGCCC  | CTCCCGCCCA | GCTCGAGTTG  | GGCACCGCGA  | 3250 |
| CCCGCAGCGG  | CCTGTGGTCA  | CCGGGCAAGA | TCCGAATTGG  | TCCATAG     | 3297 |

## 2) INFORMATION FOR SEQ ID NO: 2106

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106

GCGAGCAGAG CACGCCCTCC TCGCCGCTCG C

31

## 2) INFORMATION FOR SEQ ID NO: 2107

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107

GCGAGCTCCC CATCTCTGGT TGGCACGCTC GC

32

## 2) INFORMATION FOR SEQ ID NO: 2108

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108

GCGGGCAACT TCRTCAAGAA GGTGTTTAC AACCCGCCCC C

41

## 2) INFORMATION FOR SEQ ID NO: 2109

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109

GCGGGCCCAA TCTCTGGTTG GAAYGGTGAC AAGCCCGC

38

2) INFORMATION FOR SEQ ID NO: 2110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110

GCGGGCCCTT AACGATTTC ACGAATCTGG ATTCAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111

GCGGGCATGA TTGAAGCCAC CACCAACGCT TCCTGGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112

GCGGGCTTGA TGAAGTTTTG GGTTTCCTTG ACAATTTGCC CGC

43

2) INFORMATION FOR SEQ ID NO: 2113

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113

GCGGGCACAA GGGTTGGACT AAGGAAACCA AGGCAGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2114

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114

GCGGGCATCG ATGCTATTGA ACCACCTGTC AGACCGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2115

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115

GCGGGCTTGA TGATTTCTC GAATCTAGAT TGGGCCCCG

39

2) INFORMATION FOR SEQ ID NO: 2116

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116

GCGGGCGGTA AGTCCACCGG TAAGACCTTG TTGGCCCCG

39